

FEATURES

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 VFQSSIFGAFFVYLVLLVAEMCMQVLMKSSKSLAGTRPOLKRSSEESRT
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 HEV"

BASE COUNT 516 a 766 c 677 g 567 t 2 others
 ORIGIN

Query Match 80.9%; Score 1310.4; DB 6; Length 2528;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1325; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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 QY 89 TGCCTCTCCCGAGTTCATTTGAAATTCAGAGGTGAAGTTCAGAGATGTCAGAAA 148
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 DB 1979 TGCATCAGCTGTGCAACACCCCTTTTGTAAAGGGCCAAAGGCCAAAGAAAGGGAGAT 1920
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 DB 1919 TCTGCTCTGGGCGCTCAGAGCGAGGGCTCCGACACCATCTGTTCTCTCAAAATTAAGCCCTC 1860
 QY 389 TTCTCGGCACACTGTGAGAGCTGAGAGATGACACCCCTCTGATGATGTTCTTCCACAG 448
 DB 1859 TTCTCGGCACACTGTGAGAGCTGAGAGATGACACCCCTCTGATGATGTTCTTCCACAG 1800
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 DB 1799 CCTGCGCCCAACCCCAACCTCCCTGAGTGAATTCCTGAGGTGTCCTTTATTTCTGG 1740
 QY 509 GTAGGAGGGGAGATGCGGCTCTCTTTGTTCTGCTGCAAAATTAAGAAAGCTCGGTA 568
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 QY 1349 GCCCTGGGCAAG 1360
 DB 900 GCCCTGGGCAAG 889

RESULT 7
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 DEFINITION Homo sapiens, clone IMAGE:4026092, mRNA.
 BC011449
 VERSION BC011449.1 GI:15277472
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 826)
 AUTHORS
 TITLE
 JOURNAL
 Submitted (25-JUL-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: gcaps-remail.nih.gov
 Tissue Procurement: ATCC/DCID/DNP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadnan@systemsbiology.org
 Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia

REMARK

COMMENT

RESULT 5
 AX362255 1524 bp DNA linear PAT 15-FEB-2002
 LOCUS Sequence 15 from Patent WO0208288.
 DEFINITION AX362255
 ACCESSION AX362255
 VERSION AX362255.1 GI:18694585
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1
 AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
 Matanabe, C.K., and Wood, W.I.
 TITLES Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0208288-A 15 31-JAN-2002;
 Genentech, Inc. (US)
 FEATURES
 source 1. 1524
 Location/Qualifiers
 BASE COUNT 321 a 433 c 435 g 335 t
 ORIGIN
 Query Match 84.8%; Score 1373; DB 6; Length 1524;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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 Db 1520 AGAGA 1524

RESULT 6
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 LOCUS AX319944
 DEFINITION Sequence 3 from Patent WO0181634.
 ACCESSION AX319944
 VERSION AX319944.1 GI:17901491
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1
 AUTHORS Galvin, K.A. and Rudolph-Owen, L.A.
 TITLES Methods and compositions for the diagnosis and treatment of
 cardiovascular and tumorigenic disease using 4941
 Patent: WO 0181634-A 3 01-NOV-2001;
 Millennium Pharmaceuticals, Inc. (US)

QY 1306 ATCTGGTGGGATCCAGCATATGAGCCATGTCACACATATCAGCCCTGGGACAGACA 1365
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 DB 119312 ACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGA 119312
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 LOCUS Sequence 15 from Patent WO0193983.
 DEFINITION AX358762
 ACCESSION AX358762
 VERSION AX358762.1 GI:18675282
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 1 Baker, K.P., Desnovers, L., Gerltsen, M.E., Goddard, A.,
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
 Wetanabe, C.K., and Wood, W.I.
 Secretd and transmembrane polypeptides and nucleic acids encoding
 the same
 Patent: WO 0193983-A 15 13-DEC-2001;
 Genentech Inc. (US)
 JOURNAL Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 321 a 433 c 435 g 335 t
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 Best Local Similarity 99.9% Pred. No. 0;
 Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

DB 441 CGGGCCAGAGCCCAAGAAAAAGGGAAGTTCTGCTCGGCCCTCAGGCCAGGCTCCGCAC 500
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 DB 1520 AGAGA 1524


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DB 1791 ACAGCTTCTTTTGGCCAGACAGAGAAATTAACACTGTTTCAACCCGGGAGTTG 1850
OY 1560 GCTGTGTTAAAGAACACATTAAATGCTTTAGACAGTGT 1599
DB 1851 GCTGTGTTAAAGAACACATTAAATGCTTTAGACAGTGT 1890

RESULT 3
AC079773/c 129676 bp DNA linear PRI 09-JAN-2002
LOCUS Homo sapiens BAC clone RP11-258B17 from 2, complete sequence.
AC079773
AC079773.8 GI:15145561
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 129676)
AUTHORS Sulston, J.E. and Waterston, R.
JOURNAL Toward a complete human genome sequence
MEDLINE Genome Res. 8 (11), 1097-1108 (1998)
PUBMED 99063792
9847074
REFERENCE 2 (bases 1 to 129676)
AUTHORS Shan, N., Meyer, R., Boyer, E. and Dignan, G.
TITLE The sequence of Homo sapiens BAC clone RP11-258B17
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 129676)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 129676)
REFERENCE 4 (bases 1 to 129676)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (09-AUG-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 129676)
REFERENCE 5 (bases 1 to 129676)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Aug 9, 2001 this sequence version replaced g1:14486388.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0258B17
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis

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FEATURES
source
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MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tatenoe, M., Catenease, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://pacpac.med.buffalo.edu>)

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1122; the clone sequenced to the right is RP11-159N20, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-258B17; actual end is at base position 60003 of RP11-159N20.

QY 1501 CAGCTTCTTTGCGCAGACAGAGAGATTTTAACTGTTTCAAAACCCGGGGAGATTGG 1560
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 Db 1794 CTGCTTAAAGAACCATTAATGCTTTAGACAGTGT 1832

RESULT 2
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 ACCESSION AX136281
 VERSION AX136281.1 GI:14272687
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
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 Mammalia; Eultheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1890)
 AUTHORS Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and
 Hayashi, K.
 TITLE Secretary protein or membrane protein
 JOURNAL Patent: EP 1067182-A 203 10-JAN-2001;
 Helix Research Institute (Jp)
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 location/Qualifiers
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 PHLPE"
 BASE COUNT 419 a 528 c 533 g 410 t
 ORIGIN

Query Match 95.7%; Score 1548.8; DB 6; Length 1890;
 Best Local Similarity 99.68; Pred. No. 0;
 Matches 1594; Conservative 0; Mismatches 2; Indels 4; Gaps 4;

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 Db 712 CCAACCCCTCTCGATGTTGTTCTTCACAGCCTCGCCCCCAACCCCACTCCCTGAGTGA 771
 QY 481 GTTCTCTGGGAGTCCCTTTTATTCGGGAGGAGCGGAGTCCGTTCTTTGTT 540
 Db 772 GTTCTCTGGGAGTCCCTTTTATTCGGGAGGAGCGGAGTCCGTTCTTTGTT 831
 QY 541 CCTGTCAATTAATGAAGAAGCTCGGTAAAGCATTCGTGAATAATTCACCTGACTGAAT 600
 Db 832 CCGTGCATAATTAATGAAGAAGCTCGGTAAAGCATTCGTGAATAATTCACCTGACTGAAT 891
 QY 601 TTTTCAGTACTTCTTAAGAGAAAGAGGTGAGTGAAGTTCAACCCCACTGTCTGTAAAC 660
 Db 892 TTTTCAGTACTTCTTAAGAGAAAGAGGTGAGTGAAGTTCAACCCCACTGTCTGTAAAC 951
 QY 661 CGGAGTCAAGGCGCAGGCTGGCAGAGTCAGTCCCTTAGAGTCACTGAGTGGGCACTCTGCC 720
 Db 952 CGGAGTCAAGGCGCAGGCTGGCAGAGTCAGTCCCTTAGAGTCACTGAGTGGGCACTCTGCC 1011
 QY 721 TTTTGTAAAGCCTCCAGTGTCCATTCCTGATGGGGGCAATGATTGAGACTGCAGA 780
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 QY 781 GTGAGGTAGCTTTTCTTAGAGGCTGGAGGCGCAGTCCCATCAAGAGCTCCCTGCTTG 840
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 Db 1192 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTTAAGTGGGCTGGGCT 1251
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 Db 1431 CAGGAACACCCGCGAAACTGCTGGAGAGACACGCTGTACAGAGAGCGGTTGATGACCGA 1490
 QY 1200 GCTGAGGTAGAAAACGCTCTCGAAGAAGGAGAGAGATCATACGCCCGGAATGAGA 1259
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AUTHORS	Krakaml,B., Sugiyama,A., Takemoto,M., Sugiyama,T., Iife,R., Otsuki,T., Saito,H., Nakatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Salto,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kitayuchi,H., Kanda,K., Megatsuna,M., MuraKawa,K., Kanehor,i,K., Takahashi -Fuji,I,A., Ohlma,A., Suzuki,Y., Sugano,S., Nagahari,K., Masuno,Y., Nagai,K. and Isogai,T.
TITLE	NEDO human cDNA sequencing project
JOURNAL REFERENCE	Unpublished 2 (bases 1 to 1832)
AUTHORS TITLE JOURNAL	Isogai,T. and Yamamoto,J. Direct Submission Submitted (04-JUL-2002) Tako Isozaki, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:jgenomise@rri.co.jp; Tel:-81-438-52-3975, Fax:-81-438-52-3986) NEDO Human CDNA Sequencing Project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB) ;(CDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center), National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB. Location/Qualifiers 1..1832 / organism="Homo sapiens" / db_xref="taxon:9606" / clone="BRALZ001350" / tissue_type="alzheimer cortex" / clone_1lb="BRALZ2" / note="cloning vector : pMEI8SFL3" 215..640 / note="unnamed protein product" / codon_start=1 / protein_id="BACQ4368.1" / db_xref="GI:21753576" / translation="MAYLGIAITRCGLFPLGFAIDTQCVCCEPOLINDCCSPRETY NCTYANVDMCKEKVEWDSAGIMTKRSCHSSAACILASNGISFCSPKLMSVCSICSN TPLCNGPRPKRRGSASSALRLPGRDTTLLEFKLAFSAHC"
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:51:07 ; Search time 4118.22 Seconds

(without alignments)
11441.218 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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11	497.6	30.7	1362	6	AX319942
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14	474.6	25.5	587	6	AX136698
15	413.4	22.6	444	6	AX150120
16	365.4	22.4	366	6	AX093381
17	362	22.4	396	6	AX093191
18	285	17.6	591	6	AX136556
19	218.8	13.5	190503	2	AC128363
20	145	9.0	147131	9	AC010974
21	121.2	7.5	190503	2	AC128363
22	80.2	5.0	136799	2	AC110334
23	54.8	3.4	125020	9	AF429315
24	54.2	3.3	3917	10	AB017027
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27	52.4	3.2	4131	9	HSNEUR4
28	50.4	3.1	7218	6	E6494
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30	50	3.1	1140	6	E63120
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ALIGNMENTS

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VERSION AK094501.1 GI:21753575
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens alzheimer cortex cDNA to mRNA, clone_11b:BRAZ2
ORGANISM Homo sapiens
REFERENCE 1
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Pred. No. is the number of results predicted by chance to have a

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APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC30
CURRENT APPLICATION NUMBER: US/10/172,039A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
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PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
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PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
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SEQ ID NO 156
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TYPE: DNA
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Db 2655 TGTAAAAA 2677
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Sequence 156, Application US/10145016A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
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APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC32
CURRENT APPLICATION NUMBER: US/10/145,016A
CURRENT FILING DATE: 2001-10-18
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PRIOR APPLICATION NUMBER: 60/065311
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Remaining Prior Application data removed - See File Wrapper or PALM.
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Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: November 8, 2002, 02:03:49
Job time : 106.231 secs
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: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James;
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P26301C40
: CURRENT APPLICATION NUMBER: US/10/165,353
: PRIOR FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/064249
: PRIOR FILING DATE: 1997-11-03
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
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: PRIOR APPLICATION NUMBER: 60/077450
: PRIOR FILING DATE: 1998-03-10
: PRIOR APPLICATION NUMBER: 60/077632
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077641
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077649
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077791
: PRIOR FILING DATE: 1998-03-12
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 624
: SEQ ID NO 156
: LENGTH: 2680
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-165-353-156

```

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Query Match          1.4% Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1597 TGTAAAAAAAAAAAAAAAAAAAAA 1619
    |||||||||||||||||||
DB 2655 TGTAAAAAAAAAAAAAAAAAAAAA 2677

```

```

RESULT 43
US-10-170-481A-156
: Sequence 156, Application US/10170481A
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kljavin, Ivar J.

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: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James;
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P26301C53
: CURRENT APPLICATION NUMBER: US/10/170,481A
: PRIOR FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/064249
: PRIOR FILING DATE: 1997-11-03
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066364
: PRIOR FILING DATE: 1997-11-21
: PRIOR APPLICATION NUMBER: 60/077450
: PRIOR FILING DATE: 1998-03-10
: PRIOR APPLICATION NUMBER: 60/077632
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077641
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077649
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077791
: PRIOR FILING DATE: 1998-03-12
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 624
: SEQ ID NO 156
: LENGTH: 2680
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-170-481A-156

```

```

Query Match          1.4% Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1597 TGTAAAAAAAAAAAAAAAAAAAAA 1619
    |||||||||||||||||||
DB 2655 TGTAAAAAAAAAAAAAAAAAAAAA 2677

```

```

RESULT 44
US-10-172-039A-156
: Sequence 156, Application US/10172039A
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kljavin, Ivar J.

```

```
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James:
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC56
CURRENT APPLICATION NUMBER: US/10/162,522A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 156
LENGTH: 2680
TYPE: DNA
ORGANISM: Homo sapiens
US-10-162-522A-156
```

```
Query Match 1.4% Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 2655 TGTAAAAAAAAAAAAAAAAAAAA 2677
```

```
RESULT 41
US-10-165-038A-156
Sequence 156, Application US/10165038A
```

```
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
```

```
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James:
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC29
CURRENT APPLICATION NUMBER: US/10/165,038A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 156
LENGTH: 2680
TYPE: DNA
ORGANISM: Homo sapiens
US-10-165-038A-156
```

```
Query Match 1.4% Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 2655 TGTAAAAAAAAAAAAAAAAAAAA 2677
```

```
RESULT 42
US-10-165-353-156
Sequence 156, Application US/10165353
```

```
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
```

```
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC39
CURRENT APPLICATION NUMBER: US/10/143.031A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remainig Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 156
LENGTH: 2680
TYPE: DNA
ORGANISM: Homo sapiens
US-10-143-031A-156
```

```
Query Match 1.4%: Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1597 TGTAAAAA 1619
DB 2655 TGTAAAAA 2677
```

```
RESULT 39
US-10-145-092A-156
Sequence 156, Application US/10145092A
GENERAL INFORMATION:
```

```
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
```

```
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC45
CURRENT APPLICATION NUMBER: US/10/145.092A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remainig Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 156
LENGTH: 2680
TYPE: DNA
ORGANISM: Homo sapiens
US-10-145-092A-156
```

```
Query Match 1.4%: Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1597 TGTAAAAA 1619
DB 2655 TGTAAAAA 2677
```

```
RESULT 40
US-10-162-522A-156
Sequence 156, Application US/10162522A
GENERAL INFORMATION:
```

```
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
```

APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C79
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
REMAINING PRIOR APPLICATION data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 227
LENGTH: 2136
TYPE: DNA
ORGANISM: Homo Sapien
US-10-125-923A-227

Query Match 1.4%; Score 23; DB 6; Length 2136;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA 1619
Db 2061 TGTAAAAA 2083

RESULT 37
US-10-145-087A-156
Sequence 156, Application US/10145087A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.

APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C47
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
REMAINING PRIOR APPLICATION data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 156
LENGTH: 2680
TYPE: DNA
ORGANISM: Homo sapiens
US-10-145-087A-156

Query Match 1.4%; Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA 1619
Db 2655 TGTAAAAA 2677

RESULT 38
US-10-143-031A-156
Sequence 156, Application US/10143031A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.

US-10-145-129A-136

Query Match 1.4%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.058;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA 1619

DB 1974 TGTAAAAA 1996

RESULT 34
US-10-125-923A-53

Sequence 53, Application US/10125923A

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3430R1C79

CURRENT APPLICATION NUMBER: US/10/125, 923A

PRIOR FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: 10/052586

PRIOR FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059266

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063120

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063121

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063486

PRIOR FILING DATE: 1997-10-21

PRIOR APPLICATION NUMBER: 60/063540

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063541

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063544

PRIOR FILING DATE: 1997-10-28

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 53

LENGTH: 1998

TYPE: DNA

ORGANISM: Homo Sapien

US-10-125-923A-53

Query Match 1.4%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA 1619

DB 1974 TGTAAAAA 1996

RESULT 35

US-10-165-353A-136

Sequence 136, Application US/10165353A

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Flivarov, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630P1C40

CURRENT APPLICATION NUMBER: US/10/165, 353A

PRIOR FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791

PRIOR FILING DATE: 1998-03-12

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 624

SEQ ID NO 136

LENGTH: 1998

TYPE: DNA

ORGANISM: Homo sapiens

US-10-165-353A-136

Query Match 1.4%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA 1619

DB 1974 TGTAAAAA 1996

RESULT 36

US-10-125-923A-227

Sequence 227, Application US/10125923A

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

US-10-170-481A-136

Query Match 1.4%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
|||||
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 30

US-10-172-039A-136

; Sequence 136, Application US/10172039A

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C30
; CURRENT APPLICATION NUMBER: US/10/172.039A
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 136
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-172-039A-136

Query Match 1.4%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
|||||
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 31

US-10-145-016A-136

; Sequence 136, Application US/10145016A

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C52
; CURRENT APPLICATION NUMBER: US/10/145.016A
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 136
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-165-038A-136

Query Match	1.4%;	Score 23;	DB 6;	Length 1998;
Best Local Similarity	100.0%;	Pred. No. 0.058;		
Matches 23;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0

QY	1597	TGTAATAAAAAAAAAAAAAA	1619
Db	1974	TGTAAAAAAAAAAAAAAAAA	1996

RESULT 28
US-10-165-353-136

```

1 GENERAL INFORMATION:
2 APPLICANT: Ashkenazi, Avi
3 APPLICANT: Baker Kevin P.
4 APPLICANT: Botstein, David
5 APPLICANT: Desnovers, Luc
6 APPLICANT: Eaton, Dan
7 APPLICANT: Ferrara, Napoleon
8 APPLICANT: Flivarovf, Ellen
9 APPLICANT: Fong, Sherman
10 APPLICANT: Gao, Wei-Qiang
11 APPLICANT: Gerber, Hanspeter
12 APPLICANT: Gerlitsen, Mary E.
13 APPLICANT: Goddard, Audrey
14 APPLICANT: Godowski, Paul J.
15 APPLICANT: Grimaldi, J. Christopher
16 APPLICANT: Gunney, Austin L.
17 APPLICANT: Hillan, Kenneth J.
18 APPLICANT: Kljavin, Ivar J.
19 APPLICANT: Kuo, Sophia S.
20 APPLICANT: Napier, Mary A.
21 APPLICANT: Pan, James;
22 APPLICANT: Paonl, Nicholas F.
23 APPLICANT: Roy, Margaret Ann
24 APPLICANT: Shelton, David L.
25 APPLICANT: Stewart, Timothy A.
26 APPLICANT: Tumas, Daniel
27 APPLICANT: Williams, P. Mickey
28 APPLICANT: Wood, William I.
29 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
30 FILE OF INVENTION: Acids Encoding the Same
31 FILE REFERENCE: P2630PIC40
32 CURRENT APPLICATION NUMBER: US/10/165,353
33 CURRENT FILING DATE: 2002-10-10
34 CURRENT APPLICATION NUMBER: 09/918585
35 PRIOR FILING DATE: 2001-07-30
36 PRIOR APPLICATION NUMBER: 60/062250
37 PRIOR FILING DATE: 1997-10-17
38 PRIOR APPLICATION NUMBER: 60/064249
39 PRIOR FILING DATE: 1997-11-03
40 PRIOR APPLICATION NUMBER: 60/065311
41 PRIOR FILING DATE: 1997-11-13
42 PRIOR APPLICATION NUMBER: 60/066364
43 PRIOR FILING DATE: 1997-11-21
44 PRIOR APPLICATION NUMBER: 60/077450
45 PRIOR FILING DATE: 1998-03-10
46 PRIOR APPLICATION NUMBER: 60/077632
47 PRIOR FILING DATE: 1998-03-11
48 PRIOR APPLICATION NUMBER: 60/077641
49 PRIOR FILING DATE: 1998-03-11
50 PRIOR APPLICATION NUMBER: 60/077649
51 PRIOR FILING DATE: 1998-03-11
52 PRIOR APPLICATION NUMBER: 60/077791
53 Remaining Prior Application data removed - See file wrapper or PALM.
54 NUMBER OF SEQ ID NOS: 624
55 SEQ ID NO 136
56 LENGTH: 1998
57 TYPE: DNA
58 ORGANISM: Homo sapiens

```

US-10-165-353-136

Query Match	1.4%	Score 23;	DB 6;	Length 1998;
Best Local Similarity	100.0%	Pred. No.	0.058;	
Matches	23;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY	1597	TGTAAAAAAAAAAAAAAAAA	1619
Db	1974	TGTAAAAAAAAAAAAAAAAA	1996

RESULT 29
US-10-170-481A-136
; Sequence 136, Application US/10170481A

APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnovers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kjaevlin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2630PIC53
 CURRENT APPLICATION NUMBER: US/10/170,481A
 CURRENT FILING DATE: 2002-10-10
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/077632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077641
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077649
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077791
 PRIOR FILING DATE: 1998-03-12
 Remaining Prior Application data removed - See file Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 624
 SEQ ID NO 136
 LENGTH: 1998
 TYPE: DNA
 ORGANISM: Homo sapiens

US-10-145-092A-136

Query Match 1.4%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.058;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
|||||
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 26

US-10-162-522A-136

Sequence 136, Application US/10162522A

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630P1C56

CURRENT APPLICATION NUMBER: US/10/162,522A

PRIOR FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/074450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791

PRIOR FILING DATE: 1998-03-12

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 624

SEQ ID NO 136

LENGTH: 1998

TYPE: DNA

ORGANISM: Homo sapiens

US-10-162-522A-136

Query Match 1.4%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.058;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
|||||
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 27

US-10-165-038A-136

Sequence 136, Application US/10165038A

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630P1C29

CURRENT APPLICATION NUMBER: US/10/165,038A

PRIOR FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/074450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791

PRIOR FILING DATE: 1998-03-12

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 624

SEQ ID NO 136

LENGTH: 1998

TYPE: DNA

ORGANISM: Homo sapiens

US-10-145-087A-136

Query Match 1.4%; Score 23; DB 6; Length 1998;

Best Local Similarity 100.0%; Pred. No. 0.058;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA 1619

DB 1974 TGTAAAAA 1996

RESULT 24

US-10-143-031A-136

Sequence 136, Application US/10143031A

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC39
CURRENT APPLICATION NUMBER: US/10/143,031A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 136
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens

US-10-143-031A-136

Query Match 1.4%; Score 23; DB 6; Length 1998;

Best Local Similarity 100.0%; Pred. No. 0.058;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA 1619

DB 1974 TGTAAAAA 1996

RESULT 25

US-10-145-092A-136

Sequence 136, Application US/10145092A

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC45
CURRENT APPLICATION NUMBER: US/10/145,092A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 136
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens

```

; FILE REFERENCE: PA131PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 457
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-264-237-457

Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 1689;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 1654 TGTAAAAAAAAAAAAAAAAAAAA 1676

RESULT 21
; Sequence 19, Application US/10260046
; GENERAL INFORMATION:
; APPLICANT: Dhuga, Kanwarpal S.
; TITLE OF INVENTION: Manipulation of Plant Polysaccharide
; FILE REFERENCE: 1296
; CURRENT APPLICATION NUMBER: US/10/260,046
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/325,614
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Zea mays
; US-10-260-046-19

Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 1740;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 1711 TGTAAAAAAAAAAAAAAAAAAAA 1733

RESULT 22
; Sequence 890, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 890
; LENGTH: 1765
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```

US-10-264-237-890

Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 1765;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 1739 TGTAAAAAAAAAAAAAAAAAAAA 1761

RESULT 23
; Sequence 136, Application US/10145087A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C47
; CURRENT APPLICATION NUMBER: US/10/145,087A
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 136
; LENGTH: 136
; TYPE: DNA
; ORGANISM: Homo sapiens
```


FEATURE:
NAME/KEY: misc.feature
LOCATION: (1078)..(1078)
OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-563

Query Match 1.4%; Score 23; DB 6; Length 1092;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
|||||
Db 1037 TGTAAAAAAAAAAAAAAAAAAAA 1059

RESULT 16
US-10-264-237-40/c
Sequence 40, Application US/10264237
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 40
LENGTH: 1326
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (912)..(912)
OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-40

Query Match 1.4%; Score 23; DB 6; Length 1326;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
|||||
Db 54 TGTAAAAAAAAAAAAAAAAAAAA 32

RESULT 17
US-10-264-237-995
Sequence 995, Application US/10264237
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 995
LENGTH: 1539
TYPE: DNA
ORGANISM: Homo sapiens
US-10-264-237-995

Query Match 1.4%; Score 23; DB 6; Length 1539;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
|||||
Db 1509 TGTAAAAAAAAAAAAAAAAAAAA 1531

RESULT 18
US-10-264-237-1007
Sequence 1007, Application US/10264237
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1007
LENGTH: 1571
TYPE: DNA
ORGANISM: Homo sapiens
US-10-264-237-1007

Query Match 1.4%; Score 23; DB 6; Length 1571;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
|||||
Db 1539 TGTAAAAAAAAAAAAAAAAAAAA 1561

RESULT 19
US-09-602-472A-1
Sequence 1, Application US/09602472A
GENERAL INFORMATION:
APPLICANT: Bidney, Dennis L.
APPLICANT: Hu, Xu
TITLE OF INVENTION: Sunflower Disease Resistance Genes
FILE REFERENCE: 35718/200630
CURRENT APPLICATION NUMBER: US/09/602,472A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/140,876
PRIOR FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1593
TYPE: DNA
ORGANISM: Helianthus annuus
US-09-602-472A-1

Query Match 1.4%; Score 23; DB 5; Length 1593;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
|||||
Db 1571 TGTAAAAAAAAAAAAAAAAAAAA 1593

RESULT 20
US-10-264-237-457
Sequence 457, Application US/10264237
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

```
;; APPLICANT: Birse et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PA131P1
;; CURRENT APPLICATION NUMBER: US/10/264,237
;; CURRENT FILING DATE: 2002-10-04
;; PRIOR APPLICATION NUMBER: PCT/US01/16450
;; PRIOR FILING DATE: 2001-05-18
;; PRIOR APPLICATION NUMBER: US 60/205,515
;; PRIOR FILING DATE: 2000-05-19
;; NUMBER OF SEQ ID NOS: 2876
;; SOFTWARE: PatentIn Ver. 3.1
;; SEQ ID NO: 114
;; LENGTH: 574
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-264-237-114
```

```
Query Match
Best Local Similarity 1.4%; Score 23; DB 6; Length 574;
Pred. No. 0.061;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
DB 551 TGTAAAAAAAAAAAAAAAAAAAA 573
```

```
RESULT 12
US-10-264-237-1055
;; Sequence 1055, Application US/10264237
;; GENERAL INFORMATION:
;; APPLICANT: Birse et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PA131P1
;; CURRENT APPLICATION NUMBER: US/10/264,237
;; CURRENT FILING DATE: 2002-10-04
;; PRIOR APPLICATION NUMBER: PCT/US01/16450
;; PRIOR FILING DATE: 2001-05-18
;; PRIOR APPLICATION NUMBER: US 60/205,515
;; PRIOR FILING DATE: 2000-05-19
;; NUMBER OF SEQ ID NOS: 2876
;; SOFTWARE: PatentIn Ver. 3.1
;; SEQ ID NO: 1055
;; LENGTH: 785
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (74)..(74)
;; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1055
```

```
Query Match
Best Local Similarity 1.4%; Score 23; DB 6; Length 785;
Pred. No. 0.06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
DB 734 TGTAAAAAAAAAAAAAAAAAAAA 756
```

```
RESULT 13
US-10-264-237-687
;; Sequence 687, Application US/10264237
;; GENERAL INFORMATION:
;; APPLICANT: Birse et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PA131P1
;; CURRENT APPLICATION NUMBER: US/10/264,237
;; CURRENT FILING DATE: 2002-10-04
;; PRIOR APPLICATION NUMBER: PCT/US01/16450
;; PRIOR FILING DATE: 2001-05-18
;; PRIOR APPLICATION NUMBER: US 60/205,515
;; PRIOR FILING DATE: 2000-05-19
```

```
;; NUMBER OF SEQ ID NOS: 2876
;; SOFTWARE: PatentIn Ver. 3.1
;; SEQ ID NO: 687
;; LENGTH: 1001
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-264-237-687
```

```
Query Match
Best Local Similarity 1.4%; Score 23; DB 6; Length 1001;
Pred. No. 0.06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
DB 974 TGTAAAAAAAAAAAAAAAAAAAA 996
```

```
RESULT 14
PCT-US02-33408-5/C
;; Sequence 5, Application PC/TUS0233408
;; GENERAL INFORMATION:
;; APPLICANT: RIKEN
;; APPLICANT: HAYASHI, Yasunori
;; TITLE OF INVENTION: NR3B Receptor Subunit Compositions and Related Methods
;; FILE REFERENCE: M00656, 70068, MO
;; CURRENT APPLICATION NUMBER: PCT/US02/33408
;; CURRENT FILING DATE: 2002-10-18
;; PRIOR APPLICATION NUMBER: US 60/344,545
;; PRIOR FILING DATE: 1999-10-19
;; NUMBER OF SEQ ID NOS: 23
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO: 5
;; LENGTH: 1040
;; TYPE: DNA
;; ORGANISM: Rattus norvegicus
PCT-US02-33408-5
```

```
Query Match
Best Local Similarity 1.4%; Score 23; DB 1; Length 1040;
Pred. No. 0.06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
DB 42 TGTAAAAAAAAAAAAAAAAAAAA 20
```

```
RESULT 15
US-10-264-237-563
;; Sequence 563, Application US/10264237
;; GENERAL INFORMATION:
;; APPLICANT: Birse et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PA131P1
;; CURRENT APPLICATION NUMBER: US/10/264,237
;; CURRENT FILING DATE: 2002-10-04
;; PRIOR APPLICATION NUMBER: PCT/US01/16450
;; PRIOR FILING DATE: 2001-05-18
;; PRIOR APPLICATION NUMBER: US 60/205,515
;; PRIOR FILING DATE: 2000-05-19
;; NUMBER OF SEQ ID NOS: 2876
;; SOFTWARE: PatentIn Ver. 3.1
;; SEQ ID NO: 563
;; LENGTH: 1092
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (57)..(57)
;; OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (227)..(227)
OTHER INFORMATION: n equals a,t,g, or c
```

```

US-10-266-131-1361/c
; Sequence 1361, Application US/10266131
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Murine Polynucleotide Tags and
; FILE REFERENCE: LEX-0030-USA
; CURRENT APPLICATION NUMBER: US/10/266,131
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/09/611,675
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/143,878
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 2908
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1361
; LENGTH: 286
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(286)
; OTHER INFORMATION: n = A,T,C or G
US-10-266-131-1361

```

```

Query Match          1.4%; Score 23; DB 6; Length 286;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1597 TGTAAAAA...1619
DB 24 TGTAAAAA...2

```

```

RESULT 8
US-09-907-907A-31
; Sequence 31, Application US/09907907A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Leszczyniecka, Magdalena
; TITLE OF INVENTION: GENES DISPLAYING ENHANCED EXPRESSION DURING CELLULAR SENESENCE A
; FILE REFERENCE: A34584-A-PCT-USA (070050,1664)
; CURRENT APPLICATION NUMBER: US/09/907,907A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: US 09/243,277
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-907A-31

```

```

Query Match          1.4%; Score 23; DB 5; Length 315;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1597 TGTAAAAA...1619
DB 290 TGTAAAAA...312

```

```

RESULT 9
US-10-240-425-758/c
; Sequence 758, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.

```

```

; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 758
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AF1675419
US-10-240-425-758

```

```

Query Match          1.4%; Score 23; DB 6; Length 504;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1597 TGTAAAAA...1619
DB 23 TGTAAAAA...1

```

```

RESULT 10
US-10-240-425-525/c
; Sequence 525, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 525
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AF162104
US-10-240-425-525

```

```

Query Match          1.4%; Score 23; DB 6; Length 523;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1597 TGTAAAAA...1619
DB 52 TGTAAAAA...30

```

```

RESULT 11
US-10-264-237-114
; Sequence 114, Application US/10264237
; GENERAL INFORMATION:

```

US-10-125-923A-215

Query Match

1.5%; Score 24; DB 6; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAAGAAAAAAGAAAAA 1619

DB 1298 GTGTAAGAAAAAAGAAAAA 1321

RESULT 3

US-10-266-829-15

Sequence 15, Application US/10266829
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 29 Human secreted proteins
FILE REFERENCE: P2041P1
CURRENT APPLICATION NUMBER: US/10/266,829
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 09/756,168
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: PCT/US00/19735
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: 60/145,220
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 2057
TYPE: DNA
ORGANISM: Homo sapiens
US-10-266-829-15

Query Match

1.5%; Score 24; DB 6; Length 2057;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAAGAAAAAAGAAAAA 1619

DB 1907 GTGTAAGAAAAAAGAAAAA 1930

RESULT 4

US-10-240-425-1530/C

Sequence 1530, Application US/10240425
GENERAL INFORMATION:
APPLICANT: Williams, Amanda
APPLICANT: Bolland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Wetzel, Jon C.
APPLICANT: Scheff, Dwe
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REFERENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
PRIOR FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/193,446
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1530
LENGTH: 2305
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. X06374
US-10-240-425-1530

Query Match

1.5%; Score 24; DB 6; Length 2305;

Best Local Similarity 100.0%; Pred. No. 0.019;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAAGAAAAAAGAAAAA 1619

DB 1626 GTGTAAGAAAAAAGAAAAA 1603

RESULT 5

US-09-513-999C-20982

Sequence 20982, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclerc, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59,US2 REG
CURRENT APPLICATION NUMBER: US/09/513,999C
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 20982
LENGTH: 102
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-20982

Query Match

1.4%; Score 23; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAGAAAAAAGAAAAA 1619

DB 73 TGTAAAGAAAAAAGAAAAA 95

RESULT 6

US-09-907-907A-23

Sequence 23, Application US/09907907A
GENERAL INFORMATION:
APPLICANT: Fisher, Paul B.
APPLICANT: Leszyniecka, Magdalena
TITLE OF INVENTION: GENES DISPLAYING ENHANCED EXPRESSION DURING CELLULAR SENESENC
FILE REFERENCE: A34584-A-PCT-USA (070050,1664)
CURRENT APPLICATION NUMBER: US/09/907,907A
PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: US 09/243,277
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 198
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: unsure
FEATURE:
LOCATION: 21
OTHER INFORMATION: a or c or g or t
US-09-907-907A-23

Query Match

1.4%; Score 23; DB 5; Length 198;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAGAAAAAAGAAAAA 1619

DB 160 TGTAAAGAAAAAAGAAAAA 182

RESULT 7

Best Local Similarity 99.98; Pred. No. 0;
Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGCACCTTTTGGCGATGTTCTTCTTCAGAGCTTGGCGTGGCAATTCAGTGTACCA 60
DB 141 GGCACCTTTTGGCGATGTTCTTCTTCAGAGCTTGGCGTGGCAATTCAGTGTACCA 200

QY 61 GTGTGAAGAATTCAGTGTGAACACAGACTGCTCTCCCGAGTTCAATTGTGAATTCAC 120
DB 201 GTGTGAAGAATTCAGTGTGAACACAGACTGCTCTCCCGAGTTCAATTGTGAATTCAC 260

QY 121 GGTGAACCTTCAAGACATGTGTCAAGAAAGTGTGAGCAAAATGCGCGGATCATGTA 180
DB 261 GGTGAACCTTCAAGACATGTGTCAAGAAAGTGTGAGCAAAATGCGCGGATCATGTA 320

QY 181 CGCAGATCTCTGTGATCATCAGCGGCTGTCTCATCGCCCTCTCGCGGATACAGTCTCT 240
DB 321 CGCAGATCTCTGTGATCATCAGCGGCTGTCTCATCGCCCTCTCGCGGATACAGTCTCT 380

QY 241 CTGTCTCCCGAGGAACTGAACTCAGTTTGCATCAGCTGCTGTCACACCCCTCTTTGTA 300
DB 381 CTGTCTCCCGAGGAACTGAACTCAGTTTGCATCAGCTGCTGTCACACCCCTCTTTGTA 440

QY 301 CGGGCCAGGCGCCAGAAAGGGGAGTCTGCTCGGCGCTCAAGGCGAGGCTCCGAC 360
DB 441 CGGGCCAGGCGCCAGAAAGGGGAGTCTGCTCGGCGCTCAAGGCGAGGCTCCGAC 500

QY 361 CACCATCTGTCTCTCAAAATTAAGCCCTCTTCTGCGCACATGCTGAGCTGAAGAGATG 420
DB 501 CACCATCTGTCTCTCAAAATTAAGCCCTCTTCTGCGCACATGCTGAGCTGAAGAGATG 560

QY 421 CCACCCCTCTCTGATGTTCTTCCAGCCCTGCGCCCAACCCCTCACTCCCTGAGTGA 480
DB 561 CCACCCCTCTCTGATGTTCTTCCAGCCCTGCGCCCAACCCCTCACTCCCTGAGTGA 620

QY 481 GTTCTCTCTGCTGTCTTTTATCTGCGTGAAGAGCGGAGTCCGTCTCTTTTGT 540
DB 621 GTTCTCTCTGCTGTCTTTTATCTGCGTGAAGAGCGGAGTCCGTCTCTTTTGT 680

QY 541 CCTGTGAATTAATGAAGAGCTGCTGTAAGAGCTTCTGAATTAATTAATTAATTAAT 600
DB 681 CCTGTGAATTAATGAAGAGCTGCTGTAAGAGCTTCTGAATTAATTAATTAATTAAT 740

QY 601 TTTCAGATGATCTTGAAGAGAGAGTGAAGTGAAGTTCACCCCACTGCTGTGTAA 660
DB 741 TTTCAGATGATCTTGAAGAGAGAGTGAAGTGAAGTTCACCCCACTGCTGTGTAA 800

QY 661 CGGAGTCAGGCGCAGGCTGCGAGATGCTTGAAGTCACTGAGTGGCATCTGCC 720
DB 801 CGGAGTCAGGCGCAGGCTGCGAGATGCTTGAAGTCACTGAGTGGCATCTGCC 860

QY 721 TTTTGTAAAGCTTCCATGTCATTCATCCGATGAGGAGGCACTATTGAGACTGAC 780
DB 861 TTTTGTAAAGCTTCCATGTCATTCATCCGATGAGGAGGCACTATTGAGACTGAC 920

QY 781 GTGAGAGTGAAGTCTTCTAGGCTGAGGCGCAAGTTCACACTCAAGGCTCCCTGCTTG 840
DB 921 GTGAGAGTGAAGTCTTCTAGGCTGAGGCGCAAGTTCACACTCAAGGCTCCCTGCTTG 980

QY 841 ACATTCAAACTTCACTGCTCTGAAAACCAATTCCTGAGAGAAATGGCTGGTTGGCCG 900
DB 981 ACATTCAAACTTCACTGCTCTGAAAACCAATTCCTGAGAGAAATGGCTGGTTGGCCG 1040

QY 901 CTGAGTGGGCTTATGACTCGAGACTCAATGACTGGAGTCTAGACTGGGCTCGGCT 960
DB 1041 CTGAGTGGGCTTATGACTCGAGACTCAATGACTGGAGTCTAGACTGGGCTCGGCT 1100

QY 961 CGCTCTGAAGAGCTTAAAGAAATCTTCTCAGTCTCTTCTGAGAGAGACTGGCGCGG 1020
DB 1101 CGCTCTGAAGAGCTTAAAGAAATCTTCTCAGTCTCTTCTGAGAGAGACTGGCGCGG 1160

QY 1021 ACGGAAAGAGAGCGGCGCTGCAAAAGCGGCGCTGAGGAGTGAATGGCATGTA 1080
DB 1161 ACGGAAAGAGAGCGGCGCTGCAAAAGCGGCGCTGAGGAGTGAATGGCATGTA 1220

DB 1161 ACGGAAAGAGAGCGGCGCTGCAAAAGCGGCGCTGAGGAGTGAATGGCATGTA 1220
QY 1081 CGCGAGGCGCTTCTCTGAGTGGCGTGTGACAGAGCGGCGAGACAGACCTTGC 1140
DB 1221 CGCGAGGCGCTTCTCTGAGTGGCGTGTGACAGAGCGGCGAGACAGACCTTGC 1279
QY 1141 ACGAGACCGCGGCAATGCTGCGAGAGACACCTGTATAGAGAGCGGCTTGTATGACCGAG 1200
DB 1280 ACGAGACCGCGGCAATGCTGCGAGAGACACCTGTATAGAGAGCGGCTTGTATGACCGAG 1339
QY 1201 CTGAGTGAAGAAACCTCTCCGAGAGAGGAGAGATCATGTACGCCCGAATGAGAC 1260
DB 1340 CTGAGTGAAGAAACCTCTCCGAGAGAGGAGAGATCATGTACGCCCGAATGAGAG 1399
QY 1261 CTGTCACAGTCTGCTGAGTGGGTTTGGCCGACCATGATCTCCGAATCTGTTGGCATC 1320
DB 1400 CTGTCACAGTCTGCTGAGTGGGTTTGGCCGACCATGATCTCCGAATCTGTTGGCATC 1459
QY 1321 CAGCATACGCGCAATGTCAACAATCAGCCCTGGGCGAGACAGAGAGAGAGAGAC 1380
DB 1460 CAGCATACGCGCAATGTCAACAATCAGCCCTGGGCGAGACAGAGAGAGAGAGAC 1519
QY 1381 AGAGA 1385
DB 1520 AGAGA 1524

RESULT 2
US-10-125-923A-215
Sequence 215, Application US/10125923A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C79
CURRENT APPLICATION NUMBER: US/10/125,923A
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 215
LENGTH: 1337
TYPE: DNA
ORGANISM: Homo Sapien

326

TYPE: DNA
ORGANISM: Homo Sapien
US-10-218-631-15

Query Match 78.1% Score 1264; DB 42; Length 1524;
Best Local Similarity 99.9% Pred. No. 9,6e-234;
Matches 184; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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OY 1 GGCACATTTTTCGAGATGTTCTTCCAGGCTTTGGCTGCAAAATCCAGTGTACCA 60
DB 141 GGCACATTTTTCGAGATGTTCTTCCAGGCTTTGGCTGCAAAATCCAGTGTACCA 200
OY 61 GTGTGAAGATTCACAGTGAACAGACTGTCCTCCCGGATTCATTGTGAATGGAC 120
DB 201 GTGTGAAGATTCACAGTGAACAGACTGTCCTCCCGGATTCATTGTGAATGGAC 260
OY 121 GGTGAAGCTTCAAGCATGTGTCAAGAAAGATGTGAAGCAAAATGCCGGATATGTA 180
DB 261 GGTGAAGCTTCAAGCATGTGTCAAGAAAGATGTGAAGCAAAATGCCGGATATGTA 320
OY 181 CGCAGATCTGTGATCATCAGCGGCTGTCTATCGCTTGGCGGATACAGTCTT 240
DB 321 CGCAGATCTGTGATCATCAGCGGCTGTCTATCGCTTGGCGGATACAGTCTT 380
OY 241 CTGTCTCCAGGAAAGTGAATCACTGATTCATGCTGTGCAACACCCCTTTGTAA 300
DB 381 CTGTCTCCAGGAAAGTGAATCACTGATTCATGCTGTGCAACACCCCTTTGTAA 440
OY 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCTGCGCCCTCCAGGCCCAAGGCTCCGAC 360
DB 441 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCTGCGCCCTCCAGGCCCAAGGCTCCGAC 500
OY 361 CACCATCTCTTCTCAAAATAGCCCTCTTCGCGACACTGTGAACCTGAAGAGATG 420
DB 501 CACCATCTCTTCTCAAAATAGCCCTCTTCGCGACACTGTGAACCTGAAGAGATG 560
OY 421 CCAGCCCTCTCTGCAATGTTCTTCCAGCCCTGCCCAACCCCAACCTCTGAGTGA 480
DB 561 CCAGCCCTCTCTGCAATGTTCTTCCAGCCCTGCCCAACCCCAACCTCTGAGTGA 620
OY 481 GTTCTCTGAGGTCTCTTATCTGAGTGAAGGAGGAGTCTGCTTTTGT 540
DB 621 GTTCTCTGAGGTCTCTTATCTGAGTGAAGGAGGAGTCTGCTTTTGT 680
OY 541 CCTGTCAAAATGAAGAGAGCTCGTAAAGCATCTGAATAAATTCAGCTGAGTGAAT 600
DB 681 CCTGTCAAAATGAAGAGAGCTCGTAAAGCATCTGAATAAATTCAGCTGAGTGAAT 740
OY 601 TTTCAGTATGTAAGTGAAGAGAGGAGTGAAGTGAATCAACCCCAATGCTGTGAAC 660
DB 741 TTTCAGTATGTAAGTGAAGAGAGGAGTGAAGTGAATCAACCCCAATGCTGTGAAC 800
OY 661 CGGAGTCAAGGCGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 720
DB 801 CGGAGTCAAGGCGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 860
OY 721 TTTCGTAAGGCTCCAGTGTCCATTCCTGATGAGGAGTGAAGTGAAGTGAAGTGAAG 780
DB 861 TTTCGTAAGGCTCCAGTGTCCATTCCTGATGAGGAGTGAAGTGAAGTGAAGTGAAG 920
OY 781 GTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
DB 921 GTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 980
OY 841 ACATTCAAACTTCATGCTCTGAAAAACATCTCTGAGCAGAAATGAGTGTGCGGC 900
DB 981 ACATTCAAACTTCATGCTCTGAAAAACATCTCTGAGCAGAAATGAGTGTGCGGC 1040
OY 901 CTGAGTTGGGCTCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 960
DB 1041 CTGAGTTGGGCTCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1100
OY 961 CGCTCTGAAGAGTCTTAAGAAATCTTCTGATGTTCTTGCAGAGAGTGCAGCGGG 1020

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DB 1101 CGCTCTGAAGAGTCTTAAGAAATCTTCTGATGTTCTTCCAGTGTGAGAGACTGGCGGG 1160
OY 1021 ACAGAGAGAGTCAAGGCGCTCTGCAAAAGCGGCGCTGTGTGTGTGTGTGTGTGTGT 1080
DB 1161 ACAGAGAGAGTCAAGGCGCTCTGCAAAAGCGGCGCTGTGTGTGTGTGTGTGTGTGT 1220
OY 1081 CGCGAGAGCGCTTCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
DB 1221 CGCGAGAGCGCTTCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1279
OY 1141 ACAGAGAGAGTCAAGGCGCTCTGCAAAAGCGGCGCTGTGTGTGTGTGTGTGTGTGT 1200
DB 1280 ACAGAGAGAGTCAAGGCGCTCTGCAAAAGCGGCGCTGTGTGTGTGTGTGTGTGTGT 1339
OY 1201 CTGAGGTGAAGAAAGTCTCTGAGAGAGAGAGAGATCATGTACGCGCGAAGTGAAG 1260
DB 1340 CTGAGGTGAAGAAAGTCTCTGAGAGAGAGAGAGATCATGTACGCGCGAAGTGAAG 1399
OY 1261 CTGCTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
DB 1400 CTGCTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1459
OY 1321 CAGCATACGGCCAAATGTCAACAATCAGCCCTGGGCGAGACAGAGAGAGAGAGAC 1380
DB 1460 CAGCATACGGCCAAATGTCAACAATCAGCCCTGGGCGAGACAGAGAGAGAGAGAC 1519
OY 1381 AGAGA 1385
DB 1520 AGAGA 1524

```

RESULT 45
US-10-218-765-15

```

? Sequence 15, Application US/10218765
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Desnoyers, Luc
? APPLICANT: Geriltsen, Mary
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Gurney, Austin L.
? APPLICANT: Smith, Victoria
? APPLICANT: Stephan, Jean-Philippe F.
? APPLICANT: Wood, William I.
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE REFERENCE: P3530P1C19
? CURRENT APPLICATION NUMBER: US/10/218,765
? PRIOR FILING DATE: 2002-08-12
? PRIOR APPLICATION NUMBER: 10/119,480
? PRIOR FILING DATE: 2002-04-09
? PRIOR APPLICATION NUMBER: 60/059113
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/062287
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/063549
? PRIOR FILING DATE: 1997-10-28
? PRIOR APPLICATION NUMBER: 60/064103
? PRIOR FILING DATE: 1997-10-31
? PRIOR APPLICATION NUMBER: 60/069873
? PRIOR FILING DATE: 1997-12-17
? PRIOR APPLICATION NUMBER: 60/078910
? PRIOR FILING DATE: 1998-03-20
? PRIOR APPLICATION NUMBER: 60/079294
? PRIOR FILING DATE: 1998-03-25
? PRIOR APPLICATION NUMBER: 60/079656
? PRIOR FILING DATE: 1998-03-26
? PRIOR APPLICATION NUMBER: 60/079728
? PRIOR FILING DATE: 1998-03-27
? PRIOR APPLICATION NUMBER: 60/081819

```

Query Match 78.1%; Score 1264; DB 42; Length 1524;
 Best Local Similarity 99.9%; Pred. No. 9,6e-234;
 Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1 GGGAACTTTTGGGAGTGTCTTCTGCTCCAGAGCTTGGGCTGCAAAATCAGTGTACCA 60
 141 GGGAACTTTTGGGAGTGTCTTCTGCTCCAGAGCTTGGGCTGCAAAATCAGTGTACCA 200
 61 GTGTGAAGATTCAGAGCTGCAACAGAGCTGCTCCCTCCCGAGTTTCATTTGTAAATTGAC 120
 201 GTGTGAAGATTCAGAGCTGCAACAGAGCTGCTCCCTCCCGAGTTTCATTTGTAAATTGAC 260
 121 GGTGAAGCTTCAAGACATGTGTGAGAAAGAGTGTGAGCAAGAGTGGGGTTCATGTA 180
 261 GGTGAAGCTTCAAGACATGTGTGAGAAAGAGTGTGAGCAAGAGTGGGGTTCATGTA 320
 181 CCGCAAGTCTGTGATCATCATCAGCGGCTGTCTCATCGGCTCTGCGGGTACCAAGTCTT 240
 321 CCGCAAGTCTGTGATCATCATCAGCGGCTGTCTCATCGGCTCTGCGGGTACCAAGTCTT 380
 241 CTGCTCCCAAGGAAAGTGAATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 300
 381 CTGCTCCCAAGGAAAGTGAATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 440
 301 CCGGCAAGGCTGCAAGAAAGGAGGAGTCTGCTGCGGCTGCAAGGCTGCGGCTGCGGCT 360
 441 CCGGCAAGGCTGCAAGAAAGGAGGAGTCTGCTGCGGCTGCAAGGCTGCGGCTGCGGCT 500
 361 CACCATCTGCTCTCAAAATTTAGCCCTCTCTGCGGACACATGCTGAAGTGAAGAGATG 420
 501 CACCATCTGCTCTCAAAATTTAGCCCTCTCTGCGGACACATGCTGAAGTGAAGAGATG 560
 421 CCGAGCCCTCTCAATGCTCTGCAAGGCTGCTGCGGCTGCAAGGCTGCGGCTGCGGCT 480
 561 CCGAGCCCTCTCAATGCTCTGCAAGGCTGCTGCGGCTGCAAGGCTGCGGCTGCGGCT 620
 481 GTTCTCTGCTGCT 540
 621 GTTCTCTGCTGCT 600
 541 CCGTGTCAAAATTAATGAAGAGCTGCTGAAGAGCTGCTGAAGAGCTGCTGAAGAGCT 600
 681 CCGTGTCAAAATTAATGAAGAGCTGCTGAAGAGCTGCTGAAGAGCTGCTGAAGAGCT 740
 601 TTTAGATATGATCTGAAGAGAGGAGTGAAGAGTCAACCCCATGCTGTGAAC 660
 741 TTTAGATATGATCTGAAGAGAGGAGTGAAGAGTCAACCCCATGCTGTGAAC 800
 661 CCGAGTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 801 CCGAGTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 860
 721 TTTTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 861 TTTTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 920
 781 GTGAGAGTGAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 921 GTGAGAGTGAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 841 ACATTCAAACTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 981 ACATTCAAACTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1040
 901 CTGAGTGGGCTCTAGTACTGAGACTCAATGACTGAGACTTGAATGGGGCTGCGGCT 960
 1041 CTGAGTGGGCTCTAGTACTGAGACTCAATGACTGAGACTTGAATGGGGCTGCGGCT 1100
 961 CCGCTGGAAGAGTGTGTAAGAAATCTTCTGATCTCTGCTGCTGCTGCTGCTGCTGCTG 1020
 1101 CCGCTGGAAGAGTGTGTAAGAAATCTTCTGATCTCTGCTGCTGCTGCTGCTGCTGCTG 1160

1021 ACGGAGAGCAGACGGGGGCTGTCACAAAGCGGCGCTGTGCTGTGTGAGTGGCATGTA 1080
 1161 ACGGAGAGCAGACGGGGGCTGTCACAAAGCGGCGCTGTGCTGTGTGAGTGGCATGTA 1220
 1081 CCGGAGGCGCTTCTGCTGT 1140
 1221 CCGGAGGCGCTTCTGCTGT 1279
 1141 ACGAAGACCCCGCAAACTGT 1200
 1280 ACGAAGACCCCGCAAACTGT 1339
 1201 CTGAGTGAAGAAAGCTGTCTGAGAAAGGAGAGATCATGTACGCCGGAAGTAGAGAC 1360
 1340 CTGAGTGAAGAAAGCTGTCTGAGAAAGGAGAGATCATGTACGCCGGAAGTAGAGAC 1399
 1261 CTGCTCCAGT 1320
 1400 CTGCTCCAGT 1459
 1321 CAGCATAGGCGCAATGTCAAAATCAGCCCTGCGGCTGAGACAGCAGAGAGAGAGAC 1380
 1460 CAGCATAGGCGCAATGTCAAAATCAGCCCTGCGGCTGAGACAGCAGAGAGAGAGAC 1519
 1381 AGAGA 1385
 1520 AGAGA 1524

RESULT 44
 US-10-218-631-15
 ; Sequence 15, Application US/10218631
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C14
 ; CURRENT APPLICATION NUMBER: US/10/218,631
 ; PRIOR FILING DATE: 2002-08-12
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See file Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 15
 ; LENGTH: 1524

Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1.

```

OY 1 GGCACATTTTGGGAGTGTCTGCTCCAGGCTTTGGGCTGCAATTCATGCTACCA 60
    |||||||
Db 141 GGCACATTTTGGGAGTGTCTGCTCCAGGCTTTGGGCTGCAATTCATGCTACCA 200
OY 61 GTGTGAAGAAATTCACAGCTGACAGACAGTCTCTCCCGAGTTCATGTGAATTCAC 120
    |||||||
Db 201 GTGTGAAGAAATTCACAGCTGACAGACAGTCTCTCCCGAGTTCATGTGAATTCAC 260
OY 121 GGTGAACGTTCAAGACATGTCTCAGAAAGATGAGCAAAAGTCCCGGATCATGTA 180
    |||||||
Db 261 GGTGAACGTTCAAGACATGTCTCAGAAAGATGAGCAAAAGTCCCGGATCATGTA 320
OY 181 CCGCAAGTCTCTGATCATCATCAGGCGCTGTCTCATCGCTCTGGCGGATACCATCTT 240
    |||||||
Db 321 CCGCAAGTCTCTGATCATCATCAGGCGCTGTCTCATCGCTCTGGCGGATACCATCTT 380
OY 241 CTGTCTCCCGAGGAAAATGAACTCAGTTTGCATCAGTCTGCAACACCCCTCTTTGTA 300
    |||||||
Db 381 CTGTCTCCCGAGGAAAATGAACTCAGTTTGCATCAGTCTGCAACACCCCTCTTTGTA 440
OY 301 CGGGCCCAAGGCCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCAGGCCAGGGCTCCGAC 360
    |||||||
Db 441 CGGGCCCAAGGCCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCAGGCCAGGGCTCCGAC 500
OY 361 CACCATCTCTCTCAATTAAGCCCTCTCTCGGCGACACTGCTGAAGTGAAGATG 420
    |||||||
Db 501 CACCATCTCTCTCAATTAAGCCCTCTCTCGGCGACACTGCTGAAGTGAAGATG 560
OY 421 CCACCCCTCTCTGATGTTCTTCCAGCCCTCGCCCAACCCCACTCCCTGAGTGA 480
    |||||||
Db 561 CCACCCCTCTCTGATGTTCTTCCAGCCCTCGCCCAACCCCACTCCCTGAGTGA 620
OY 481 GTTCTCTGCGGTCCTTTTATTTCTGGTGGGAGCGGGAGTCCGTTCTTTTGT 540
    |||||||
Db 621 GTTCTCTGCGGTCCTTTTATTTCTGGTGGGAGCGGGAGTCCGTTCTTTTGT 680
OY 541 CCTGTGCAATTAATGAAGAGCTCGGTAAAGCATCTGAATTAATTAATTAATTAAT 600
    |||||||
Db 681 CCTGTGCAATTAATGAAGAGCTCGGTAAAGCATCTGAATTAATTAATTAATTAAT 740
OY 601 TTTTCAGTATGTAATGAAGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 660
    |||||||
Db 741 TTTTCAGTATGTAATGAAGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 800
OY 661 CGGAGTCAAGGCGCAGGCTGGAGAGTGTCTTGAAGTCAAGTGAAGTGAAGTGAAGT 720
    |||||||
Db 801 CGGAGTCAAGGCGCAGGCTGGAGAGTGTCTTGAAGTCAAGTGAAGTGAAGTGAAGT 860
OY 721 TTTTGTAAAGCTCCAGTGTCCATTCATCCCTGATGGGGGCAATGTTGAGACTGAGA 780
    |||||||
Db 861 TTTTGTAAAGCTCCAGTGTCCATTCATCCCTGATGGGGGCAATGTTGAGACTGAGA 920
OY 781 GTGAGAGTGAAGTGTCTTGAAGGCTGGAGGCGCAATTCCTCAAGGCTCCCTGCTTG 840
    |||||||
Db 921 GTGAGAGTGAAGTGTCTTGAAGGCTGGAGGCGCAATTCCTCAAGGCTCCCTGCTTG 980
OY 841 ACATTCAAACTCAATGCTCTGAAACCATCTCTGAGAGGAGATTTGGGCTTCCGCG 900
    |||||||
Db 981 ACATTCAAACTCAATGCTCTGAAACCATCTCTGAGAGGAGATTTGGGCTTCCGCG 1040
OY 901 CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACTGGGATTAAGACTGGGGCTCGGCT 960
    |||||||
Db 1041 CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACTGGGATTAAGACTGGGGCTCGGCT 1100
OY 961 CGCTCTGAAAGTCTTAAAGAAATCTTCTCAGTTCTCTTGAAGAGACTGGGCGCGG 1020
    |||||||
Db 1101 CGCTCTGAAAGTCTTAAAGAAATCTTCTCAGTTCTCTTGAAGAGACTGGGCGCGG 1160
OY 1021 ACGGGAAGAGCAAGGCGCTGCAACAAGGCGGCGTGTGGGTTGGAGATGGGCAATGTA 1080
    |||||||
Db 1161 ACGGGAAGAGCAAGGCGCTGCAACAAGGCGGCGTGTGGGTTGGAGATGGGCAATGTA 1220

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OY 1081 CGCCAGAGCGCTTCTGCTGTGGTGGCTGCTGACGACAGGCGGACAGACACCTTGC 1140
    |||||||
Db 1221 CGCCAGAGCGCTTCTGCTGTGGTGGCTGCTGACGACAGGCGGACAGACACCTTGC 1279
OY 1141 ACGAACCACCGCGCAAACTGTGCGAGAGACACCGTGAACAGAGCGGTTGATGACCGAG 1200
    |||||||
Db 1280 ACGAACCACCGCGCAAACTGTGCGAGAGACACCGTGAACAGAGCGGTTGATGACCGAG 1339
OY 1201 CTGAGGTAGAAAACGTCCTCGAAGAGGAGAGAGATCATGTACGCCCGGAATGAGAC 1260
    |||||||
Db 1340 CTGAGGTAGAAAACGTCCTCGAAGAGGAGAGAGATCATGTACGCCCGGAATGAGAC 1399
OY 1261 CTGCTCAGTGTGCTGTTGGTTGGCGACACCATGATCTCGGAATCTGTTGGCATC 1320
    |||||||
Db 1400 CTGCTCAGTGTGCTGTTGGTTGGCGACCATGATCTCGGAATCTGTTGGCATC 1459
OY 1321 CAGCATAGGCGCATGTACAAACATCAGCCCTGGGCGAGACAGAGAGAGAGAGAC 1380
    |||||||
Db 1460 CAGCATAGGCGCATGTACAAACATCAGCCCTGGGCGAGACAGAGAGAGAGAGAC 1519
OY 1381 AGAGA 1385
    |||||
Db 1520 AGAGA 1524

```

```

RESULT 43
US-10-218-612-15
? Sequence 15, Application us/10218612
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Desnoyers, Luc
? APPLICANT: Gerritsen, Mary
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Gurney, Austin L.
? APPLICANT: Smith, Victoria
? APPLICANT: Stephan, Jean-Philippe F.
? APPLICANT: Watanabe, Colin L.
? APPLICANT: Wood, William I.
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE REFERENCE: P35301C21
? CURRENT APPLICATION NUMBER: US/10/218,612
? PRIOR FILING DATE: 2002-08-12
? PRIOR APPLICATION NUMBER: 10/119,480
? PRIOR FILING DATE: 2002-04-09
? PRIOR APPLICATION NUMBER: 60/059113
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/062287
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/063549
? PRIOR FILING DATE: 1997-10-28
? PRIOR APPLICATION NUMBER: 60/064103
? PRIOR FILING DATE: 1997-10-31
? PRIOR APPLICATION NUMBER: 60/069873
? PRIOR FILING DATE: 1997-12-17
? PRIOR APPLICATION NUMBER: 60/078910
? PRIOR FILING DATE: 1998-03-20
? PRIOR APPLICATION NUMBER: 60/079294
? PRIOR FILING DATE: 1998-03-25
? PRIOR APPLICATION NUMBER: 60/079656
? PRIOR FILING DATE: 1998-03-26
? PRIOR APPLICATION NUMBER: 60/079728
? PRIOR FILING DATE: 1998-03-27
? Remaining Prior Application data removed - See file Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 246
? SEQ ID NO 15
? LENGTH: 1524
? TYPE: DNA
? ORGANISM: Homo Sapien
US-10-218-612-15

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|||||
Db 141 GGCACATTTTTCGAGATGTTCTTCTTCACAGGCTTTGCGTGCAGAAATCCAGTCTTACCA 200
Oy 61 GTGTGAAGAAATTCAGAGTGAACAGACAGTGTCTCTCCCGAGTTCATTTGAAATTCAC 120
Db 201 GTGTGAAGAAATTCAGAGTGAACAGACAGTGTCTCTCCCGAGTTCATTTGAAATTCAC 260
Oy 121 GGTGAACGTTTCAAGACATGTCTCAGAAAGAGTGTGAGCAAGATGCGGGGATCATGTA 180
Db 261 GGTGAACGTTTCAAGACATGTCTCAGAAAGAGTGTGAGCAAGATGCGGGGATCATGTA 320
Oy 181 CCGCAGTGTCTGTGCAATCAGAGGCGGTCTCATGCGCTGTGCGGGTACAGTCTT 240
Db 321 CCGCAGTGTCTGTGCAATCAGAGGCGGTCTCATGCGCTGTGCGGGTACAGTCTT 380
Oy 241 CTGCTCCCGAGGAAAGTCAAGTCAAGTTCATCAGCTGTGCAACACCCCTTTTGTAA 300
Db 381 CTGCTCCCGAGGAAAGTCAAGTTCATCAGCTGTGCAACACCCCTTTTGTAA 440
Oy 301 CCGGCGCAAGGCGCAAGAAAGGGAAGTCTGCGCGCCCTCAGAGGCGTCCGAGC 360
Db 441 CCGGCGCAAGGCGCAAGAAAGGGAAGTCTGCGCGCCCTCAGAGGCGTCCGAGC 500
Oy 361 CACATCTCTTCTCTCAAAATTAACCTCTTCTCGGACACTGTGAGAGAGATG 420
Db 501 CACATCTCTTCTCTCAAAATTAACCTCTTCTCGGACACTGTGAGAGAGATG 560
Oy 421 CCACCCCTCTCTCAATTTTTCACAGCCCTGCGCCCAACCCCGCCACTCTCTAGTA 480
Db 561 CCACCCCTCTCTCAATTTTTCACAGCCCTGCGCCCAACCCCGCCACTCTCTAGTA 620
Oy 481 GTTCTCTCTGCGGTCTCTTATTTCTGGGAGGAGCGGAGCGTCTTCTTGT 540
Db 621 GTTCTCTCTGCGGTCTCTTATTTCTGGGAGGAGCGGAGCGTCTTCTTGT 680
Oy 541 CCTGTGCAAAATTAAGAAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGACTGA 600
Db 681 CCTGTGCAAAATTAAGAAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGACTGA 740
Oy 601 TTTTGAATGTACTTGAAGAGAGAGGTGAGTGAAGATTCACCCCATGTCTGTATAC 660
Db 741 TTTTGAATGTACTTGAAGAGAGAGGTGAGTGAAGATTCACCCCATGTCTGTATAC 800
Oy 661 CCGAGTCAAGGCGAGCTGCGAGAGTCACTTGAAGAGTCACTGAGTGGGATCTGCGC 720
Db 801 CCGAGTCAAGGCGAGCTGCGAGAGTCACTTGAAGAGTCACTGAGTGGGATCTGCGC 860
Oy 721 TTTTGAATGTACTTGAAGAGAGAGGTGAGTGAAGATTCACCCCATGTCTGTATAC 780
Db 861 TTTTGAATGTACTTGAAGAGAGAGGTGAGTGAAGATTCACCCCATGTCTGTATAC 920
Oy 781 GTGAGAGTGAAGTCTTCTTGAAGGCTGAGAGGAGTCCCACTCAAGAGCTCCCTGCTTG 840
Db 921 GTGAGAGTGAAGTCTTCTTGAAGGCTGAGAGGAGTCCCACTCAAGAGCTCCCTGCTTG 980
Oy 841 ACATTTCAAACTTCATGCTCTCTGAAACCATTTCTCTGACGACGAATGCGTTCGCGC 900
Db 981 ACATTTCAAACTTCATGCTCTCTGAAACCATTTCTCTGACGACGAATGCGTTCGCGC 1040
Oy 901 CTGAGTGTGGCTGTAGTACCTGAGACATGATGAGTGGGATGAGTGGGCGCT 960
Db 1041 CTGAGTGTGGCTGTAGTACCTGAGACATGATGAGTGGGATGAGTGGGCGCT 1100
Oy 961 CCGTCTGAAGAGTCTTGAAGAAATCTTCTCAAGTTCCTTTCGACAGAGTGGCGCGG 1020
Db 1101 CCGTCTGAAGAGTCTTGAAGAAATCTTCTCAAGTTCCTTTCGACAGAGTGGCGCGG 1160
Oy 1021 ACGCGAAGAGCAGCGGCGCTGACACAAAGCGGCGCTGTGGTGGTGGATGGCGCATGTA 1080
Db 1161 ACGCGAAGAGCAGCGGCGCTGACACAAAGCGGCGCTGTGGTGGTGGATGGCGCATGTA 1220
Oy 1081 CCGCGAGGCGCTTCTGTGTGGTGGCTGACAGAGAGCGCGACAGCATCTTGC 1140

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Db 1221 CCGCGAGGCGCTTCTGTGTGGTGGCTGTGACGACGACAGGCGCGACAGCACC-TGC 1279
Oy 1141 AGGAACACCCCGCGAAGTGTGCGAGAGACACGATGACAGAGCGGGTGTGATGACCGAG 1200
Db 1280 ACGAACACCCCGCGAAGTGTGCGAGAGACACGATGACAGAGCGGGTGTGATGACCGAG 1339
Oy 1201 CTGAGGTGAAGAAAGTCTCTCGAAGAGGAGGAGATGATGATGATGATGATGATGATGAT 1260
Db 1340 CTGAGGTGAAGAAAGTCTCTCGAAGAGGAGGAGATGATGATGATGATGATGATGATGAT 1399
Oy 1261 CTGCTCAGTCTGTCTGTGGTGTGGCGCCAGCCATGATCTCCAAATCTGGTGGCATC 1320
Db 1400 CTGCTCAGTCTGTCTGTGGTGTGGCGCCAGCCATGATCTCCAAATCTGGTGGCATC 1459
Oy 1321 CACGATACGCGCAAGTGTCAACATTCAGCCCTGCGGACAGCAGCAGCAGCAGCAGCAG 1380
Db 1460 CACGATACGCGCAAGTGTCAACATTCAGCCCTGCGGACAGCAGCAGCAGCAGCAGCAG 1519
Oy 1381 AGAGA 1385
Db 1520 AGAGA 1524

```

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RESULT 42
US-10-216-168-15
; Sequence 15, Application US/10216168
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C10
; CURRENT APPLICATION NUMBER: US/10/216,168
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-168-15

```

Query Match 78.1% Score 1264; DB 42; Length 1524;
Best Local Similarity 99.9%; Pred. No. 9,6e-234;

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0Y 61 GTGTGAAGATTCACAGACAGACGTCCTCCCCGAGTTCATTGTGAATGAC 120
    |||
Db 201 GTGTGAAGATTCACAGACAGACGTCCTCCCCGAGTTCATTGTGAATGAC 260
0Y 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGTAGAGCAAGTCCGGATCATSTA 180
    |||
Db 261 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGTAGAGCAAGTCCGGATCATSTA 320
0Y 181 CCAGAGTCCTGTGATCATCAGCGGCGTCTCATCCGCTCTGCGGGTACAGTCTT 240
    |||
Db 321 CCAGAGTCCTGTGATCATCAGCGGCGTCTCATCCGCTCTGCGGGTACAGTCTT 380
0Y 241 CTGCTCCCAAGGAAACTGAATTCAGTTGATCAGCTGTGAACACCCCTTTGTA 300
    |||
Db 381 CTGCTCCCAAGGAAACTGAATTCAGTTGATCAGCTGTGAACACCCCTTTGTA 440
0Y 301 CGGGCCCAAGGAAAGGAAAGGAAAGTTCGCTCGGCTCAGGCCAGGGCTCCGAC 360
    |||
Db 441 CGGGCCCAAGGAAAGGAAAGGAAAGTTCGCTCGGCTCAGGCCAGGGCTCCGAC 500
0Y 361 CACCATCTCTCTCAAAATTCAGCCCTCTCTCGGACACCTGGAAGCTGAAGAGATG 420
    |||
Db 501 CACCATCTCTCTCAAAATTCAGCCCTCTCTCGGACACCTGGAAGCTGAAGAGATG 560
0Y 421 CCACCCCTCTCTCAATTCCTTCACGCCCTCGGCCCAACCCCTCCCTGAGTGA 480
    |||
Db 561 CCACCCCTCTCTCAATTCCTTCACGCCCTCGGCCCAACCCCTCCCTGAGTGA 620
0Y 481 GTTCTCTGCGGTCCTTTATTCCTGGGTAGGAGCGGAGTCCGTTCTTTGTT 540
    |||
Db 621 GTTCTCTGCGGTCCTTTATTCCTGGGTAGGAGCGGAGTCCGTTCTTTGTT 680
0Y 541 CCTGTGCAAAATTAATGAAGAGCTCGGTAAAGCATTCGAATTAATTCAGCTCAGTGAAT 600
    |||
Db 681 CCTGTGCAAAATTAATGAAGAGCTCGGTAAAGCATTCGAATTAATTCAGCTCAGTGAAT 740
0Y 601 TTTGAGTGTACTTGAAGAGAGAGAGTGGAGTAAAGTTACCCCTCATCTGTGTAA 660
    |||
Db 741 TTTGAGTGTACTTGAAGAGAGAGAGTGGAGTAAAGTTACCCCTCATCTGTGTAA 800
0Y 661 CGAGATCAAGGCGCAGGCTGAGAGAGTCAAGTCTTGAAGTCACTGAGTGGGATGCGC 720
    |||
Db 801 CGAGATCAAGGCGCAGGCTGAGAGAGTCAAGTCTTGAAGTCACTGAGTGGGATGCGC 860
0Y 721 TTTTGTAAAGCTTCAAGTGTCCATTCCTGATGGGGGATGATTTGAGACTGACA 780
    |||
Db 861 TTTTGTAAAGCTTCAAGTGTCCATTCCTGATGGGGGATGATTTGAGACTGACA 920
0Y 781 GTGAGAGTCAAGTGTCTTGAAGGCTGAGAGGCGCATTCACATCAAGGCTCCCTGCTTG 840
    |||
Db 921 GTGAGAGTCAAGTGTCTTGAAGGCTGAGAGGCGCATTCACATCAAGGCTCCCTGCTTG 980
0Y 841 ACATTTCAAACTTCATGCTCTGAAAAACATTTCTGACAGAGAAATGGGTGGTTCGGC 900
    |||
Db 981 ACATTTCAAACTTCATGCTCTGAAAAACATTTCTGACAGAGAAATGGGTGGTTCGGC 1040
0Y 901 CTGAGTGGGCTTCAAGTGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 960
    |||
Db 1041 CTGAGTGGGCTTCAAGTGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1100
0Y 961 CGCTCTGAAAAAGTCTTGAAGAAATCTTCAAGTCTCTTCTGACAGAGACTGGCCGGG 1020
    |||
Db 1101 CGCTCTGAAAAAGTCTTGAAGAAATCTTCTCAAGTCTCTTCTGACAGAGACTGGCCGGG 1160
0Y 1021 ACGCGAAGAGCAACGGGCGCTGCACAAAGCGGCGCTGCGGTGGAGTGGCGCATGTA 1080
    |||
Db 1161 ACGCGAAGAGCAACGGGCGCTGCACAAAGCGGCGCTGCGGTGGAGTGGCGCATGTA 1220
0Y 1081 CGGCGAGGCGCTTCTGCTGGTGGCTGTGACGAGACAGGCGGAGAGCAACGACTTGC 1140
    |||
Db 1221 CGGCGAGGCGCTTCTGCTGGTGGCTGTGACGAGACAGGCGGAGAGCAACGACTTGC 1279
0Y 1141 ACGAACAACCGCGAAGACTGCTGCGAGGACACCGGTACAGAGAGCGGTTGATGACGAG 1200

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Db 1280 ACGAACAACCGCGAAGACTGTGCGAGGACACCGTGTACAGAGAGCGGTTGATACCGAG 1339
0Y 1201 CTGAGGTAGAAAAAGCTCTCCGAGAAAGGAGAGAGATCATGTACGCCGGAATGAGAC 1260
    |||
Db 1340 CTGAGGTAGAAAAAGCTCTCCGAGAAAGGAGAGAGATCATGTACGCCGGAATGAGAC 1399
0Y 1261 CTGCTCACTGCTGCTTGGGTTGGCCGACGACATGATCTCCGAATCTGGTGGCATC 1320
    |||
Db 1400 CTGCTCACTGCTGCTTGGGTTGGCCGACGACATGATCTCCGAATCTGGTGGCATC 1459
0Y 1321 CAGCATACGCGCAATGTCAACAATTCAGCCCTGGGACAGACAGAGAGAGAGAGAC 1380
    |||
Db 1460 CAGCATACGCGCAATGTCAACAATTCAGCCCTGGGACAGACAGAGAGAGAGAGAC 1519
0Y 1381 AGAGA 1385
    |||
Db 1520 AGAGA 1524

```

```

RESULT 41
US-10-216-167-15
; Sequence 15, Application US/10216167
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1CA
; CURRENT APPLICATION NUMBER: US/10/216,167
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-167-15

```

```

Query Match 78.1%; Score 1264; DB 42; Length 1524;
Best Local Similarity 99.9%; Pred. No. 9.6e-234;
Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
0Y 1 GGCACCTTTTTCGCGATGTCTCTTCACAGGCTTTCGCGTGCAGAAATCCAGTGTACCA 60

```


QY 121 GGTGAAGCTTCAAGCATGTGTCAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 180
 DB 261 GGTGAAGCTTCAAGCATGTGTCAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 320
 QY 181 CGGCAAGTCTGTGATCATGAGCGGCTGTCTATCGCTCTGCGGGTACAGTCTT 240
 DB 321 CGGCAAGTCTGTGATCATGAGCGGCTGTCTATCGCTCTGCGGGTACAGTCTT 380
 QY 241 CTGTCTCCCGAGGAAAGTCACTAGTTGATGATGCTGCTGCAACACCCCTTTGTA 300
 DB 381 CTGTCTCCCGAGGAAAGTCACTAGTTGATGATGCTGCTGCAACACCCCTTTGTA 440
 QY 301 CGGGCCAAAGGCGCCAGAAAGGGAGTTGCTGCGGCGCTCAGGGCAGGCTCCGAC 360
 DB 441 CGGGCCAAAGGCGCCAGAAAGGGAGTTGCTGCGGCGCTCAGGGCAGGCTCCGAC 500
 QY 361 CACCATCTGTCTCTCAAAATTAAGCCCTCTCTGCGCACACTGTGAAGCTGAAGAGATG 420
 DB 501 CACCATCTGTCTCTCAAAATTAAGCCCTCTCTGCGCACACTGTGAAGCTGAAGAGATG 560
 QY 421 CCACCCCTCTGCAATGTTGTTCTTCAGCCCTGCGCCCAACCCCTCCCTGAGTGA 480
 DB 561 CCACCCCTCTGCAATGTTGTTCTTCAGCCCTGCGCCCAACCCCTCCCTGAGTGA 620
 QY 481 GTTCTCTGCGGTCTCTTTATCTGCGGTAGGAGCGGAGTCCGTCTCTTTGTT 540
 DB 621 GTTCTCTGCGGTCTCTTTATCTGCGGTAGGAGCGGAGTCCGTCTCTTTGTT 680
 QY 541 CCTGTGCAAAATATGAAGAGCTCGTAAAGCATTTCTGAATTAATTCAGCTGACTGAT 600
 DB 681 CCTGTGCAAAATATGAAGAGCTCGTAAAGCATTTCTGAATTAATTCAGCTGACTGAT 740
 QY 601 TTTCAGTACTGTTGAAGAGAGGAGTGAAGTCAACCCCTGCTGCTGATG 660
 DB 741 TTTCAGTACTGTTGAAGAGAGGAGTGAAGTCAACCCCTGCTGCTGATG 800
 QY 661 CGGAGTCAAGGCGGAGGCTGGCAGAGTCACTCTTAGAATCACTGAGTGGGCTGCC 720
 DB 801 CGGAGTCAAGGCGGAGGCTGGCAGAGTCACTCTTAGAATCACTGAGTGGGCTGCC 860
 QY 721 TTTTGTAAAGCTCCAGTCTCATTCATCCCTGATGGGCGATGTTGAGACTGACGA 780
 DB 861 TTTTGTAAAGCTCCAGTCTCATTCATCCCTGATGGGCGATGTTGAGACTGACGA 920
 QY 781 GTGAGAGTACGTTTCTTAGGCTGGAGGCGGAGTCCCACTCAAGGCTCCCTGCTTG 840
 DB 921 GTGAGAGTACGTTTCTTAGGCTGGAGGCGGAGTCCCACTCAAGGCTCCCTGCTTG 980
 QY 841 ACATTCAAATTCATGCTCTGTAACCAATTCCTGACAGCAATTTGGCTTGGCGC 900
 DB 981 ACATTCAAATTCATGCTCTGTAACCAATTCCTGACAGCAATTTGGCTTGGCGC 1040
 QY 901 CTGAGTGTGGGCTCTAGTACTGAGACTAATGACTGAGGACTTAAGTGGGCTGGGCT 960
 DB 1041 CTGAGTGTGGGCTCTAGTACTGAGACTAATGACTGAGGACTTAAGTGGGCTGGGCT 1100
 QY 961 CGCTGTGAAAGTCTTAAGAAATCTTCTCAGTTCTCTTCAAGAGACTGGCGCGG 1020
 DB 1101 CGCTGTGAAAGTCTTAAGAAATCTTCTCAGTTCTCTTCAAGAGACTGGCGCGG 1160
 QY 1021 ACAGCAAGAGCAAGGCGCTGCAAAAGCGGCGCTGTGCTGTGAGTGGCGCATGTA 1080
 DB 1161 ACAGCAAGAGCAAGGCGCTGCAAAAGCGGCGCTGTGCTGTGAGTGGCGCATGTA 1220
 QY 1081 CGGCGAGGCGCTCTGCTGTGCTGCTGCTGCAAGGCGAGCGGCGGACAGCACTTGG 1140
 DB 1221 CGGCGAGGCGCTCTGCTGTGCTGCTGCTGCAAGGCGAGCGGCGGACAGCACTTGG 1200
 QY 1141 ACAGCAAGAGCAAGGCGCTGCAAGAGCACTGTAAGAGAGCGGCTTGAATGACGAG 1280
 DB 1280 ACAGCAAGAGCAAGGCGCTGCAAGAGCACTGTAAGAGAGCGGCTTGAATGACGAG 1339

QY 1201 CTGAGTGTGAAAGAGTCTCTCCGAGAGGAGGAGGATCATGTACCCCGAAGTAGAC 1260
 DB 1340 CTGAGTGTGAAAGAGTCTCTCCGAGAGGAGGAGGATCATGTACCCCGAAGTAGAC 1399
 QY 1261 CTGCTCCAGTCTGCTGTTGGGTTGGCCGACAGCATATCTCGAATCTGTTGGGATC 1320
 DB 1400 CTGCTCCAGTCTGCTGTTGGGTTGGCCGACAGCATATCTCGAATCTGTTGGGATC 1459
 QY 1321 CAGCATACGGGCAATGTCACAAATCAGCCCTGGGCGAGACAGCAGAGAGAGAGAC 1380
 DB 1460 CAGCATACGGGCAATGTCACAAATCAGCCCTGGGCGAGACAGCAGAGAGAGAGAC 1519
 QY 1381 AGAGA 1385
 DB 1520 AGAGA 1524

RESULT 40
 US-10-216-166-15
 : Sequence 15, Application US/10216166
 : GENERAL INFORMATION:
 : APPLICANT: Baker, Kevin P.
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Gerilsen, Mary
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, J. Christopher
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Smith, Victoria
 : APPLICANT: Stephan, Jean-Philippe F.
 : APPLICANT: Watanabe, Colin L.
 : APPLICANT: Wood, William I.
 : TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 : FILE REFERENCE: P3530P1C9
 : CURRENT APPLICATION NUMBER: US/10/216,166
 : CURRENT FILING DATE: 2002-08-09
 : PRIOR APPLICATION NUMBER: 10/119,480
 : PRIOR FILING DATE: 2002-04-09
 : PRIOR APPLICATION NUMBER: 60/059113
 : PRIOR FILING DATE: 1997-09-17
 : PRIOR APPLICATION NUMBER: 60/062287
 : PRIOR FILING DATE: 1997-10-17
 : PRIOR APPLICATION NUMBER: 60/063549
 : PRIOR FILING DATE: 1997-10-28
 : PRIOR APPLICATION NUMBER: 60/064103
 : PRIOR FILING DATE: 1997-10-31
 : PRIOR APPLICATION NUMBER: 60/069873
 : PRIOR FILING DATE: 1997-12-17
 : PRIOR APPLICATION NUMBER: 60/078910
 : PRIOR FILING DATE: 1998-03-20
 : PRIOR APPLICATION NUMBER: 60/079294
 : PRIOR FILING DATE: 1998-03-25
 : PRIOR APPLICATION NUMBER: 60/079656
 : PRIOR FILING DATE: 1998-03-26
 : PRIOR APPLICATION NUMBER: 60/079728
 : PRIOR FILING DATE: 1998-03-27
 : Remaining Prior Application data removed - See file Wrapper or PALM.
 : NUMBER OF SEQ ID NOS: 246
 : SEQ ID NO 15
 : LENGTH: 1524
 : TYPE: DNA
 : ORGANISM: Homo Sapien
 US-10-216-166-15
 Query March 78.1% Score 1264: DB 42: Length 1524:
 Best Local Similarity 99.9%: Pred. NO. 9.6e-234:
 Matches 1384: Conservative 0: Mismatches 0: Indels 1: Gaps 1:
 QY 1 GGCACATTTTGGCGGATGTTCTGCTTCCAGGCTTTCGCTGCAAAATCCAGTGTACCA 60
 DB 141 GGCACATTTTGGCGGATGTTCTGCTTCCAGGCTTTCGCTGCAAAATCCAGTGTACCA 200

Db 261 GGTGACGTTCAAGCATGTCTCAGAAAGATGAGCAAAAGTCCGGGATCATGTA 320
 Qy 181 CGGCAAGTCTGTGCATCATCAGGCGCTGTCTCATGCGCTCTGCGGGTACAGTCTT 240
 Db 321 CGGCAAGTCTGTGCATCATCAGGCGCTGTCTCATGCGCTCTGCGGGTACAGTCTT 380
 Qy 241 CTGCTCCCCAGGAAACGAACTCAGTTTGCATAGCTGCTGCAACACCCCTTTTAA 300
 Db 381 CTGCTCCCCAGGAAACGAACTCAGTTTGCATAGCTGCTGCAACACCCCTTTTAA 440
 Qy 301 CGGCGCAAGGCGCAAGAAAGGGAAGTTCGCTCGGCGCTCGGCGCGGCTCGGCG 360
 Db 441 CGGCGCAAGGCGCAAGAAAGGGAAGTTCGCTCGGCGCTCGGCGCGGCTCGGCG 500
 Qy 361 CACATCTCTTCTCTCAATTAAGCCCTCTCTCGGCACTGCTGAAGTGAAGAGATG 420
 Db 501 CACATCTCTTCTCTCAATTAAGCCCTCTCTCGGCACTGCTGAAGTGAAGAGATG 560
 Qy 421 CCAGCCCTCTCTGATGTTCTTCTGACAGCCCTCGGCGCGGCGCGGCTCGGCGTGA 480
 Db 561 CCAGCCCTCTCTGATGTTCTTCTGACAGCCCTCGGCGCGGCGCGGCTCGGCGTGA 620
 Qy 481 GTTCTCTCTGAGTCTCTTCTTATCTGGTGAAGGAGCGGCGGCGGCTCTCTTCTT 540
 Db 621 GTTCTCTCTGAGTCTCTTCTTATCTGGTGAAGGAGCGGCGGCGGCTCTCTTCTT 680
 Qy 541 CCTGTCAATTAATGAAGAGCTCGTGAAGATCTGAATTAATTAATTAATTAATTA 600
 Db 681 CCTGTCAATTAATGAAGAGCTCGTGAAGATCTGAATTAATTAATTAATTAATTA 740
 Qy 601 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 Db 741 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 800
 Qy 661 CGGAGTCAAGGCGCAGGCTGCGAGAGTCACTTGAAGTCACTGAGTGGGATCTGCC 720
 Db 801 CGGAGTCAAGGCGCAGGCTGCGAGAGTCACTTGAAGTCACTGAGTGGGATCTGCC 860
 Qy 721 TTTTGTAAAGCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATG 780
 Db 861 TTTTGTAAAGCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATG 920
 Qy 781 GTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 Db 921 GTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 980
 Qy 841 ACATTTCAATCTATGCTCTCTGAAACCAATCTCTGACAGAGATGCTGCTTGGCG 900
 Db 981 ACATTTCAATCTATGCTCTCTGAAACCAATCTCTGACAGAGATGCTGCTTGGCG 1040
 Qy 901 CTGAGTTGGGCTCTAGTGAAGTCAATGATGATGATGATGATGATGATGATGATGAT 960
 Db 1041 CTGAGTTGGGCTCTAGTGAAGTCAATGATGATGATGATGATGATGATGATGATGAT 1100
 Qy 961 CGCTCTGAAAGTCTTAAAGAAATCTTCTCACTTCTCTGAGAGAGATGCTGCGCGG 1020
 Db 1101 CGCTCTGAAAGTCTTAAAGAAATCTTCTCACTTCTCTGAGAGAGATGCTGCGCGG 1160
 Qy 1021 ACCGGAAGAGCAAGCGGCGCTGCAAAAGCGGCGCTGCTGCTGCTGCTGCTGCTG 1080
 Db 1161 ACCGGAAGAGCAAGCGGCGCTGCAAAAGCGGCGCTGCTGCTGCTGCTGCTGCTG 1220
 Qy 1081 CGGCGAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 Db 1221 CGGCGAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1279
 Qy 1141 ACAGAACCCCGCGGAAGTCTGCGAGGACACGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 Db 1280 ACAGAACCCCGCGGAAGTCTGCGAGGACACGCTGCTGCTGCTGCTGCTGCTGCTGCT 1339
 Qy 1201 CTGAGGTAAAGAAAGCTCTGCGAGAGGAGAGATCATGAGCCCGGAAGTGAAGAC 1260
 Db 1340 CTGAGGTAAAGAAAGCTCTGCGAGAGGAGAGATCATGAGCCCGGAAGTGAAGAC 1399

Qy 1261 CTGTCACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 Db 1400 CTGTCACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1459
 Qy 1321 CACATACGCGCAATGTCAACAAATCAGCCCTGCGGAGACAGAGAGAGAGAGAC 1380
 Db 1460 CACATACGCGCAATGTCAACAAATCAGCCCTGCGGAGACAGAGAGAGAGAGAC 1519
 Qy 1381 AGAGA 1385
 Db 1520 AGAGA 1524
 RESULT 39
 US-10-216-165-15
 ; Sequence 15, Application US/10216165
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerlitsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C7
 ; CURRENT APPLICATION NUMBER: US/10/216,165
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 15
 ; LENGTH: 1524
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-216-165-15
 Query Match 78.1%; Score 1264; DB 42; Length 1524;
 Best Local Similarity 99.9%; Pred. No. 9.6e-234;
 Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

Db 321 CCGCAGATCTGTGATATATAGGGGCTGTCTCATGCTCTCGGGGTACAGTCTTT
380
Qy 241 CTGCTCCCGGAGAACTGAACTAGTTCATGACGTGTCGAACACCCCTTTGTA
300
Db 381 CTGCTCCCGGAGAACTGAACTAGTTCATGACGTGTCGAACACCCCTTTGTA
440
Qy 301 CGGCGCAAGGCGGCAAGAAAGGGGAGTTGCTCGGCTCGGCGGAGGCGCTCCGAC
360
Db 441 CGGCGCAAGGCGGCAAGAAAGGGGAGTTGCTCGGCTCGGCGGAGGCGCTCCGAC
500
Qy 361 CACCATCTGTTCCTCAATTAAGCCCTCTTCGCGACACGTGTAAGCTAAGAGATG
420
Db 501 CACCATCTGTTCCTCAATTAAGCCCTCTTCGCGACACGTGTAAGCTAAGAGATG
560
Qy 421 CCACCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
480
Db 561 CCACCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
620
Qy 481 GTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
540
Db 621 GTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
680
Qy 541 CCTGTGCAATATATGAAGAGCTCGCTGAAGCATTTCTGAATTAATTCAGCTGACTGAT
600
Db 681 CCTGTGCAATATATGAAGAGCTCGCTGAAGCATTTCTGAATTAATTCAGCTGACTGAT
740
Qy 601 TTTTCTGATGCTGGAAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA
660
Db 741 TTTTCTGATGCTGGAAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA
800
Qy 661 CGGAGTCAAGGCGGAGCTGCGAGAGTCACTTGAAGTCACTGAGTGGGCTGCTGCC
720
Db 801 CGGAGTCAAGGCGGAGCTGCGAGAGTCACTTGAAGTCACTGAGTGGGCTGCTGCC
860
Qy 721 TTTTCTGAAAGCTCCAGTGTCCATTCCTGATGCGGGCATGTTGAGACTGCGAGA
780
Db 861 TTTTCTGAAAGCTCCAGTGTCCATTCCTGATGCGGGCATGTTGAGACTGCGAGA
920
Qy 781 GTGAGAGTACGCTTTTCTGAGGCTGAGAGGCGGCTGCGGCTGCGGCTGCTG
840
Db 921 GTGAGAGTACGCTTTTCTGAGGCTGAGAGGCGGCTGCGGCTGCGGCTGCTG
980
Qy 841 ACATTCAAACTTCATGCTCTGAAAAACCAATTCCTGACAGCAAAATTTGCTGCTGCGGC
900
Db 981 ACATTCAAACTTCATGCTCTGAAAAACCAATTCCTGACAGCAAAATTTGCTGCTGCGGC
1040
Qy 901 CTGAGTGGGCTCTAGTACTGAGACTCAATGACTGGGCTGAGCTGGGCTGAGCT
960
Db 1041 CTGAGTGGGCTCTAGTACTGAGACTCAATGACTGGGCTGAGCTGGGCTGAGCT
1100
Qy 961 CGCTCTGAAAAAGTGTCTGAAAAATCTTCTCAGTTCTCTCTGACAGAGACTGCGCGG
1020
Db 1101 CGCTCTGAAAAAGTGTCTGAAAAATCTTCTCAGTTCTCTCTGACAGAGACTGCGCGG
1160
Qy 1021 ACGCAAGAGCAAGCGGCGCTGACAAAGCGGCGCTGCTGCTGCTGCTGCTGCTG
1080
Db 1161 ACGCAAGAGCAAGCGGCGCTGACAAAGCGGCGCTGCTGCTGCTGCTGCTGCTG
1220
Qy 1081 CGCGGAGGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
1140
Db 1221 CGCGGAGGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
1279
Qy 1141 ACGAAGACCGCGGCAAACTGCTGAGAGCAACGCTGACAGAGCGGCTGCTGCTGCTG
1200
Db 1280 ACGAAGACCGCGGCAAACTGCTGAGAGCAACGCTGACAGAGCGGCTGCTGCTGCTG
1339
Qy 1201 CTGAGGTAGAAAAAGCTCTCCGAGAGGGGAGAGATCATGTACGCCCGAAGTAGGAC
1260
Db 1340 CTGAGGTAGAAAAAGCTCTCCGAGAGGGGAGAGATCATGTACGCCCGAAGTAGGAC
1399
Qy 1261 CTCGTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
1320

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Db 1400 CTGCTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
1459
Qy 1321 CAGCATAGGCGCAATGTCACACATCAGGCTGCGGAGACAGAGAGGAGAGAC
1380
Db 1460 CAGCATAGGCGCAATGTCACACATCAGGCTGCGGAGACAGAGAGGAGAGAC
1519
Qy 1381 AGAGA 1385
1381
Db 1520 AGAGA 1524
1520

RESULT 38
US-10-216-164-15
; Sequence 15, Application US/10216164
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P105
; CURRENT APPLICATION NUMBER: US/10/216, 164
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119, 480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-164-15

Query Match 78.18; Score 1264; DB 42; Length 1524;
Best Local Similarity 99.9%; Pred. No. 9, 6e-234;
Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

241 CTGCTCCCGAGGAACTGAACTGAGTTGATGATGCTGCAACACCCCTCTTTGTA 300
| | | | |
Db 381 CTGCTCCCGAGGAACTGAACTGAGTTGATGATGCTGCAACACCCCTCTTTGTA 440
| | | | |
Qy 301 CGGGCCAAAGGCGGCAAGAAAGGAGGAGTTGCTGCTGCGCCCTCAGGCCAGGCTCCGAC 360
| | | | |
Db 441 CGGGCCAAAGGCGGCAAGAAAGGAGGAGTTGCTGCTGCGCCCTCAGGCCAGGCTCCGAC 500
| | | | |
Qy 361 CACCATCTGTTCTGCAATTAAGCCCTCTGCGGCAACAGCTGGAACCTGAAGAGATG 420
| | | | |
Db 501 CACCATCTGTTCTGCAATTAAGCCCTCTGCGGCAACAGCTGGAACCTGAAGAGATG 560
| | | | |
Qy 421 CCACCCCTCTGCAATTAAGCCCTCTGCGGCAACAGCTGGAACCTGAAGAGATG 480
| | | | |
Db 561 CCACCCCTCTGCAATTAAGCCCTCTGCGGCAACAGCTGGAACCTGAAGAGATG 620
| | | | |
Qy 481 GTTCTTCTGGGTGCTCTTTATTTCTGGGTAGGAGCGGAGTCCGTCTCTTTGTT 540
| | | | |
Db 621 GTTCTTCTGGGTGCTCTTTATTTCTGGGTAGGAGCGGAGTCCGTCTCTTTGTT 680
| | | | |
Qy 541 CCTGTGCAATTAAGAGCTGCTGTAAGCAATTCGAATTAATTCAGCTGATGAT 600
| | | | |
Db 661 CCTGTGCAATTAAGAGCTGCTGTAAGCAATTCGAATTAATTCAGCTGATGAT 740
| | | | |
Qy 601 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
| | | | |
Db 741 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 800
| | | | |
Qy 661 CGGAGTCAAGGCGGAGGCTGCGAGAGTCACTCTTGAAGAGTCACTGAGGTGGCATCTGCC 720
| | | | |
Db 801 CGGAGTCAAGGCGGAGGCTGCGAGAGTCACTCTTGAAGAGTCACTGAGGTGGCATCTGCC 860
| | | | |
Qy 721 TTTTGAAGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 780
| | | | |
Db 861 TTTTGAAGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 920
| | | | |
Qy 781 GTGAGAGTGAAGTTTCTTGAAGGCTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGG 840
| | | | |
Db 921 GTGAGAGTGAAGTTTCTTGAAGGCTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGG 980
| | | | |
Qy 841 ACATTCAAACTTCACTGCTCTGAAACCATCTCTGCAAGCAATTTGGCTGCTGCGC 900
| | | | |
Db 981 ACATTCAAACTTCACTGCTCTGAAACCATCTCTGCAAGCAATTTGGCTGCTGCGC 1040
| | | | |
Qy 901 CTGAGTTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
| | | | |
Db 1041 CTGAGTTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1100
| | | | |
Qy 961 CGCTCTGAAAGTGTGTAAGAAATCTTCTGAGTTCTCTTGCAGAGAGACTGGCGCGG 1020
| | | | |
Db 1101 CGCTCTGAAAGTGTGTAAGAAATCTTCTGAGTTCTCTTGCAGAGAGACTGGCGCGG 1160
| | | | |
Qy 1021 ACCGGAAGAGCAAGCGGCGCTGCAACAAAGCGGCGCTGCTGCTGCTGCTGCTGCTGCT 1080
| | | | |
Db 1161 ACCGGAAGAGCAAGCGGCGCTGCAACAAAGCGGCGCTGCTGCTGCTGCTGCTGCTGCT 1220
| | | | |
Qy 1081 CGCGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
| | | | |
Db 1221 CGCGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1279
| | | | |
Qy 1141 ACAGAACACCCCGCAAACTGCTGAGAGACACCTGTACAGAGAGCGGTTGATACCGAG 1200
| | | | |
Db 1280 ACAGAACACCCCGCAAACTGCTGAGAGACACCTGTGTACAGAGAGCGGTTGATACCGAG 1339
| | | | |
Qy 1201 CTGAGGTGAGAAAGAGTCTCGAGAGAGGAGAGATCATGTACGCCCGGAGATGAGAC 1260
| | | | |
Db 1340 CTGAGGTGAGAAAGAGTCTCGAGAGAGGAGAGATCATGTACGCCCGGAGATGAGAC 1399
| | | | |
Qy 1261 CTGAGGTGAGAAAGAGTCTCGAGAGAGGAGAGATCATGTACGCCCGGAGATGAGAC 1320
| | | | |
Db 1400 CTGAGGTGAGAAAGAGTCTCGAGAGAGGAGAGATCATGTACGCCCGGAGATGAGAC 1459
| | | | |
Qy 1321 CAGCATACGGCAATGTACAAACATCAGCCCTGGGAGAGACAGAGAGAGAGAGAC 1380
| | | | |

Db 1460 CAGCATACGGCAATGTACAAACATCAGCCCTGGGAGAGACAGAGAGAGAGAGAC 1519
| | | | |
Qy 1381 AGAGA 1385
| | | | |
Db 1520 AGAGA 1524
| | | | |
RESULT 37
US-10-216-163-15
; Sequence 15, Application US/10216163
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C3
; CURRENT APPLICATION NUMBER: US/10/216,163
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-163-15
Query Match 78.1%; Score 1264; DB 42; Length 1524;
Best Local Similarity 99.9%; Pred. No. 9, 6e-234;
Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 GGAACATTTTGGGAGTGTGTTGCTTCAGGCTTGGGCTGCAAAATCAGTGTACCA 60
| | | | |
Db 141 GGAACATTTTGGGAGTGTGTTGCTTCAGGCTTGGGCTGCAAAATCAGTGTACCA 200
| | | | |
Qy 61 GTGTGAAGATTCACCTGACACAGACAGTCTCTCCCGAGTTCAATGTGATTTGAC 120
| | | | |
Db 201 GTGTGAAGATTCACCTGACACAGACAGTCTCTCCCGAGTTCAATGTGATTTGAC 260
| | | | |
Qy 121 GTGTGAAGATTCACAGATGTGTGAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180
| | | | |
Db 261 GTGTGAAGATTCACAGATGTGTGAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 320
| | | | |
Qy 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGGCTCTGCCGGGTACCATGCTT 240
| | | | |

QY 301 CGGGCCCAAGGCCAAGAAAAAGGGAAGTTCTGCTCGGCGCTCAGGGCCAGGGCTCCGAC 360
 DB 441 CGGGCCCAAGGCCAAGAAAAAGGGAAGTTCTGCTCGGCGCTCAGGGCCAGGGCTCCGAC 500
 QY 361 CACATCTCTGTTCTTCAATTAATTAAGCCCTCTTCGCGACACTGCTGAAGCTGAAGAGATG 420
 DB 501 CACATCTCTGTTCTTCAATTAATTAAGCCCTCTTCGCGACACTGCTGAAGCTGAAGAGATG 560
 QY 421 CCACCCCTCGGCAATGTTCTTCAAGCCCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
 DB 561 CCACCCCTCGGCAATGTTCTTCAAGCCCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 620
 QY 481 GTTCTCTGCGGCTGCTCTTCTTCTGCGGTAGGAGCGGAGTCCGTTCTTCTTCTTCTTCTT 540
 DB 621 GTTCTCTGCGGCTGCTCTTCTTCTGCGGTAGGAGCGGAGTCCGTTCTTCTTCTTCTTCTT 680
 QY 541 CCTGTGCAATTAATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTAATTAATTAATTAAT 600
 DB 681 CCTGTGCAATTAATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTAATTAATTAATTAAT 740
 QY 601 TTTTCAATTAATTAATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTAATTAATTAATTAAT 660
 DB 741 TTTTCAATTAATTAATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTAATTAATTAATTAAT 800
 QY 661 CGGAGTCAAGGCGCAGGCTGCGAGAGTCACTTCTGAAGTCACTGAGTGGGCTATCTGCC 720
 DB 801 CGGAGTCAAGGCGCAGGCTGCGAGAGTCACTTCTGAAGTCACTGAGTGGGCTATCTGCC 860
 QY 721 TTTTGAAGGCTTCCAGTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780
 DB 861 TTTTGAAGGCTTCCAGTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 920
 QY 781 GTGAGAGTACCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 840
 DB 921 GTGAGAGTACCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 980
 QY 841 ACATTTCAAACTTATGCTCTTCAAAAAACATTTCTGCAAGCAATTTGGCTGTTTCCGCGC 900
 DB 981 ACATTTCAAACTTATGCTCTTCAAAAAACATTTCTGCAAGCAATTTGGCTGTTTCCGCGC 1040
 QY 901 CTGAGTGGGCTCTAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 960
 DB 1041 CTGAGTGGGCTCTAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1100
 QY 961 CGCTCTGAAAAGTGTCTTGAAGAAATCTTCTCAGTTCTCTTCTGACAGAGACTGGCGCGCGG 1020
 DB 1101 CGCTCTGAAAAGTGTCTTGAAGAAATCTTCTCAGTTCTCTTCTGACAGAGACTGGCGCGCGG 1160
 QY 1021 ACCGCAAGAGCAAGGCGCGCTGACAAAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 DB 1161 ACCGCAAGAGCAAGGCGCGCTGACAAAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1220
 QY 1081 CGCGAGGCGGCTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 DB 1221 CGCGAGGCGGCTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1279
 QY 1141 ACGAACAACCCCGGAAGTGTGCGAGGACACCTGTGACAGAGCGGGTGTGATGACCGAG 1200
 DB 1280 ACGAACAACCCCGGAAGTGTGCGAGGACACCTGTGACAGAGCGGGTGTGATGACCGAG 1339
 QY 1201 CTGAGGTAAAGAAAGTGTGCGAGAGGAGAGAGATCATGTACGCCCGGAAGTAGAGAC 1260
 DB 1340 CTGAGGTAAAGAAAGTGTGCGAGAGGAGAGAGATCATGTACGCCCGGAAGTAGAGAC 1399
 QY 1261 CTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 DB 1400 CTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1459
 QY 1321 CAGCATATGAGGCAATGTCAACAATCAAGCCTTGGGCAAGACAGAGAGAGAGAGAGAC 1380
 DB 1460 CAGCATATGAGGCAATGTCAACAATCAAGCCTTGGGCAAGACAGAGAGAGAGAGAGAC 1519

QY 1381 AGAGA 1385
 DB 1520 AGAGA 1524
 RESULT 36
 US-10-216-162-15
 : Sequence 15, Application US/10216162
 : GENERAL INFORMATION:
 : APPLICANT: Baker, Kevin P.
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Gerritsen, Mary
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, J. Christopher
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Smith, Victoria
 : APPLICANT: Stephan, Jean-Philippe F.
 : APPLICANT: Watanabe, Colin L.
 : APPLICANT: Wood, William I.
 : TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 : FILE REFERENCE: P3530PIC2
 : CURRENT APPLICATION NUMBER: US/10/216,162
 : PRIOR FILING DATE: 2002-08-09
 : PRIOR APPLICATION NUMBER: 10/119,480
 : PRIOR FILING DATE: 2002-04-09
 : PRIOR APPLICATION NUMBER: 60/059113
 : PRIOR FILING DATE: 1997-09-17
 : PRIOR APPLICATION NUMBER: 60/062287
 : PRIOR FILING DATE: 1997-10-17
 : PRIOR APPLICATION NUMBER: 60/063549
 : PRIOR FILING DATE: 1997-10-28
 : PRIOR APPLICATION NUMBER: 60/064103
 : PRIOR FILING DATE: 1997-10-31
 : PRIOR APPLICATION NUMBER: 60/069873
 : PRIOR FILING DATE: 1997-12-17
 : PRIOR APPLICATION NUMBER: 60/078910
 : PRIOR FILING DATE: 1998-03-20
 : PRIOR APPLICATION NUMBER: 60/079294
 : PRIOR FILING DATE: 1998-03-25
 : PRIOR APPLICATION NUMBER: 60/079656
 : PRIOR FILING DATE: 1998-03-26
 : PRIOR APPLICATION NUMBER: 60/079728
 : Remaining Prior Application data removed - See File Wrapper or PALM.
 : NUMBER OF SEQ ID NOS: 246
 : SEQ ID NO 15
 : LENGTH: 1524
 : TYPE: DNA
 : ORGANISM: Homo Sapien
 : US-10-216-162-15
 Query Match 78.18; Score 1264; DB 42; Length 1524;
 Best Local Similarity 99.9%; Pred. No. 9, 6e-234;
 Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 GGCACATTTTGGCGAGTGTCTTCTTCCAGGCTTGGCGTCAAAATCCAGTGTACCA 60
 DB 141 GGCACATTTTGGCGAGTGTCTTCTTCCAGGCTTGGCGTCAAAATCCAGTGTACCA 200
 QY 61 GTGTGAAGAAATTCAGGTGAACAACGACTGCTCCGCCGAGTGTATGTGATTTGAC 120
 DB 201 GTGTGAAGAAATTCAGGTGAACAACGACTGCTCCGCCGAGTGTATGTGATTTGAC 260
 QY 121 GGTAAAGCTTCAAGACATGTGTCTGAGAAAGATGATGAGCAAAAGTCCGGGATCTGTGA 180
 DB 261 GGTAAAGCTTCAAGACATGTGTCTGAGAAAGATGATGAGCAAAAGTCCGGGATCTGTGA 320
 QY 181 CCGCAATCTCTGTGCAATCATCAGCGGCTGTCTCATGCGCTTGGCGGATACAGTCTT 240
 DB 321 CCGCAATCTCTGTGCAATCATCAGCGGCTGTCTCATGCGCTTGGCGGATACAGTCTT 380

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Db 141 GGCACATTTTGGCGGATTGTTCTTCCAGGCTTTGCGGTGCAATTCAGTGTACCA 200
QY 61 GTGTAAATAATTCAGCTGAGAACAGACTGCTCCCTCCCGAGTTTCATTTGAAATGAC 120
Db 201 GTGTAAATAATTCAGCTGAGAACAGACTGCTCCCTCCCGAGTTTCATTTGAAATGAC 260
QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 180
Db 261 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 320
QY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCGCTCTGCGGGTACAGTCTT 240
Db 321 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCGCTCTGCGGGTACAGTCTT 380
QY 241 CTGCTCCCGAGGAAAGTGAATCAGTTGATGATGATGATGATGATGATGATGATGAT 300
Db 381 CTGCTCCCGAGGAAAGTGAATCAGTTGATGATGATGATGATGATGATGATGATGAT 440
QY 301 CCGGCCAAGGCCCAAGAAAGGGAAGTTCGCTCGGCGCTCAGGCCAGGGCTCCGAC 360
Db 441 CCGGCCAAGGCCCAAGAAAGGGAAGTTCGCTCGGCGCTCAGGCCAGGGCTCCGAC 500
QY 361 CACCATCTCTGTCTCAAAATTTAGCCCTCTCTCGGACACACTGCTGAAGAGATG 420
Db 501 CACCATCTCTGTCTCAAAATTTAGCCCTCTCTCGGACACACTGCTGAAGAGATG 560
QY 421 CACCCCTCTCTGTCTCAAAATTTAGCCCTCTCTCGGACACACTGCTGAAGAGATG 480
Db 561 CACCCCTCTCTGTCTCAAAATTTAGCCCTCTCTCGGACACACTGCTGAAGAGATG 620
QY 481 GTTCTCTGCGGTCTCTTTTATTTCTGAGTGAAGAGCGGAGTCCGTCTCTTTTGT 540
Db 621 GTTCTCTGCGGTCTCTTTTATTTCTGAGTGAAGAGCGGAGTCCGTCTCTTTTGT 680
QY 541 CCTGTGCAAAATTAAGAGAGTGGTAAAGATCTCTGAATTAATTCAGCTGACTGAT 600
Db 681 CCTGTGCAAAATTAAGAGAGTGGTAAAGATCTCTGAATTAATTCAGCTGACTGAT 740
QY 601 TTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 741 TTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 800
QY 661 CCGAGTCAAGGCGGAGGCTGAGAGTCAAGTCTTGAAGTCACTGAGGTGGCATCTGCC 720
Db 801 CCGAGTCAAGGCGGAGGCTGAGAGTCAAGTCTTGAAGTCACTGAGGTGGCATCTGCC 860
QY 721 TTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db 861 TTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 920
QY 781 GTGAGAGTGAATTTTCTTGAAGGCTGAGAGGCGCAATTCCTCAAGGCTCCCTGCTTG 840
Db 921 GTGAGAGTGAATTTTCTTGAAGGCTGAGAGGCGCAATTCCTCAAGGCTCCCTGCTTG 980
QY 841 ACATTCAAATCTCATGCTCTGAGAAACATTTCTGACAGCAAGATTTGGCTGGTTCGCGC 900
Db 981 ACATTCAAATCTCATGCTCTGAGAAACATTTCTGACAGCAAGATTTGGCTGGTTCGCGC 1040
QY 901 CTGAGTGTGGGCTCTAGTGAATCTGAGACATCAATGATGATGATGATGATGATGATGAT 960
Db 1041 CTGAGTGTGGGCTCTAGTGAATCTGAGACATCAATGATGATGATGATGATGATGATGAT 1100
QY 961 CCGTCTGAAGAAATGCTTGAAGAAATCTTCTGATGATGATGATGATGATGATGATGAT 1020
Db 1101 CCGTCTGAAGAAATGCTTGAAGAAATCTTCTGATGATGATGATGATGATGATGATGAT 1160
QY 1021 ACGGCAAGAGCAAGGCGGCTGACAAAGCGGCGCTGTGCGTGTGAGAGTGGCATGTA 1080
Db 1161 ACGGCAAGAGCAAGGCGGCTGACAAAGCGGCGCTGTGCGTGTGAGAGTGGCATGTA 1220
QY 1081 CCGGCAAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db 1221 CCGGCAAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1279

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QY 1141 ACGAACCACCGCGAATCTGTGAGAGACACCGTGTACAGAGAGGAGGTTGATACCGAG 1200
Db 1280 ACGAACCACCGCGAATCTGTGAGAGACACCGTGTACAGAGAGGAGGTTGATACCGAG 1339
QY 1201 CTGAGGTAGAAAAACGTCCTCGAAGAGGAGAGAGATCATGTAGCCCGCGAAGTAGAGAC 1260
Db 1340 CTGAGGTAGAAAAACGTCCTCGAAGAGGAGAGAGATCATGTAGCCCGCGAAGTAGAGAC 1399
QY 1261 CTGCTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db 1400 CTGCTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1459
QY 1321 CAGCATACGGCAATGTCAACAATATGAGCCCTGAGGAGACAGACAGAGAGAGAGAGAC 1380
Db 1460 CAGCATACGGCAATGTCAACAATATGAGCCCTGAGGAGACAGACAGAGAGAGAGAGAC 1519
QY 1381 AGAGA 1385
Db 1520 AGAGA 1524

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RESULT 35
US-10-216-160-15
; Sequence 15, Application us/10216160
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Geriltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Malanbe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C8
; CURRENT APPLICATION NUMBER: US/10/216,160
; CURRENT FILING DATE: 2002-08-09
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-216-160-15

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Query Match 78.1%; Score 1264; DB 42; Length 1524;
Best Local Similarity 99.9%; Pred. No. 9, 6e-234;
Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGCACATTTTGGCGGATTGTTCTTCCAGGCTTTGCGGTGCAATTCAGTGTACCA 60
Db 141 GGCACATTTTGGCGGATTGTTCTTCCAGGCTTTGCGGTGCAATTCAGTGTACCA 200
QY 61 GTGTGAAGATTCAGAGTGAAGAACAGACTGCTCTCCCGAGTTTCATTTGAAATGAC 120
Db 201 GTGTGAAGATTCAGAGTGAAGAACAGACTGCTCTCCCGAGTTTCATTTGAAATGAC 260
QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 180
Db 261 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 320
QY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCGCTCTGCGGGTACAGTCTT 240
Db 321 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCGCTCTGCGGGTACAGTCTT 380
QY 241 CTGCTCCCGAGGAAAGTGAATCAGTTGATGATGATGATGATGATGATGATGATGAT 300
Db 381 CTGCTCCCGAGGAAAGTGAATCAGTTGATGATGATGATGATGATGATGATGATGAT 440

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|||||
Db 201 GTGTGAAGATTCAGAGTGAACAGACGCTGCTCCCGGAGTTCAATTGAAATGAC 260
Oy 121 GGTGAACGTTCAAGACATGTGTGAGAAAGATGATGAGAGCAATGCGGGATATGTA 180
Db 261 GGTGAACGTTCAAGACATGTGTGAGAAAGATGATGAGAGCAATGCGGGATATGTA 320
Oy 181 CGCAAGTCTGTGATCATCAGCGCGCTGTCTCATCGCCTTGGCGGGTACAGTCTT 240
Db 321 CGCAAGTCTGTGATCATCAGCGCGCTGTCTCATCGCCTTGGCGGGTACAGTCTT 380
Oy 241 CTGCTTCCAGGGAATGAACTCACTGTTGATCACTGCTGCAACACCCCTTTTGA 300
Db 381 CTGCTTCCAGGGAATGAACTCACTGTTGATCACTGCTGCAACACCCCTTTTGA 440
Oy 301 CGGGCCAAAGGGCCAAAGAAAGGGAAGTTCTGCGCGCCCTGAGGCGAGGCTCCGAC 360
Db 441 CGGGCCAAAGGGCCAAAGAAAGGGAAGTTCTGCGCGCCCTGAGGCGAGGCTCCGAC 500
Oy 361 CACCATCTCTGTTCTCAAAATTAAGCCCTCTTCTGCGCACACTGCTGAGCTGAGAGATG 420
Db 501 CACCATCTCTGTTCTCAAAATTAAGCCCTCTTCTGCGCACACTGCTGAGCTGAGAGATG 560
Oy 421 CCACCCCTCTGATGTTGTTCTTCCAGCCCTGCGCCCAACCCCGACCTCCCTGATGA 480
Db 561 CCACCCCTCTGATGTTGTTCTTCCAGCCCTGCGCCCAACCCCGACCTCCCTGATGA 620
Oy 481 GTTCTCTGCGGTGCTTTTATCTGGGTAGGAGCGGGATCCGTGTCTTTTGT 540
Db 621 GTTCTCTGCGGTGCTTTTATCTGGGTAGGAGCGGGATCCGTGTCTTTTGT 680
Oy 541 CCTGTGCAATATGAAAGAGCTCGTAAAGCATCTGATTAATTAATTCAGCTGATGAT 600
Db 681 CCTGTGCAATATGAAAGAGCTCGTAAAGCATCTGATTAATTAATTCAGCTGATGAT 740
Oy 601 TTTTCAATATGTTGAAGAGAGAGGTGAGTGAAGTTCAACCCCATGTCTGTATAC 660
Db 741 TTTTCAATATGTTGAAGAGAGAGGTGAGTGAAGTTCAACCCCATGTCTGTATAC 800
Oy 661 CGAGAGTCAAGGCGAGGCTGGAGAGTCACTCTTGAAGTCACTGAGGCGCATCTGCC 720
Db 801 CGAGAGTCAAGGCGAGGCTGGAGAGTCACTCTTGAAGTCACTGAGGCGCATCTGCC 860
Oy 721 TTTTGAAGAGCTTCCATGTCATTCATCCCTGATGGGGCATATGTTGAGATGACGA 780
Db 861 TTTTGAAGAGCTTCCATGTCATTCATCCCTGATGGGGCATATGTTGAGATGACGA 920
Oy 781 GTGAGAGTACCTTTTCTTGAAGGCTGAGGCGCACTTCCCACTCAAGGCTCCCTGCTTG 840
Db 921 GTGAGAGTACCTTTTCTTGAAGGCTGAGGCGCACTTCCCACTCAAGGCTCCCTGCTTG 980
Oy 841 ACATTCAAACTTCATGCTGCTGAAAAACATCTCTGACAGCAGATTTGGTGTGGGCG 900
Db 981 ACATTCAAACTTCATGCTGCTGAAAAACATCTCTGACAGCAGATTTGGTGTGGGCG 1040
Oy 901 CTGAGTTGGGCTCTAGTGACTGAGAGTCAATGACTGGGACTTGAAGTGGGGCTGGGCT 960
Db 1041 CTGAGTTGGGCTCTAGTGACTGAGAGTCAATGACTGGGACTTGAAGTGGGGCTGGGCT 1100
Oy 961 CGCTCTGAAAATGCTTGAAGAAATCTTCTCAAGTTCTCTTGAAGAGACTGGGCGGG 1020
Db 1101 CGCTCTGAAAATGCTTGAAGAAATCTTCTCAAGTTCTCTTGAAGAGACTGGGCGGG 1160
Oy 1021 ACAGCAAGAGCAAGGCGCTGACAAAGCGGCGCTGCGGTGGTGGAGTGCAGATGTA 1080
Db 1161 ACAGCAAGAGCAAGGCGCTGACAAAGCGGCGCTGCGGTGGTGGAGTGCAGATGTA 1220
Oy 1081 CGGCAAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db 1221 CGGCAAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1279
Oy 1141 AGCAACACCGCGCAAACTGCTGCGAGAGCAGCTGTACAGAGCGGCTGATGACCGAG 1200
|||||

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Db 1280 AGCAACACCGCGCAAACTGCTGAGAGACACCGTGTACAGAGCGGGTGTATGACCGAG 1339
Oy 1201 CTGAGTAGAAGAAACGCTCCGAGAAAGGAGAGATCTATGACCCCGAGTAGAGAC 1260
Db 1340 CTGAGTAGAAGAAACGCTCCGAGAAAGGAGAGATCTATGACCCCGAGTAGAGAC 1399
Oy 1261 CTGCTCAGTCTGCTTGGGTTTGGCGCGCAGCCATGATCTCCGAAATCTGTTGGGCATC 1320
Db 1400 CTGCTCAGTCTGCTTGGGTTTGGCGCGCAGCCATGATCTCCGAAATCTGTTGGGCATC 1459
Oy 1321 CAGCATACGGCCATGTACACAAATCAGCCCTGGGCGACAGCAGAGAGAGAGAC 1380
Db 1460 CAGCATACGGCCATGTACACAAATCAGCCCTGGGCGACAGCAGAGAGAGAGAGAC 1519
Oy 1381 AGAGA 1385
Db 1520 AGAGA 1524

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RESULT 34
US-10-216-159A-15
; Sequence 15, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P16
; CURRENT APPLICATION NUMBER: US/10/216,159A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-159A-15
Query Match 78.1%; Score 1264; DB 42; Length 1524;
Best Local Similarity 99.9%; Pred. No. 9,6e-234;
Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Oy 1 GGCACATTTTGGCGGATGTTCTTCTTCCAGGCTTGGCCTGCAAAATCCAGTGTACCA 60
|||||

```

Query Match 80.2%; Score 1299; DB 31; Length 1917;
 Best Local Similarity 99.8%; Pred. No. 1.7e-240;
 Matches 1519; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```

QY 79 GAACAACGACTGCTCCCTCCCGAGTTCATTTGTAATTCACGAGTGAACGTTCAAGACAT 138
    |||
Db 373 GAACAACGACTGCTCCCTCCCGAGTTCATTTGTAATTCACGAGTGAACGTTCAAGACAT 432
QY 139 GTGTGAGAAGAAGTGAAGAGACAAAGTCCGGGATCATATCCCAAGTCTCTGATC 198
    |||
Db 433 GTGTGAGAAGAAGTGAAGAGACAAAGTCCGGGATCATATCCCAAGTCTCTGATC 492
QY 199 ATCAGGGGCTGCTCATAGCTGCTGCGGGATCAGTCTCTGCTCCGAGGAAACT 258
    |||
Db 493 ATCAGGGGCTGCTCATAGCTGCTGCGGGATCAGTCTCTGCTCCGAGGAAACT 552
QY 259 GAATCTAGTTTCATCAGTCTGCTGCAACACCCCTTTTGTAAAGGGCCAAAGCCCAAGAA 318
    |||
Db 553 GAATCTAGTTTCATCAGTCTGCTGCAACACCCCTTTTGTAAAGGGCCCAAGAA 612
QY 319 AAGGGGAATTCGCTGCGCTGCGGCTCAGGGCCAGGGCTCCGACACCATCTGTTCTGAA 378
    |||
Db 613 AAGGGGAATTCGCTGCGCTGCGGCTCAGGGCCAGGGCTCCGACACCATCTGTTCTGAA 672
QY 379 ATTTAGCCCTCTTCTGCGACACTGCTGAAGCTGAAGAGATCCACCCCTCTGATG 438
    |||
Db 673 ATTTAGCCCTCTTCTGCGACACTGCTGAAGCTGAAGAGATCCACCCCTCTGATG 732
QY 439 TTCTTCACAGCCCTGCGCCCAACCCCAACCTCCTGAGTGAATTTCTTGGGTGCT 498
    |||
Db 733 TTCTTCACAGCCCTGCGCCCAACCCCAACCTCCTGAGTGAATTTCTTGGGTGCT 792
QY 499 TTTATTTCTGGGTGAGGAGGCGGATCGGTCTCTTTGTCTCTGCTCAATAATATGAA 558
    |||
Db 793 TTTATTTCTGGGTGAGGAGGCGGATCGGTCTCTTTGTCTCTGCTCAATAATATGAA 852
QY 559 GAGCTCGTAAGACATTTGTAATTAATTCAGCTGACTGAATTTTCAATATGACTTGA 618
    |||
Db 853 GAGCTCGTAAGACATTTGTAATTAATTCAGCTGACTGAATTTTCAATATGACTTGA 912
QY 619 GGAAGAGAGTGAAGTGAAGTTCACCCCATGTCGTGTAAACCGAGTCAAGGGCAGCT 678
    |||
Db 913 GGAAGAGAGTGAAGTGAAGTTCACCCCATGTCGTGTAAACCGAGTCAAGGGCAGCT 972
QY 679 GGCAGAGTCACTCTTAAGAGTCACTGAGTGGGATCTGCCCTTTTGTAAAGCCCTCAGT 738
    |||
Db 973 GGCAGAGTCACTCTTAAGAGTCACTGAGTGGGATCTGCCCTTTTGTAAAGCCCTCAGT 1032
QY 739 GTCCATTTCCATCCCTGATGGGGGATAGTTTGAAGTCAAGAGTGAAGTGGTTC 798
    |||
Db 1033 GTCCATTTCCATCCCTGATGGGGGATAGTTTGAAGTCAAGAGTGAAGTGGTTC 1092
QY 799 TAGGGCTGAGGGGAGTTCCTCCTCACTCAAGGCTCCCTGCTTGAATTCAAATTCATCT 858
    |||
Db 1093 TAGGGCTGAGGGGAGTTCCTCCTCACTCAAGGCTCCCTGCTTGAATTCAAATTCATCT 1152
QY 859 CCTGAAACCATTTCTCTGACAGAGAAATGGCTGGTTTGGCGCTGAGTTGGGCTATGTG 918
    |||
Db 1153 CCTGAAACCATTTCTCTGACAGAGAAATGGCTGGTTTGGCGCTGAGTTGGGCTATGTG 1212
QY 919 ACTGAGACTCAATGACTGAGTGAAGTGGGCTGCGGCTCGCTGAAAGTGGCTTA 978
    |||
Db 1213 ACTGAGACTCAATGACTGAGTGAAGTGGGCTGCGGCTCGCTGAAAGTGGCTTA 1272
QY 979 AGAAATATCTTCTCAGTTCCTTCTGACAGAGTGGCGCGGAGCCGGAAGCAAGCGGC 1038
    |||
Db 1273 AGAAATATCTTCTCAGTTCCTTCTGACAGAGTGGCGCGGAGCCGGAAGCAAGCGGC 1332
QY 1039 GCTGCACAAAGCGGCGCTGCTGGTGGTGGAGTGGCATGTACGGCAGCGGCTTCTGCT 1098
    |||
Db 1333 GCTGCACAAAGCGGCGCTGCTGGTGGTGGAGTGGCATGTACGGCAGCGGCTTCTGCT 1392
  
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QY 1099 GGTGGCGGTGCTGACGAGACAGCGGCGAGCAGACACTTTCAGCAACACCCGCGAAAC 1158
    |||
Db 1393 GGTGGCGGTGCTGACGAGACAGCGGCGAGCAGACACTTTCAGCAACACCCGCGAAAC 1451
QY 1159 TGTGCGAGGACACCGGTGACAGAGCGGGGTGATGACGAGTGAAGTGAAGAAACGTC 1218
    |||
Db 1452 TGTGCGAGGACACCGGTGACAGAGCGGGGTGATGACGAGTGAAGTGAAGAAACGTC 1511
QY 1219 TCCGAGAAGGGGAGAGATCATGTACGGCGGAGTGAAGAGCTCGTCCAGTGGCTTG 1278
    |||
Db 1512 TCCGAGAAGGGGAGAGATCATGTACGGCGGAGTGAAGAGCTCGTCCAGTGGCTTG 1571
QY 1279 GGTGGCGCGGACGATGATCTCCGAATCTGTTGGGTCATCCAGCATACGGCCAAATGTC 1338
    |||
Db 1572 GGTGGCGCGGACGATGATCTCCGAATCTGTTGGGTCATCCAGCATACGGCCAAATGTC 1631
QY 1339 ACAACATCAGCCCTGGGCGACACGACGAGAGGAGAGACAGAGAAAGAAACACA 1398
    |||
Db 1632 ACAACATCAGCCCTGGGCGACACGACGAGAGGAGAGACAGAGAAAGAAACACA 1691
QY 1399 GCATGAGACACAGTAAATGATTAACATTAATTAATTAATTAATTAATTAATTAAT 1458
    |||
Db 1692 GCATGAGACACAGTAAATGATTAACATTAATTAATTAATTAATTAATTAATTAAT 1751
QY 1459 ACTGCGCAGGAATGTACCAATTTTCAAGTGTGACTTGAAGCTTCTTTGCGACAA 1518
    |||
Db 1752 ACTGCGCAGGAATGTACCAATTTTCAAGTGTGACTTGAAGCTTCTTTGCGACAA 1811
QY 1519 GCAAGAGAGATTTAACAAGTTCCTCAACCCGGGGAGTGGCTGTGTTAAAGAAAGAC 1578
    |||
Db 1812 GCAAGAGAGATTTAACAAGTTCCTCAACCCGGGGAGTGGCTGTGTTAAAGAAAGAC 1871
QY 1579 ATTAATGCTTTAGACAGTGA 1600
    |||
Db 1872 ATTAATGCTTTAGACAGTGA 1893
  
```

RESULT 33

US-10-119-480-15

Sequence 15, Application US/10119480

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.

TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE OR INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3530P1C1

CURRENT APPLICATION NUMBER: US/10/119,480

CURRENT FILING DATE: 2002-04-09

NUMBER OF SEQ ID NOS: 246

Prior Application removed - See file wrapper or Palm

SEQ ID NO 15

LENGTH: 1524

TYPE: DNA

ORGANISM: Homo Sapien

US-10-119-480-15

Query Match 78.1%; Score 1264; DB 40; Length 1524;

Best Local Similarity 99.9%; Pred. No. 9.6e-234;

Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

QY 1 GGCACATTTTGGCGGATTTGTTTCTTCCAGGCTTTCGCTGCAATTCAGTGTACCA 60
    |||
Db 141 GGCACATTTTGGCGGATTTGTTTCTTCCAGGCTTTCGCTGCAATTCAGTGTACCA 200
QY 61 GTGTGAAGAATTCAGCTGAACAACGACTGCTCCTCCCGGAGTTCATTTGTGAATTGCA 120
  
```



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; TITLE OF INVENTION: THERAPY
; FILE REFERENCE: 1600.1170-001
; CURRENT APPLICATION NUMBER: US/09/652.917
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,422
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 3855
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2477
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-652-917-2477

Query Match      80.2%  Score 1299; DB 25; Length 1917;
Best Local Similarity 99.8%; Pred. No. 1,76-240;
Matches 1519; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 79 GAACAAAGCAGCTGCTCTCCGAGTTCATTTGTAATGCAAGGTGAACGTTCAAGACAT 138
    |||||||
DB 373 GAAACAAAGCAGCTGCTCTCCGAGTTCATTTGTAATGCAAGGTGAACGTTCAAGACAT 432
QY 139 GTGTGAGAAAGATGATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATC 198
    |||||||
DB 433 GTGTGAGAAAGATGATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATC 492
QY 199 ATCAGCGGCTGTCTCATCGCTCTCCGAGTTCATTTGTAATGCAAGGTGAACGTTCAAGACAT 258
    |||||||
DB 493 ATCAGCGGCTGTCTCATCGCTCTCCGAGTTCATTTGTAATGCAAGGTGAACGTTCAAGACAT 552
QY 259 GAACATCAGTTTGCATCAGTGTGCAACACCCCTTTTGTAAAGGCGCAAGGCGCAAGAA 318
    |||||||
DB 553 GAACATCAGTTTGCATCAGTGTGCAACACCCCTTTTGTAAAGGCGCAAGGCGCAAGAA 612
QY 319 AAGGGAGATTTGCTGCTGCGCCCTCAGGCGAGGCTCCGACACCAATCTGTTCTTCAA 378
    |||||||
DB 613 AAGGGAGATTTGCTGCTGCGCCCTCAGGCGAGGCTCCGACACCAATCTGTTCTTCAA 672
QY 379 ATTAGGCTCTTCTGGGACATGCTGGAAGGAGAGATGCCACCCCTCTGCTGATTTG 438
    |||||||
DB 673 ATTAGGCTCTTCTGGGACATGCTGGAAGGAGAGATGCCACCCCTCTGCTGATTTG 732
QY 439 TTCTTTCACGCTCTGCGCCCAACCCCACTCCCTGATGAGTTCTTCTGCTGCTGCT 498
    |||||||
DB 733 TTCTTTCACGCTCTGCGCCCAACCCCACTCCCTGATGAGTTCTTCTGCTGCTGCT 792
QY 499 TTTATTTCTGGGATGAGGAGCGGAGTCCGTTCTTTTGTGTTCTGCTGCAAAATTAAGAA 558
    |||||||
DB 793 TTTATTTCTGGGATGAGGAGCGGAGTCCGTTCTTTTGTGTTCTGCTGCAAAATTAAGAA 852
QY 559 GAGCTCGGTAAGGATTTGAATTAATTCAGCTGACGTAATTTTCAGTATGATGAA 618
    |||||||
DB 853 GAGCTCGGTAAGGATTTGAATTAATTCAGCTGACGTAATTTTCAGTATGATGAA 912
QY 619 GGAAGAGGTGAGAGTGAAGTTTCAACCCCATGCTGTGTACCCGAGATCAAGGCGAGCT 678
    |||||||
DB 913 GGAAGAGGTGAGAGTGAAGTTTCAACCCCATGCTGTGTACCCGAGATCAAGGCGAGCT 972
QY 679 GGAAGAGTCACTCTTGAAGTCACTGAGGTGGGATCTGCTTTTGTAAAGCTTCAAT 738
    |||||||
DB 973 GGAAGAGTCACTCTTGAAGTCACTGAGGTGGGATCTGCTTTTGTAAAGCTTCAAT 1032
QY 739 GTCCATTTCCATCCCTGANTGGGGGAGTATGTTGAGTGTGAGAGTGAAGTGAAGTCTTCT 798
    |||||||
DB 1033 GTCCATTTCCATCCCTGANTGGGGGAGTATGTTGAGTGTGAGAGTGAAGTGAAGTCTTCT 1092
QY 799 TAGGGCTGAGGGGCGAGTTCCACTCAAGGCTCCCTGCTTGAATTAAGTCTGCT 858
    |||||||
DB 1093 TAGGGCTGAGGGGCGAGTTCCACTCAAGGCTCCCTGCTTGAATTAAGTCTGCT 1152
QY 859 CCGTGAAGAACATTTCTGCGAGAGAAATTTGGCTGTTTCCGGCTGAGTGGGCTGAGTG 918
    |||||||
DB 1153 CCGTGAAGAACATTTCTGCGAGAGAAATTTGGCTGTTTCCGGCTGAGTGGGCTGAGTG 1212

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QY 919 ACTGAGACTCAATGACTGGGACTTAGACTGGGGCTCGGCTCTGCTGTAAGTGTCTTA 978
    |||||||
DB 1213 ACTGAGACTCAATGACTGGGACTTAGACTGGGGCTCGGCTCTGCTGTAAGTGTCTTA 1272
QY 979 AGAAATCTTCTCAGTTCCTTTCAGAGAGTGGGCGGAGCGGAGAGCAACGAGGCT 1038
    |||||||
DB 1273 AGAAATCTTCTCAGTTCCTTTCAGAGAGTGGGCGGAGCGGAGAGCAACGAGGCT 1332
QY 1039 GCTGACAAAGCGGGGCTGTGGTGTGGAGTGGGCTGATGAGCGGAGGCTTCTGCT 1098
    |||||||
DB 1333 GCTGACAAAGCGGGGCTGTGGTGTGGAGTGGGCTGATGAGCGGAGGCTTCTGCT 1392
QY 1099 GGTGGGCTGCTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1158
    |||||||
DB 1393 GGTGGGCTGCTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1451
QY 1159 TGCTGCGAGGACACCGTGTACAGAGGCGGTTGATGACCGAGCTGAGTGAAGAAACGTC 1218
    |||||||
DB 1452 TGCTGCGAGGACACCGTGTACAGAGGCGGTTGATGACCGAGCTGAGTGAAGAAACGTC 1511
QY 1219 TCCGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1278
    |||||||
DB 1512 TCCGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1571
QY 1279 GGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1338
    |||||||
DB 1572 GGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1631
QY 1339 ACANCAATCAGCCCTGGGAGACAGACAGACAGAGAGGAGAGACAGAGAGAGAGAGAGAG 1398
    |||||||
DB 1632 ACANCAATCAGCCCTGGGAGACAGACAGACAGAGAGGAGAGAGAGAGAGAGAGAGAGAG 1691
QY 1399 GCATGAGACAGTAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1458
    |||||||
DB 1692 GCATGAGACAGTAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1751
QY 1459 ACTGGCCAGGAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1518
    |||||||
DB 1752 ACTGGCCAGGAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1811
QY 1519 GCAAGAGAGATTTTAACTGTTTCAAAACCCGGGGAGTGGCTGTGTTTAAAGAAAGACC 1578
    |||||||
DB 1812 GCAAGAGAGATTTTAACTGTTTCAAAACCCGGGGAGTGGCTGTGTTTAAAGAAAGACC 1871
QY 1579 ATTAATGCTTTAGCAGTGTGA 1600
    |||||||
DB 1872 ATTAATGCTTTAGCAGTGTGA 1893

```

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RESULT 32
US-09-801-833-7188
; Sequence 7188, Application us/09801833
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, M. Alexandra
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: 1600.1037-005
; CURRENT APPLICATION NUMBER: US/09/801.833
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 09/371,168
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/095,907
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/103,145
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 8285
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7188
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-833-7188

```


OY	1039	GCTGCACAAAGCGGGCGGTGTCGGTGGAGATGCCATATGTACGCCAGCGCCTCTTGCT	1098
Db	1333	GCTGCACAAGGGGGCGGTGTGCGGTGTGAAGTAGTCCGATGTATACGGCAGCGCCTCTTGCT	1392
OY	1099	GGGTTGGCGTGTGTACAGCCACAGGGGGGAGCACAGCACTTTCGACGAAACACCCCGCGAACC	1158
Db	1393	GGTGGCGGTGCTGCACGACGCGACAGGGCGGCACAGCACAGCAC-TCACAGCAACCCGCGGAAC	1451
OY	1159	TGCTCGAGAGCAACCGTGTACAGAGGCGGGTTGATGACGAGCTGAGTAGTAAGAAAAGCTC	1218
Db	1452	TGCTCGAGAGCAACCGTGTACAGAGGCGGGTTGATGACCGAGCTGAGTAGTAAGAAAAGCTC	1511
OY	1219	TCCGAGAAGGGGAGGAGAGCATATGTACGCCCGGAATAGAGACTCTGTCCAGTGTGCTTGG	1278
Db	1512	TCCGAGAAGGGGAGGAGATCATGTATACGCCCGGAATAGAGACTCTGTCCAGTGTGCTTGG	1571
OY	1279	GGTWTGGCCGACGCCATGATCTCCGAATGTGTTGGGCATCCACATATACGGCCAAATGC	1338
Db	1572	GTTTTGGCCGACGCATGATCTCTCCAGTCTGTTTGGCATCCACATATACGGCCAAATGCTC	1631
OY	1339	ACMACATCAGCCCTTGGGCGACAGCAGCAGNAGGAGAGACAGAGAAAAAGAAAAACACA	1398
Db	1632	ACAACATCAGCCCTTGGGCGACAGCAGCAGNAGGAGAGACAGAGAAAAAGAAAAACACA	1681
OY	1399	GCATGAGAAACAGCTAATAATTAATAAACCATATAATATTATAGCCCTGTGTTGTGCTT	1458
Db	1692	GCATGAGAAACAGCTAATAATAATAAACCATATAATATTATAGCCCTGTGTTGTGCTT	1751
OY	1459	ACTGGCCAGGAAATGTAACCAATTTTTCAGTGTGTGAGCTTGACAGCTTCTTTTCCCAA	1518
Db	1752	ACTGGCCAGGAAATGTAACCAATTTTTCAGTGTGTGAGCTTGACAGCTTCTTTTCCCAA	1811
OY	1519	GCAAGAGAGATTTAAACACTGTTCAAAACCCGCGGGAGTGGCTGTGTTAAAGAAAGAC	1578
Db	1812	GCAAGAGAGATTTAAACACTGTTCAAAACCCGCGGGAGTGGCTGTGTTAAAGAAAGAC	1871
OY	1579	ATTAAATGCTTTAGACAGTGA 1600	
Db	1872	ATTAAATGCTTTAGACAGTGA 1893	

```

RESULT 28
US-09-652-128-7518
: Sequence 7518 Application US/09652128
: GENERAL INFORMATION:
: APPLICANT: Shyjan, Andrew W.
: APPLICANT: Holcman, Douglas A.
: TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
: TITLE OR INVENTION: THEREFOR
: FILE REFERENCE: 1600,1171-001
: CURRENT APPLICATION NUMBER: US/09/652,128
: CURRENT FILING DATE: 2000-08-30
: PRIOR APPLICATION NUMBER: 60/151,133
: PRIOR FILING DATE: 1999-08-30
: NUMBER OF SEQ ID NOS: 10265
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 7518
: LENGTH: 1917
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-652-128-7518

```

Query Match	80.2%	Score 1299;	DB 25;	Length 1917;
Best Local Similarity	99.8%	Pred. No. 1.7e-240;		
Matches 1519;	Conservative	0;	Mismatches 2;	Indels 1; Gaps 1
QY 79	GACACGACTGCTCCTCCCGACATTCATTGTGATTGCACGGGTGAACGTTCAAGCAT	138		
Db 373	GACACACGACTGCTCCTCCCGACATTCATTGTGATTGCACGGGTGAACGTTCAAGCAT	432		
QY 139	GTGTCAAGAAGAGTGTGGACCAAGTCCCGGATTCATGTACCGCAAGTCGTGTGCATC	198		

Db	433	GTGTCAGAAAAGTAATGATGAGCAAAAGTCCGGGATCATGTACCCCAAGTCTGTGCATC	492
QY	139	ATCAGCGGCTGTCTCATGCCCTCTCCGGGATACAGTCCCTTCTGCTCCCGAGGAAACT	258
Db	493	ATCAGCGGCTGTCTCATGCCCTCTCCGGGATACAGTCCCTTCTGCTCCCGAGGAAACT	552
QY	259	GAATCTCATGTTGCATCAGTGCCTGCAACACCCCTCTTGTAAAGGGGCCAAGGCCAAGAA	318
Db	553	GAATCTCATGTTGCATCAGTGCCTGCAACACCCCTCTTGTAAAGGGGCCAAGGCCAAGAA	612
QY	319	AAGGGGAAGTTCTGCTCGGCCCCAGGCCAGGGCTCCGACACACATCTGTTCTCA	378
Db	613	AAGGGGAAGTTCTGCTCGGCCCCAGGCCAGGGCTCCGACACACATCTGTTCTCA	672
QY	379	ATTGAGCCCTTCTCGGCACTGCTGGAAGCGTGAAGAGATGCCACCCCTCTGCATTTG	438
Db	673	ATTGAGCCCTTCTCGGCACTGCTGGAAGCGTGAAGAGATGCCACCCCTCTGCATTTG	732
QY	439	TTCCTCCAGCCCTCGCCCCAACCCCCACACTCCCTGATGATGTTCTTCTGGGTGCT	498
Db	733	TTCCTCCAGCCCTCGCCCCAACCCCCACACTCCCTGATGATGTTCTTCTGGGTGCT	792
QY	499	TTTATTCTGGGTGAGGAGGGGAGTCCGTGTTCTCTTTGTCTGTGCATAATATGAAA	558
Db	793	TTTATTCTGGGTGAGGAGGGGAGTCCGTGTTCTCTTTGTCTGTGCATAATATGAAA	852
QY	559	GACCTCGGTAAGACATCTGATAAATTCACGCTGACGTAATTTTCATGTTACTGAA	618
Db	853	GACCTCGGTAAGACATCTGATAAATTCACGCTGACGTAATTTTCATGTTACTGAA	912
QY	619	GGAAGAGGTGGAGTGAAGAAATGCACCCCACTGTCTGTGTAAACGGAGTCAAGGCCAGCT	678
Db	913	GGAAGAGGTGGAGTGAAGAAATGCACCCCACTGTGTGTAAACGGAGTCAAGGCCAGCT	972
QY	679	GGCAGAGTCAGTCCCTTAAGAGTCACTAGAGTGGGCACTCCTTTTGTAAAGCTCACT	738
Db	973	GGCAGAGTCAGTCCCTTAAGAGTCACTAGAGTGGGCACTCCTTTTGTAAAGCTCACT	1032
QY	739	GTCCATTCCTCATCCCTGATGAGGGGCATAGTTTGAGACTGCAGAAGTGAAGTGAAGTTTCT	798
Db	1033	GTCCATTCCTCATCCCTGATGAGGGGCATAGTTTGAGACTGCAGAAGTGAAGTGAAGTTTCT	1092
QY	799	TAGGGCTGAGGGGCACTGTTCCACTCAAGGCTCCCTCGCTGACATTCAACTCATGCT	858
Db	1093	TAGGGCTGAGGGGCACTGTTCCACTCAAGGCTCCCTCGCTGACATTCAACTCATGCT	1152
QY	859	CCTGAAAACCATTTCTCTGACAGCAAGATTTGCGCTGGCGCTGAGTTGGGCTCTAGTG	918
Db	1153	CCTGAAAACCATTTCTCTGACAGCAAGATTTGCGCTGGCGCTGAGTTGGGCTCTAGTG	1212
QY	919	ACTCAGACTCAATGACATGGGACTTAACTAGGGGGCTCGGCTCGCTCTGAAAAGTCTTA	978
Db	1213	ACTCAGACTCAATGACATGGGACTTAACTAGGGGGCTCGGCTCGCTCTGAAAAGTCTTA	1272
QY	979	AGAAATCTTCTCAGTTCTCCTTGCAGAGGACTGCGCCGGGACGCAAGACCAACGGGC	1038
Db	1273	AGAAATCTTCTCAGTTCTCCTTGCAGAGGACTGCGCCGGGACGCAAGACCAACGGGC	1332
QY	1039	GCTGCACAAACCGGGGCTGTGGTGGTGGTGAAGTGGCCATGTACGGCAGCGCTTCTGCT	1098
Db	1333	GCTGCACAAACCGGGGCTGTGGTGGTGGTGAAGTGGCCATGTACGGCAGCGCTTCTGCT	1392
QY	1099	GATTGGCGTGTGTGACGACAGGCGGCACACAGCACTTGCACGAACACCGCGCGAAG	1158
Db	1393	GATTGGCGTGTGTGACGACAGGCGGCACACAGCACTTGCACGAACACCGCGCGAAG	1452
QY	1159	TGTCGACAGACACCGGTGTACAGAGACGGGTTGATGACCGAGCTGAGGTAGAAAAAGCT	1218
Db	1452	TGTCGACAGACACCGGTGTACAGAGACGGGTTGATGACCGAGCTGAGGTAGAAAAAGCT	1512
QY	1219	TCCGAGAAAGGGAGAGAGATCATGTACGCCCGGAGTATGAGACCTGTCACATGCTGCTTG	1278
Db	1512	TCCGAGAAAGGGAGAGAGATCATGTACGCCCGGAGTATGAGACCTGTCACATGCTGCTTG	1572

Db	1033	GTCCATTCATCCCTCAGTAGGGGGCATATATTGGACACTGCAGAGTGAAGAGTGGACGTTTCT	1092
Qy	799	TAGGGCTGAGGGGCCAGTTCCCACTCAAGGCTCCCTGCCTTGACATTCAAATTCATGCT	858
Db	1093	TAGGGCTGAGGGGCCAGTTCCCACTCAAGGCTCCCTGCCTTGACATTCAAATTCATGCT	1152
Qy	859	CTGGAACCAATTCCTCGAGAGAAATGGCGGTTTGGCGCCGAGTTGAGGCTCAGTG	918
Db	1153	CTGGAACCAATTCCTCGAGAGAAATGGCGGTTTGGCGCCGAGTTGAGGCTCAGTG	1212
Qy	919	ACTGAGACTCAATGACTGGGACTTAGACTGGGGCTCGGCTCGCTCGTAAGAAAGTGGTTA	978
Db	1213	ACTGAGACTCAATGACTGGGACTTAGACTGGGGCTCGGCTCGCTCGTAAGAAAGTGGTTA	1272
Qy	979	AGAAATCTTCTCAATTCCTCTCGAGAGGACTGGCGCGGGAGCGCAAGGACAGGGG	1038
Db	1273	AGAAATCTTCTCAATTCCTCTCGAGAGGACTGGCGCGGGAGCGCAAGGACAGGGG	1332
Qy	1039	GCTGCACAAAGCCGGGCGCTGTCTGGTGGAGTGGCATGTACGGCAGGCGCTTCGT	1098
Db	1333	GCTGCACAAAGCCGGGCGCTGTCTGGTGGAGTGGCATGTACGGCAGGCGCTTCGT	1392
Qy	1099	GCTTGGCGCTCTGCAGCGACAGGCGGCACACAGCACTTGACACAACCCGCGGAAC	1158
Db	1393	GCTTGGCGCTCTGCAGCGACAGGCGGCACACAGCACTTGACACAACCCGCGGAAC	1451
Qy	1159	TGCTGCAGGACACCCGTACAGAGACCGGGTTGATGACGAGCTGAGTAGAAAAAGTC	1218
Db	1452	TGCTGCAGGACACCCGTACAGAGACCGGGTTGATGACGAGCTGAGTAGAAAAAGTC	1511
Qy	1219	TCCGAGAAAGGGAGAGGAGATCATGTACGCCCGGAGTAGAGACTCTGCTCAGTCTGCTG	1278
Db	1512	TCCGAGAAAGGGAGAGGAGATCATGTACGCCCGGAGTAGAGACTCTGCTCAGTCTGCTG	1571
Qy	1279	GCTTGGCGCGGACGATGATCTCCGATCTGTTGGGATCAGCATACGGCCATGTC	1338
Db	1572	GCTTGGCGCGGACGATGATCTCCGATCTGTTGGGATCAGCATACGGCCATGTC	1631
Qy	1339	ACACAAATCAGCCCTGGGGACACACGACGAGGAGGAGACAGAGAAAAACAAACCA	1398
Db	1633	ACACAAATCAGCCCTGGGGACACACGAGCGAGGAGGAGAGACAGAGAAAAACAAACCA	1691
Qy	1399	GCATGAGAAACAGTAATATGATTAACCACTTAATAATATTAGCCCTCTGTTCTGCTT	1458
Db	1692	GCATGAGAAACAGTAATATGATTAACCACTTAATAATATTAGCCCTCTGTTCTGCTT	1751
Qy	1459	ACTGGCCAGGAATGGTACCAATTTTTCAGTGTGGACTTGACAGCTCTTTTGGCCACA	1518
Db	1752	ACTGGCCAGGAATGGTACCAATTTTTCAGTGTGGACTTGACAGCTCTTTTGGCCACA	1811
Qy	1519	GCAAGAGCAATTTTACACTGTTTCAAAACCCGGGGAGTGGGTGTGTTAAAGAAAGAC	1578
Db	1812	GCAAGAGCAATTTTACACTGTTTCAAAACCCGGGGAGTGGGTGTGTTAAAGAAAGAC	1871
Qy	1579	ATTTAATGCTTAGACAGTGTGA 1600	
Db	1872	ATTTAATGCTTAGACAGTGTGA 1893	
RESULT 27			
US-09-652-121-6191			
: Sequence 6191, Application US/09652121			
: GENERAL INFORMATION:			
: APPLICANT: Distefano, Peter			
: TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES			
: FILE REFERENCE: 1600.1188-001			
: CURRENT APPLICATION NUMBER: US/09/652.121			
: CURRENT FILING DATE: 2000-08-30			
: PRIOR APPLICATION NUMBER: 60/151.129			
: PRIOR FILING DATE: 1999-08-30			
: NUMBER OF SEQ ID NOS: 7615			
: SOFTWARE: FASTSEQ for Windows Version 4.0			

Query Match	Best Local Similarity	Score	DB	Length
Matches 1519;	Conservative	99.8%	Pred. No. 1,7e-240;	Indels 1; Gaps 1.
US-09-652-121-6191	ORGANISM: Homo sapiens			
SEQ ID NO 6191	LENGTH: 1917			
TYPE: DNA				
Query Match	80.2%;	Score 1299;	DB 25;	Length 1917;
Best Local Similarity	99.8%;	Pred. No. 1,7e-240;	Indels 1; Gaps 1.	
Matches 1519;	Conservative	0;	Mismatches 2;	
US-09-652-121-6191	ORGANISM: Homo sapiens			
SEQ ID NO 6191	LENGTH: 1917			
TYPE: DNA				
Query Match	80.2%;	Score 1299;	DB 25;	Length 1917;
Best Local Similarity	99.8%;	Pred. No. 1,7e-240;	Indels 1; Gaps 1.	
Matches 1519;	Conservative	0;	Mismatches 2;	
US-09-652-121-6191	ORGANISM: Homo sapiens			
SEQ ID NO 6191	LENGTH: 1917			
TYPE: DNA				
Query Match	80.2%;	Score 1299;	DB 25;	Length 1917;
Best Local Similarity	99.8%;	Pred. No. 1,7e-240;	Indels 1; Gaps 1.	
Matches 1519;	Conservative	0;	Mismatches 2;	
US-09-652-121-6191	ORGANISM: Homo sapiens			
SEQ ID NO 6191	LENGTH: 1917			
TYPE: DNA				
Query Match	80.2%;	Score 1299;	DB 25;	Length 1917;
Best Local Similarity	99.8%;	Pred. No. 1,7e-240;	Indels 1; Gaps 1.	
Matches 1519;	Conservative	0;	Mismatches 2;	
US-09-652-121-6191	ORGANISM: Homo sapiens			
SEQ ID NO 6191	LENGTH: 1917			
TYPE: DNA				
Query Match	80.2%;	Score 1299;	DB 25;	Length 1917;
Best Local Similarity	99.8%;	Pred. No. 1,7e-240;	Indels 1; Gaps 1.	
Matches 1519;	Conservative	0;	Mismatches 2;	
US-09-652-121-6191	ORGANISM: Homo sapiens			
SEQ ID NO 6191	LENGTH: 1917			
TYPE: DNA				
Query Match	80.2%;	Score 1299;	DB 25;	Length 1917;
Best Local Similarity	99.8%;	Pred. No. 1,7e-240;	Indels 1; Gaps 1.	
Matches 1519;	Conservative	0;	Mismatches 2;	
US-09-652-121-6191	ORGANISM: Homo sapiens			
SEQ ID NO 6191	LENGTH: 1917			
TYPE: DNA				
Query Match	80.2%;	Score 1299;	DB 25;	Length 1917;
Best Local Similarity	99.8%;	Pred. No. 1,7e-240;	Indels 1; Gaps 1.	
Matches 1519;	Conservative	0;	Mismatches 2;	
US-09-652-121-6191	ORGANISM: Homo sapiens			
SEQ ID NO 6191	LENGTH: 1917			
TYPE: DNA				
Query Match	80.2%;	Score 1299;	DB 25;	Length 1917;
Best Local Similarity	99.8%;	Pred. No. 1,7e-240;	Indels 1; Gaps 1.	
Matches 1519;	Conservative	0;	Mismatches 2;	
US-09-652-121-6191	ORGANISM: Homo sapiens			
SEQ ID NO 6191	LENGTH: 1917			
TYPE: DNA				
Query Match	80.2%;	Score 1299;	DB 25;	Length 1917;
Best Local Similarity	99.8%;	Pred. No. 1,7e-240;	Indels 1; Gaps 1.	
Matches 1519;	Conservative	0;	Mismatches 2;	
US-09-652-121-6191	ORGANISM: Homo sapiens			
SEQ ID NO 6191	LENGTH: 1917			
TYPE: DNA				
Query Match	80.2%;	Score 1299;	DB 25;	Length 1917;
Best Local Similarity	99.8%;	Pred. No. 1,7e-240;	Indels 1; Gaps 1.	
Matches 1519;	Conservative	0;	Mismatches 2;	
US-09-652-121-6191	ORGANISM: Homo sapiens			
SEQ ID NO 6191	LENGTH: 1917			
TYPE: DNA				
Query Match	80.2%;	Score 1299;	DB 25;	Length 1917;
Best Local Similarity	99.8%;	Pred. No. 1,7e-240;	Indels 1; Gaps 1.	
Matches 1519;	Conservative	0;	Mismatches 2;	
US-09-652-121-6191	ORGANISM: Homo sapiens			
SEQ ID NO 6191	LENGTH: 1917			
TYPE: DNA				
Query Match	80.2%;	Score 1299;	DB 25;	Length 1917;
Best Local Similarity	99.8%;	Pred. No. 1,7e-240;	Indels 1; Gaps 1.	
Matches 1519;	Conservative	0;	Mismatches 2;	
US-09-652-121-6191	ORGANISM: Homo sapiens			
SEQ ID NO 6191	LENGTH: 1917			
TYPE: DNA				

|||||
Db 553 GAACCTGATTTTCATCAGTGTGCTGCAACACCCCTTTTGTACGGGGCCAAAGCCCAAA 612
Oy 319 AAGGGGAATTTTGCCTGGCCCTCAGGCGCAGGGCTCCGACACACATCTCTTCTCA 378
Db 613 AAGGGGAATTTTGCCTGGCCCTCAGGCGCAGGGCTCCGACACACATCTCTTCTCA 672
Oy 379 ATTAGCCCTCTTCTGGGCACTGTGTAAGCTGAAGAGATGCCACCCCTTCCATCTG 438
Db 673 ATTAGCCCTCTTCTGGGCACTGTGTAAGCTGAAGAGATGCCACCCCTTCCATCTG 732
Oy 439 TTCTTCCACCCCTCGGCCCAACCCCGACCTCCCTGAGTGTCTTTCTTGGGTGCT 498
Db 733 TTCTTCCACCCCTCGGCCCAACCCCGACCTCCCTGAGTGTCTTTCTTGGGTGCT 792
Oy 499 TTATATCTGGGTAGGAGAGGGAGTCCGTTCTCTTTTGTCTCTGTGCAATAATTA 558
Db 793 TTATATCTGGGTAGGAGAGGGAGTCCGTTCTCTTTTGTCTCTGTGCAATAATTA 852
Oy 559 GAGCTCGGTAAAGCATTTCTGAATTAATTCAGCCTGACGTGAATTTTCAATATG 618
Db 853 GAGCTCGGTAAAGCATTTCTGAATTAATTCAGCCTGACGTGAATTTTCAATATG 912
Oy 619 GGAAGAGGTGAGAGTAAGATTCAACCCCATCTCTGTGTAAACCGAGTCAAGGCT 678
Db 913 GGAAGAGGTGAGAGTAAGATTCAACCCCATCTCTGTGTAAACCGAGTCAAGGCT 972
Oy 679 GGCAGAGTGTAGTCTTGTAGAGTCACTGAGTGGGATCGCTTTTGTAAAGCTCCAGT 738
Db 973 GGCAGAGTGTAGTCTTGTAGAGTCACTGAGTGGGATCGCTTTTGTAAAGCTCCAGT 1032
Oy 739 GTCCATTTCCATCCCTGTATGGGGGATGTTTGTAGAGTCAAGTGAAGTGAAGT 798
Db 1033 GTCCATTTCCATCCCTGTATGGGGGATGTTTGTAGAGTCAAGTGAAGTGAAGT 1092
Oy 799 TAGGGCTGAGGGGCACTTCCACATCAAGGCTCCCTCGTTTACATTCAAATTTATGCT 858
Db 1093 TAGGGCTGAGGGGCACTTCCACATCAAGGCTCCCTCGTTTACATTCAAATTTATGCT 1152
Oy 859 CCTGAACCATTTCTGTCAGAGAGAAATTTGGTTCGCGGCTGAGTGGGCTCTAGTG 918
Db 1153 CCTGAACCATTTCTGTCAGAGAGAAATTTGGTTCGCGGCTGAGTGGGCTCTAGTG 1212
Oy 919 ACTCGAGCTCAATGACTGGGACTTAGACTGGGGCTCGGCTCGCTGTGAAAAGTCTTA 978
Db 1213 ACTCGAGCTCAATGACTGGGACTTAGACTGGGGCTCGGCTCGCTGTGAAAAGTCTTA 1272
Oy 979 AGAAATCTTCTCAGTTCTCTTGCAGAGAGTGGGCGCGGAGCGGAAGACCAAGGCG 1038
Db 1273 AGAAATCTTCTCAGTTCTCTTGCAGAGAGTGGGCGCGGAGCGGAAGACCAAGGCG 1332
Oy 1039 GGTGCACAAAGCGGGGCTGTGCTGTGTGTGAGTGGCATGTACGGCAGGCTCTCTGT 1098
Db 1333 GGTGCACAAAGCGGGGCTGTGCTGTGTGTGAGTGGCATGTACGGCAGGCTCTCTGT 1392
Oy 1099 GGTGTGCGT 1158
Db 1393 GGTGTGCGT 1451
Oy 1159 TGTGTGAGAGACCGGT 1218
Db 1452 TGTGTGAGAGACCGGT 1511
Oy 1219 TCCGAGAAAGGAGAGATCATGTACGCCCGGAAGTAGAGACTGTCTCAGTGTCTTG 1278
Db 1512 TCCGAGAAAGGAGAGATCATGTACGCCCGGAAGTAGAGACTGTCTCAGTGTCTTG 1571
Oy 1279 GGTGTGCGGCGGACCATGTATCTCGGAATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1338
Db 1572 GGTGTGCGGCGGACCATGTATCTCGGAATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1631
Oy 1339 ACACAAATAGAGCCTGTGGAGAGACGAGAGGAGGAGAGAGAGAGAGAGAGAGAGAG 1398
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Db 1632 ACAACATCAGCCCTGGGACACGACGAGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1691
Oy 1399 GCATGAGAACACAGTAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1458
Db 1692 GCATGAGAACACAGTAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1751
Oy 1459 ACTGGCCAGGAATGTGATCAATTTTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1518
Db 1752 ACTGGCCAGGAATGTGATCAATTTTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1811
Oy 1519 GCAGAGAGAGATTTTAACACTTTTCAACCCCGGGGAGTGTGTGTGTGTGTGTGTGTGT 1578
Db 1812 GCAAGAGAGAGATTTTAACACTTTTCAACCCCGGGGAGTGTGTGTGTGTGTGTGTGT 1871
Oy 1579 ATTAAATGCTTTAGACAGTGA 1600
Db 1872 ATTAAATGCTTTAGACAGTGA 1893

RESULT 25

US-09-644-873-9077
: Sequence 9077, Application US/09644873
: GENERAL INFORMATION:
: APPLICANT: SIOS-Santlago, Immaculada
: APPLICANT: Holtzman, Douglas A.
: TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
: FILE REFERENCE: 1600.1169-001
: CURRENT APPLICATION NUMBER: US/09/644,873
: PRIOR FILING DATE: 2000-08-28
: PRIOR APPLICATION NUMBER: 60/151,064
: NUMBER OF SEQ ID NOS: 11286
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9077
: LENGTH: 1917
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-644-873-9077

Query Match 80.2%; Score 1299; DB 25; Length 1917;

Best Local Similarity 99.8%; Pred. No. 1.7e-240;

Matches 1519; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Oy 79 GAACACGACGTCTCTCCGCCGATTCATTTGTGACAGGCTGAAGCTTCAAGACAT 138
Db 373 GAACACGACGTCTCTCCGCCGATTCATTTGTGACAGGCTGAAGCTTCAAGACAT 432
Oy 139 GTGTGAGAAAGATGATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATC 198
Db 433 GTGTGAGAAAGATGATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATC 492
Oy 199 ATCAGGGGCTGTGTCATCGCTGCGGCTGCGGCTGACACCTCTGCTGCCAGGAACT 258
Db 493 ATCAGGGGCTGTGTCATCGCTGCGGCTGCGGCTGACACCTCTGCTGCCAGGAACT 552
Oy 259 GAACATGTTTGCATCAGCTGCTGCAACACCCCTCTTTTGAAGGCGGCAAGGCGCAAGAA 318
Db 553 GAACATGTTTGCATCAGCTGCTGCAACACCCCTCTTTTGAAGGCGGCAAGGCGCAAGAA 612
Oy 319 AAGGGGAAGTTCTGCTGTGCGCTCAGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 378
Db 613 AAGGGGAAGTTCTGCTGTGCGCTCAGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 672
Oy 379 ATTAGCCCTCTTCTCGGACACCTGTGAGCTGAAGAGATGCCACCCCTCTCGCATTG 438
Db 673 ATTAGCCCTCTTCTCGGACACCTGTGAGCTGAAGAGATGCCACCCCTCTCGCATTG 732
Oy 439 TTCTTCCAGCCCTCGCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCA 498
Db 733 TTCTTCCAGCCCTCGCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCA 792
Oy 499 TTATATCTGGGTAGGAGAGGAGGAGTCCGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 558
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; SEQ ID NO 4458
; LENGTH: 1925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-710-281-4458

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Query Match	85.18;	Score 1377;	DB 28;	Length 1925;
Best Local Similarity	99.88;	Pred. No. 1.9e-255;		
Matches 1597;	Conservative 0;	Mismatches 2;	Indels 1;	Gaps 1.

Qy	1	GGCAACATTTTGGGGAATTGTTCTTGCTTCACAGGCTTTGGGCTGCAAAATCCAGTGTCTACCA	60
Db	1627	GGCAACTTTTGGGGANTGTCTTGCTTCCAGGCTTTGGGCTGCAAAATCCAGTGTCTACCA	1568
Qy	61	GTTGGAAGAATTCACAGTGAACACACACACTGTCTCTCCCCGAGTTTCATTGTGAATTGCAC	120
Db	1567	GTTGGAAGAATTCACAGTGAACACACACACTGTCTCTCCCCGAGTTTCATTGTGAATTGCAC	1508
Qy	121	GGTGAAGTTCGAAGACATGTGTGCAGAAAGAGTGAAGAGGAGCAAAATGGCCGGGATCATCTA	180
Db	1507	GGTGAAGTTCGAAGACATGTGTGCAGAAAGAGTGAAGAGGAGCAAAATGGCCGGGATCATCTA	1448
Qy	181	CCGAGATCTCTGTGCATCATCACAGCGGCTGTCTCATACGCTCTGCGGGGTACCACTCTT	240
Db	1447	CCGAGATCTCTGTGCATCATCACAGCGGCTGTCTCATACGCTCTGCGGGGTACCACTCTT	1388
Qy	241	CTGTCTCCCCAGGGAACTGAATCACTAGTTTGATCACTCACTGTCTGCACACACCCCTCTTTGTA	300
Db	1387	CTGTCTCCCCAGGGAACTGAATCACTAGTTTGATCACTCACTGTCTGCACACACCCCTCTTTGTA	1328
Qy	301	CGGGGCCAAGGCCCAAGAAAGGGGGAAGTTGTGTCTGGGCGCTCAGGGCCAGGGGCTCCGGAC	360
Db	1327	CGGGGCCAAGGCCCAAGAAAGGGGGAAGTTGTGTCTGGGCGCTCAGGGCCAGGGGCTCCGGAC	1268
Qy	361	CACCATCCTGTTCCCTCAAAATTAAGCCCTCTTCTGTGGACACTGTGTGAAGCTGAAGAGATG	420
Db	1267	CACCATCCTGTTCTCAAAATTAAGCCCTCTTCTGTGGACACTGTGTGAAGCTGAAGAGATG	1208
Qy	421	CCACCCCTCTCTGCATGTTCTTCCACAGCCCTGCGCCCCAACCCCCACCTCCCTGTAGTGA	480
Db	1207	CCACCCCTCTCTGCATGTTCTTCCACAGCCCTGCGCCCCAACCCCCACCTCCCTGTAGTGA	1148
Qy	481	GTTTCTCTGGGTCCTCTTTATTTCTGGGTAAGGACGGGAGTCGCTGTTCTCTTTGTT	540
Db	1147	GTTTCTCTGGGTCCTCTTTATTTCTGGGTAAGGACGGGAGTCGCTGTTCTCTTTGTT	1088
Qy	541	CCTGTGCAAAATGAAGAAAGAGCTCGTGAAGACATTTCTGAATAATTCACTCTGACTGAT	600
Db	1087	CCTGTGCAAAATGAAGAAAGAGCTCGTGAAGACATTTCTGAATAATTCACTCTGACTGAT	1028
Qy	601	TTTTCAGTATGTACTTGAAGGAGGAGGTGAGTGAAGTTCACCCCATGCTGTGTGAAC	660
Db	1027	TTTTCAGTATGTACTTGAAGGAGGAGGTGAGTGAAGTTCACCCCATGCTGTGTGAAC	968
Qy	661	CGGAGTCAAGGCCAAGGCTGGCAGAGTCAGTCTTTAGAAGTCACTGAAGGTGGCATCTGCC	720
Db	967	CGGAGTCAAGGCCAAGGCTGGCAGAGTCAGTCTTTAGAAGTCACTGAAGGTGGCATCTGCC	908
Qy	721	TTTTTAAAGCTCAGAGTCCATTCATCCCGATGAGGGGGCAATFATTTTGAGACTGCACA	780
Db	907	TTTTTAAAGCTCAGAGTCCATTCATCCCGATGAGGGGGCAATFATTTTGAGACTGCACA	848
Qy	781	GTTGAAGTGAAGTTCCTTCTTGAAGGCTGAGAGGCCAGTTCCACACTCAAGGCTCCCTGCTTG	840
Db	847	GTTGAAGTGAAGTTCCTTCTTGAAGGCTGAGAGGCCAGTTCCACACTCAAGGCTCCCTGCTTG	788
Qy	841	ACATTTCAAACTTCATGCTCTCTGAAAACCATTTCTCTGCACAGATTGGCTGTTTCGGCC	900
Db	787	ACATTTCAAACTTCATGCTCTCTGAAAACCATTTCTCTGCACAGATTGGCTGTTTCGGCC	728
Qy	901	CTGAGTCTGGGCTCTGTGTACTGTGACATCAATGATCGGGCACTTAAAGATCGGGGCTGGGCT	960
Db	727	CTGAGTCTGGGCTCTGTGTACTGTGACATCAATGATCGGGCACTTAAAGATCGGGGCTGGGCT	668

QY	961	CGCCTCGAAAGATGCTTAAGAAAATTTCTCAGTTCCTCTTCGACAGGACGATGGCGCGG	1020
Db	667	CGCTCTGAAAGATGCTTAAAGAAATTTCTCAGTTCCTCTTCGACAGGACGATGGCGCGG	608
QY	1021	ACCGGAAGAGCAACGGGCGCTGCACAAAGCGGGCGCTGTGGTGGTGAATGGCCATGTA	1080
Db	607	ACCGGAAGAGCAACGGGCGCTGCACAAAGCGGGCGCTGTGGTGGTGAATGGCCATGTA	548
QY	1081	CGCGCAGGGCCTTCTGCTGTTTGGCTGCTGCAGCAGACAGGCGGCGACACGACCTTGC	1140
Db	547	CGCGCAGGGCCTTCTGCTGTTTGGCTGCTGCAGCAGCAGGCGGCGACACGACCTTGC	489
QY	1141	ACGAACACCCCGCGAAACTCTGCGAGGACACCGTGTACAGGAGCGGGTTGATGCCAG	1200
Db	488	ACGAACACCCCGCGAAACTCTGCGAGGACACCGTGTACAGGAGCGGGTTGATGCCAG	429
QY	1201	CTGAGTAGAAGAAACGTCTCCGGAAGGGGAGGAGATCATGTACGCCCGGAATGAGAC	1260
Db	428	CTGAGTAGAAGAAACGTCTCCGGAAGGGGAGGAGATCATGTACGCCCGGAATGAGAC	369
QY	1261	CTGCTCCAGTCGTCGTGGGTTTGGCCGAGCCATATCCTCGAATCGTGTGGGCGATC	1320
Db	368	CTGCTCCAGTCGTCGTGGGTTTGGGCTTGGCCGAGCCATATCCTCGAATCGTGTGGGCGATC	309
QY	1321	CAGCATACGGCCAAATGTCACACAAATCAGCCCTGGGCGAGACAGACGAGGAGGAGAC	1380
Db	308	CAGCATACGGCCAAATGTCACACAAATCAGCCCTGGGCGAGACAGACGAGGAGGAGAC	249
QY	1381	AGAGAAAAAGAAAAACACAGCATGAGAACACAGTAAATGAAATTAACCAATTAATTTTNG	1440
Db	248	AGAGAAAAAGAAAAACACAGCATGAGAACACAGTAAATTAATTAACCAATTAATTTTNG	189
QY	1441	CCCCCTGTTCTGTGCTTACTGTGCGCAGGAATGTATACCAATTTTTCAGTGTGAGATTGA	1500
Db	188	CCCCCTGTTCTGTGCTTACTGTGCGCAGGAATGTATACCAATTTTTCAGTGTGAGATTGA	129
QY	1501	CAGCTTCTTTTGCACAAGCAGACAGACAAATTTAACTGTTTTCAAAACCCGGGGAGATTGG	1560
Db	128	CAGCTTCTTTTGCACAAGCAGACAGGAGAAATTTAACTGTTTTCAAAACCCGGGGAGATTGG	69
QY	1561	CTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTGA 1600	
Db	68	CTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTGA 29	

```

RESULT 23
US-09-726-805-1608/C
: Sequence 1608, Application US/09726805
: GENERAL INFORMATION:
: APPLICANT: Gealing, David P.
: APPLICANT: Holzman, Douglas A.
: TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 1600, 2017-001
: CURRENT APPLICATION NUMBER: US/09/726, 805
: CURRENT FILING DATE: 2000-11-30
: PRIOR APPLICATION NUMBER: 60/168,140
: PRIOR FILING DATE: 1999-11-30
: NUMBER OF SEQ ID NOS: 2158
: SOFTWARE: PastSeq for Windows Version 4.0
: SEQ ID NO 1608
: LENGTH: 1925
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-726-805-1608

```

Query Match	85.1%	Score 1377	DB 29	length 1925
Best Local Similarity	99.8%	Pred. 1.9e-255		
Matches 1597	Conservative	0	Mismatches 2	Indels 1
<p>QY 1 GGCACCTTTGGGGGCTTCTTCCTCCAGGCTTGGCGTCGCAATACAGTACCA 60</p> <p> </p>				

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; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Stefano, Peter
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2020-001
; CURRENT APPLICATION NUMBER: US/09/699,997
; CURRENT FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 60/162,359
; NUMBER OF SEQ ID NOS: 12714
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 11085
; LENGTH: 1925
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-699-997-11085

```

```

Query Match      85.1%; Score 1377; DB 27; Length 1925;
Best Local Similarity 99.8%; Pred. No. 1.9e-255;
Matches 1597; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```

```

QY 1 GGCACCTTTTGGGATTTGTTCTTCTCCAGGCTTTGCGTCAAAATCCAGTGTACCA 60
Db 1627 GGCACCTTTTGGGATTTGTTCTTCTCCAGGCTTTGCGTCAAAATCCAGTGTACCA 1568
QY 61 GTGTGAAGATTCAGCTGAACAAAGACTGCTCCCGGAGTTTCAATTTGAATTGGAC 120
Db 1567 GTGTGAAGATTCAGCTGAACAAAGACTGCTCCCGGAGTTTCAATTTGAATTGGAC 1508
QY 121 GGTGAAGCTTCAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180
Db 1507 GGTGAAGCTTCAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 1448
QY 181 CCGCAAGTCTGTGATCATCAGGGGCTGTCTATGCGCTCTGCGGGTACAGTCTT 240
Db 1447 CCGCAAGTCTGTGATCATCAGGGGCTGTCTATGCGCTCTGCGGGTACAGTCTT 1388
QY 241 CTGTCTCCCGAGGAAATGAACCTGATTGATCAGTGTGCAACACCCCTTTTGTAA 300
Db 1387 CTGTCTCCCGAGGAAATGAACCTGATTGATCAGTGTGCAACACCCCTTTTGTAA 1328
QY 301 CGGGCCAGGCCCCAAGAAAGGGAAGTTCGCTCGGCCCTCAGGCCAGGGCTCCGAC 360
Db 1327 CGGGCCAGGCCCCAAGAAAGGGAAGTTCGCTCGGCCCTCAGGCCAGGGCTCCGAC 1268
QY 361 CACATCTCTGTTCCTCAATATAGCCCTTCTCGGCACTGTGAAGCTGAAGAGATG 420
Db 1267 CACATCTCTGTTCCTCAATATAGCCCTTCTCGGCACTGTGAAGCTGAAGAGATG 1208
QY 421 CCACCCCTCTGCAATTTGTTCTTCCAGCCCTGCCCCCAACCCCACTCCCTGAGTGA 480
Db 1207 CCACCCCTCTGCAATTTGTTCTTCCAGCCCTGCCCCCAACCCCACTCCCTGAGTGA 1148
QY 481 GTTCTCTTGGGTGCTCTTATCTGGGTAGGAGAGGGGAGTCCGTTCTCTTTTGT 540
Db 1147 GTTCTCTTGGGTGCTCTTATCTGGGTAGGAGAGGGGAGTCCGTTCTCTTTTGT 1088
QY 541 CCGTGCATAATATGAAGAGCTCGTAAAGCATTTGAATTAATTAAGCTGACTGAAT 600
Db 1087 CCGTGCATAATATGAAGAGCTCGTAAAGCATTTGAATTAATTAAGCTGACTGAAT 1028
QY 601 TTTTCAGTATGACTTGAAGAGAGAGGTGAGTGAAGATTCACCCCATGTCTGTGAAC 660
Db 1027 TTTTCAGTATGACTTGAAGAGAGAGGTGAGTGAAGATTCACCCCATGTCTGTGAAC 968
QY 661 CGGAGTCAAGGCGCAGGCTGGAGAGTCAAGTCTTAAGAGTCACTGAGGTGGCATCTGCC 720
Db 967 CGGAGTCAAGGCGCAGGCTGGAGAGTCAAGTCTTAAGAGTCACTGAGGTGGCATCTGCC 908
QY 721 TTTTGAAGAGCTCAGTGTTCATTCATCCCTGATGAGGGGCAATGATTGAGACTGAGA 780
Db 907 TTTTGAAGAGCTCAGTGTTCATTCATCCCTGATGAGGGGCAATGATTGAGACTGAGA 848

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QY 781 GTGAGAGTACCTTTTCTTAAAGGCTGAGGGCCAGTTCACCACTCAAGGCTCCCTCGCTTG 840
Db 847 GTGAGAGTACCTTTTCTTAAAGGCTGAGGGCCAGTTCACCACTCAAGGCTCCCTCGCTTG 788
QY 841 ACATTTCAAACTTCATGCTCTCTGAAAACCAATTCCTGACGAGATTTGGCTGTTGGCG 900
Db 787 ACATTTCAAACTTCATGCTCTCTGAAAACCAATTCCTGACGAGATTTGGCTGTTGGCG 728
QY 901 CTGAGTTGGGCTCTAGTACTCCAGACTCAATAGCTGGGACTTAAGACTGCGGCT 960
Db 727 CTGAGTTGGGCTCTAGTACTCCAGACTCAATAGCTGGGACTTAAGACTGCGGCT 668
QY 961 CGCTCTGAAAAGTCTTAAGAAAATCTTCAGTTCTCTTGAAGAGTGGCGCGG 1020
Db 667 CGCTCTGAAAAGTCTTAAGAAAATCTTCAGTTCTCTTGAAGAGTGGCGCGG 608
QY 1021 ACGGAAAGACAAAGGCGCTGCAAAAGGCGGCTGTGCTGTGAGTGGCATGTA 1080
Db 607 ACGGAAAGACAAAGGCGCTGCAAAAGGCGGCTGTGCTGTGAGTGGCATGTA 548
QY 1081 CGGCGAGGCGCTTCTGTTGCTGTTGGCGTGTGACAGCAGCGGCGACAGCACCCTTGC 1140
Db 547 CGGCGAGGCGCTTCTGTTGCTGTTGGCGTGTGACAGCAGCGGCGACAGCACC -TGC 489
QY 1141 ACGAAGACCGCGGAAACCTGCTGAGAGACACCGTGTACAGAGCGGGTGTATGACCGAG 1200
Db 488 ACGAAGACCGCGGAAACCTGCTGAGAGACACCGTGTACAGAGCGGGTGTATGACCGAG 429
QY 1201 CTGAGTAGAAAAACGCTCTCGAGAGGAGGAGATCATGTACGCCCGGAAAGTAGAGAC 1260
Db 428 CTGAGTAGAAAAACGCTCTCGAGAGGAGGAGATCATGTACGCCCGGAAAGTAGAGAC 369
QY 1261 CTGTCTCAGTCTGCTGTTGGTGGTGGCGGACGACATGCTCCGAATCTGTGGGCAATC 1320
Db 368 CTGTCTCAGTCTGCTGTTGGTGGTGGCGGACGACATGCTCCGAATCTGTGGGCAATC 309
QY 1321 CAGCATACGGCCATGTCAACAATCAGCCCTGGGAGACAGACGAGCAGAGGAGAGAC 1380
Db 308 CAGCATACGGCCATGTCAACAATCAGCCCTGGGAGACAGACGAGCAGAGGAGAGAC 249
QY 1381 AGAGAAAAGAAAAACACAGCATGAGAACAGTAAATGAATAAACCATTAATATTAG 1440
Db 248 AGAGAAAAGAAAAACACAGCATGAGAACAGTAAATGAATAAACCATTAATATTAG 189
QY 1441 CCCCTCTGTTCTGCTTACTGCTTAAAGGCAAGAAATGTTTAAAGTGTGGACTTGA 1500
Db 188 CCCCTCTGTTCTGCTTACTGCTTAAAGGCAAGAAATGTTTAAAGTGTGGACTTGA 129
QY 1501 CAGCTCTTTTGGCACAAGCAAGAGAAATTTAACTCTTTCAAAACCCGGGAGATTGG 1560
Db 128 CAGCTCTTTTGGCACAAGCAAGAGAAATTTAACTCTTTCAAAACCCGGGAGATTGG 69
QY 1561 CTGTGTTAAAGAAACCATTAATGCTTTTACAGTGTGA 1600
Db 68 CTGTGTTAAAGAAACCATTAATGCTTTTACAGTGTGA 29

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RESULT 22
US-09-710-281-4458/c
; Sequence 4458, Application US/09710281
; GENERAL INFORMATION:
; APPLICANT: Hunter, John J.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Stidal, Hilde
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2036-001
; CURRENT APPLICATION NUMBER: US/09/710,281
; CURRENT FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 60/164,254
; NUMBER OF SEQ ID NOS: 5803
; SOFTWARE: FastSeq for Windows Version 4.0

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QY 1561 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTGA 1600
    |||
    68 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTGA 29

RESULT 20
US-09-652-917-3346/c
; Sequence 3346, Application US/09652917
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Holzman, Douglas A.
; APPLICANT: Disleffano, Peter
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1170-001
; CURRENT APPLICATION NUMBER: US/09/652.917
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,422
; NUMBER OF SEQ ID NOS: 3855
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3346
; LENGTH: 1925
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-652-917-3346

Query Match 85.1%; Score 1377; Db 25; Length 1925;
Best Local Similarity 99.8%; Pred. No. 1.9e-255;
Matches 1597; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GGCACATTTTTCGGGATGTTCTTCTTCAGAGCTTGGCGTTCGCAAAATCCAGTGTACCA 60
    |||
    1627 GGCACATTTTTCGGGATGTTCTTCTTCAGAGCTTGGCGTTCGCAAAATCCAGTGTACCA 1568

QY 61 GTGGAAGAAATTCAGCTGAACAACGACTCTCTCCCGAGTTGATTTGTAATTTGAC 120
    |||
    1567 GTGGAAGAAATTCAGCTGAACAACGACTCTCTCCCGAGTTGATTTGTAATTTGAC 1508

QY 121 GGTGAAGCTTCACATGTTGTCTGAGAAAGATGATGAGCAAGTCCGGATCTCTTA 180
    |||
    1507 GGTGAAGCTTCACATGTTGTCTGAGAAAGATGATGAGCAAGTCCGGATCTCTTA 1448

QY 181 CCGGAAGCTTCAGCTGAACAACGACTCTCTCCCGAGTTGATTTGTAATTTGAC 240
    |||
    1447 CCGGAAGCTTCAGCTGAACAACGACTCTCTCCCGAGTTGATTTGTAATTTGAC 1388

QY 241 CTGCTCCCGAGGAAAGTGAACCTGATTTGATGATGATGATGATGATGATGATGAT 300
    |||
    1387 CTGCTCCCGAGGAAAGTGAACCTGATTTGATGATGATGATGATGATGATGATGAT 1328

QY 301 CCGGCAAGGCTTCAGCTGAACAACGACTCTCTCCCGAGTTGATTTGTAATTTGAC 360
    |||
    1327 CCGGCAAGGCTTCAGCTGAACAACGACTCTCTCCCGAGTTGATTTGTAATTTGAC 1268

QY 361 CAGCATCTGTTCTCAATATAGCCCTTCTTCGCAACACTGCTGAAGTGAAGAGATG 420
    |||
    1267 CAGCATCTGTTCTCAATATAGCCCTTCTTCGCAACACTGCTGAAGTGAAGAGATG 1208

QY 421 CCAACCCCTCTGATGATTTCTTCAGAGCCCTCCGCAACCCCTCCGCAACCCCTG 480
    |||
    1207 CCAACCCCTCTGATGATTTCTTCAGAGCCCTCCGCAACCCCTCCGCAACCCCTG 1148

QY 481 GTTCTCTGAGGATCTTTTATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
    |||
    1147 GTTCTCTGAGGATCTTTTATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1088

QY 541 CCTGTGCAATATATGAAGAGCTCGTAAGCATTTGTAATTAATTAATTAATTAATTA 600
    |||
    1087 CCTGTGCAATATATGAAGAGCTCGTAAGCATTTGTAATTAATTAATTAATTAATTA 1028

QY 601 TTTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
    |||

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    |||
    1027 TTTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 968

QY 661 CGGAGTCAAGGCGGAGGCTGCGAGAGTCACTCTTAAGATGATGATGATGATGATGATG 720
    |||
    967 CGGAGTCAAGGCGGAGGCTGCGAGAGTCACTCTTAAGATGATGATGATGATGATGATGATG 908

QY 721 TTTGTAAGGCTCCAGTGTCCATTCATCCCTGATGGGGCATAGTTTGAAGTCACTGAGA 780
    |||
    907 TTTGTAAGGCTCCAGTGTCCATTCATCCCTGATGGGGCATAGTTTGAAGTCACTGAGA 848

QY 781 GTGAGAGTCACTCTTCTTAAGGCTGAGAGGCGGAGTCCCACTCAAGGCTCCCTGCTT 840
    |||
    847 GTGAGAGTCACTCTTCTTAAGGCTGAGAGGCGGAGTCCCACTCAAGGCTCCCTGCTT 788

QY 841 ACATTTAACTCATGCTCCGTAAGAAACATTCCTGCGAGCAATTTGCTGCTTCCGCG 900
    |||
    787 ACATTTAACTCATGCTCCGTAAGAAACATTCCTGCGAGCAATTTGCTGCTTCCGCG 728

QY 901 CTGAGTTGGGCTCTAGTGAAGTCACTGAGTCAATGACTGGGACTTGAAGTGGGCTTGG 960
    |||
    727 CTGAGTTGGGCTCTAGTGAAGTCACTGAGTCAATGACTGGGACTTGAAGTGGGCTTGG 668

QY 961 CGCTGTAAGAGTCTTAAAGAAATCTTCTCACTTCTCTTCTGAGAGAGTCCGCGCGG 1020
    |||
    667 CGCTGTAAGAGTCTTAAAGAAATCTTCTCACTTCTCTTCTGAGAGAGTCCGCGCGG 608

QY 1021 ACGGAAAGAGCAAGGCGGCTGACAAAGGCGGCTGCGTGGTGGAGTGGCGATGTA 1080
    |||
    607 ACGGAAAGAGCAAGGCGGCTGACAAAGGCGGCTGCGTGGTGGAGTGGCGATGTA 548

QY 1081 CCGGACAGGCTTCTGAGTGGGCTGCTGCTGAGAGAGGCGGCGGAGAGAGAGAGAGAG 1140
    |||
    547 CCGGACAGGCTTCTGAGTGGGCTGCTGCTGAGAGAGGCGGCGGAGAGAGAGAGAGAG 489

QY 1141 ACGAAGACCGGCGGAAAGCTCTGAGAGACCGTGTACAGAGAGGAGGAGTGTAGACGAG 1200
    |||
    489 ACGAAGACCGGCGGAAAGCTCTGAGAGACCGTGTACAGAGAGGAGGAGTGTAGACGAG 429

QY 1201 CTGAGTAGAAGAAAGCTCTCCGAGAAAGGAGAGGATATGATGAGGCGGAGTATGAGAC 1260
    |||
    428 CTGAGTAGAAGAAAGCTCTCCGAGAAAGGAGAGGATATGATGAGGCGGAGTATGAGAC 369

QY 1261 CTGCTCCAGTCTGCTTGGGTTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
    |||
    368 CTGCTCCAGTCTGCTTGGGTTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 309

QY 1321 CAGCATAGGCGCAATGTCACACATTCAGGCTGGGAGAGAGAGAGAGAGAGAGAGAG 1380
    |||
    308 CAGCATAGGCGCAATGTCACACATTCAGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAG 249

QY 1381 AGAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
    |||
    248 AGAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 189

QY 1441 CCGCTCTGTTGCTGCTTACAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
    |||
    188 CCGCTCTGTTGCTGCTTACAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 129

QY 1501 CAGCTTCTTTCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
    |||
    128 CAGCTTCTTTCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 69

QY 1561 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTGA 1600
    |||
    68 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTGA 29

RESULT 21
US-09-699-997-11085/c
; Sequence 11085, Application US/09699997
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.

```

OY 1381 AGAGAAAAGAAAACACAGATGAGAAACAGTAAATGAATTAACCAATTAATTTAG 1440
 |||||
 Db 248 AGAGAAAAGAAAACACAGATGAGAAACAGTAAATGAATTAACCAATTAATTTAG 189
 |||||
 OY 1441 CCCCTCTGTTCTGCTTACTGCGCAGAAATGTTACCAATTTTTCAGTGTGACCTGA 1500
 |||||
 Db 188 CCCCTCTGTTCTGCTTACTGCGCAGAAATGTTACCAATTTTTCAGTGTGACCTGA 129
 |||||
 OY 1501 CAGCTTCTTTGCGCAACAGAGAGAAATTAACACGTTTTCACACCCGGGAGTTGG 1560
 |||||
 Db 128 CAGCTTCTTTGCGCAACAGAGAGAAATTAACACGTTTTCACACCCGGGAGTTGG 69
 |||||
 OY 1561 CTGTGTTAAAGAAACCATTAATGCTTTAGACAGTGA 1600
 |||||
 Db 68 CTGTGTTAAAGAAACCATTAATGCTTTAGACAGTGA 29
 |||||

RESULT 19

US-09-652-128-9375/c
 : Sequence 9375, Application US/09652128
 : GENERAL INFORMATION:
 : APPLICANT: Shyjan, Andrew W.
 : APPLICANT: Holtzman, Douglas A.
 : TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
 : FILE REFERENCE: 1600.1171-001
 : CURRENT APPLICATION NUMBER: US/09/652.128
 : PRIOR FILING DATE: 2000-08-30
 : PRIOR APPLICATION NUMBER: 60/151.133
 : NUMBER OF SEQ ID NOS: 10265
 : SOFTWARE: FASTSEQ for Windows Version 4.0
 : SEQ ID NO 9375
 : LENGTH: 1925
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-09-652-128-9375

Query Match 85.18; Score 1377; DB 25; Length 1925;
 Best Local Similarly 99.8%; Pred. No. 1.9e-255;
 Matches 1597; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 1 GGCACACTTTTGGCGATGTTCTTCTCCAGGCTTTGGCGTCAATCCAGTCTACCA 60
 |||||
 Db 1627 GGCACACTTTTGGCGATGTTCTTCTCCAGGCTTTGGCGTCAATCCAGTCTACCA 1568
 |||||
 OY 61 GTGTGAAGAAATTCAGCTGAACAAGACTGCTCTCCCGAGTTTCATTGTGAATTGGAC 120
 |||||
 Db 1567 GTGTGAAGAAATTCAGCTGAACAAGACTGCTCTCCCGAGTTTCATTGTGAATTGGAC 1508
 |||||
 OY 121 GGTGAACGTTCAAGACATGTTGTGAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 180
 |||||
 Db 1507 GGTGAACGTTCAAGACATGTTGTGAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 1448
 |||||
 OY 181 CCGCAAGTCTGTGCATCATCAAGCGCTGTCTCATCGGCTGTGGCGGATACAGTCTT 240
 |||||
 Db 1447 CCGCAAGTCTGTGCATCATCAAGCGCTGTCTCATCGGCTGTGGCGGATACAGTCTT 1388
 |||||
 OY 241 CTGCTCTCCCAAGGAAATCTAAGTCTGATGATGATGATGATGATGATGATGATGAT 300
 |||||
 Db 1387 CTGCTCTCCCAAGGAAATCTAAGTCTGATGATGATGATGATGATGATGATGATGAT 1328
 |||||
 OY 301 CCGGCCAAGGCCCAAGAAAAGGGAAGTTCTGCTCCGCGCTCAGGCCAGGCGTCCGAC 360
 |||||
 Db 1327 CCGGCCAAGGCCCAAGAAAAGGGAAGTTCTGCTCCGCGCTCAGGCCAGGCGTCCGAC 1268
 |||||
 OY 361 CACCATCTGTTCTCAATTAAGCCCTCTCTCGGCACTGCTGAAAGCTGAAGAGATG 420
 |||||
 Db 1267 CACCATCTGTTCTCAATTAAGCCCTCTCTCGGCACTGCTGAAAGCTGAAGAGATG 1208
 |||||
 OY 421 CCACCCCTCCGCAATGTTCTTCCAGCCCTGCGCCCAACCCCAACCTCCGAGTGA 480
 |||||

Db 1207 CCACCCCTCTGCAATGTTCTTCCAGCCCTGCCCCCAACCCCACTCCCTGAGTGA 1148
 |||||
 OY 481 GTTCTTCTGGGTTGCTCTTATTCGTTGGGTAGGAGCGGGAGTCCGTCTCTTTGTT 540
 |||||
 Db 1147 GTTCTTCTGGGTTGCTCTTATTCGTTGGGTAGGAGCGGGAGTCCGTCTCTTTGTT 1088
 |||||
 OY 541 CCTGTCAATTAATGAAGAGCTCGTAAAGCATCTGAATTAATAGCTGACTGAAT 600
 |||||
 Db 1087 CCTGTCAATTAATGAAGAGCTCGTAAAGCATCTGAATTAATAGCTGACTGAAT 1028
 |||||
 OY 601 TTTCAATATGTTCTGAAGAGAGGTGAGTGAATTAATTAATTAATTAATTAATTAAT 660
 |||||
 Db 1027 TTTCAATATGTTCTGAAGAGAGGTGAGTGAATTAATTAATTAATTAATTAATTAAT 968
 |||||
 OY 661 CCGAGTCAAGCGCAGGCTGCGAGAGTCAAGTCTTGAAGAGTCAAGTCTGAGTGGCA 720
 |||||
 Db 967 CCGAGTCAAGCGCAGGCTGCGAGAGTCAAGTCTTGAAGAGTCAAGTCTGAGTGGCA 908
 |||||
 OY 721 TTTTGAAGCTCCAGTGTCCATTCATCCCTGATGGGGCATAGTTGAGACTGAGA 780
 |||||
 Db 907 TTTTGAAGCTCCAGTGTCCATTCATCCCTGATGGGGCATAGTTGAGACTGAGA 848
 |||||
 OY 781 GTGAGAGTGAAGTCTTCTTGAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 |||||
 Db 847 GTGAGAGTGAAGTCTTCTTGAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 788
 |||||
 OY 841 ACATTCAACTTCATGCTCTCTGAAGAACCATTCCTGAGAGAGAAATGAGTGGCTGGCC 900
 |||||
 Db 787 ACATTCAACTTCATGCTCTCTGAAGAACCATTCCTGAGAGAGAAATGAGTGGCTGGCC 728
 |||||
 OY 901 CTGAGTGGGCTGAGTGAAGTCAAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGT 960
 |||||
 Db 727 CTGAGTGGGCTGAGTGAAGTCAAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGT 668
 |||||
 OY 961 CGTCTGAAAAGTCTTAAGAAAATCTTCTCAATTCCTCTGAGAGAGTGGCGCGGG 1020
 |||||
 Db 667 CGTCTGAAAAGTCTTAAGAAAATCTTCTCAATTCCTCTGAGAGAGTGGCGCGGG 608
 |||||
 OY 1021 ACGGGAAGAGCAACGGCGCTGCAAAAGCGGCGTGTGCGGTGAGTGGAGTGGATGA 1080
 |||||
 Db 607 ACGGGAAGAGCAACGGCGCTGCAAAAGCGGCGTGTGCGGTGAGTGGAGTGGATGA 548
 |||||
 OY 1081 CGCGCAGGCTTCTGCTGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGG 1140
 |||||
 Db 547 CGCGCAGGCTTCTGCTGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGG 489
 |||||
 OY 1141 ACGAACAACCGCGGAAATCTGCTCGAGGACACCGTGTACAGAGCGGGTGTGATGACGAG 1200
 |||||
 Db 488 ACGAACAACCGCGGAAATCTGCTCGAGGACACCGTGTACAGAGCGGGTGTGATGACGAG 429
 |||||
 OY 1201 CTGAGGTAGAAAACGTTCCCGAAGAGGAGGAGGATCATGACCCCGAAGTAGAGAC 1260
 |||||
 Db 428 CTGAGGTAGAAAACGTTCCCGAAGAGGAGGAGGATCATGACCCCGAAGTAGAGAC 369
 |||||
 OY 1261 CTGCTCAAGTCTGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTG 1320
 |||||
 Db 368 CTGCTCAAGTCTGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTG 309
 |||||
 OY 1321 CAGCATACGCGCAATGTCAACAATACAGCTGGGCAAGACGAGCAGAGGAGAGAGAC 1380
 |||||
 Db 308 CAGCATACGCGCAATGTCAACAATACAGCTGGGCAAGACGAGCAGAGGAGAGAGAC 249
 |||||
 OY 1381 AGAGAAAAGAAAACACACATGAGAAACAGTAAATGAATTAACCAATTAATTTAG 1440
 |||||
 Db 248 AGAGAAAAGAAAACACACATGAGAAACAGTAAATGAATTAACCAATTAATTTAG 189
 |||||
 OY 1441 CCCCTCTGTTCTGCTTACTGCGCAGAAATGTTACCAATTTTTCAGTGTGACCTGA 1500
 |||||
 Db 188 CCCCTCTGTTCTGCTTACTGCGCAGAAATGTTACCAATTTTTCAGTGTGACCTGA 129
 |||||
 OY 1501 CAGCTTCTTTGCGCAACAGAGAGAAATTAACACGTTTTCACACCCGGGAGTTGG 1560
 |||||
 Db 128 CAGCTTCTTTGCGCAACAGAGAGAAATTAACACGTTTTCACACCCGGGAGTTGG 69
 |||||

Db 1435 ACGAACACCCGCCAACTGCTGCGAGACACCGTGTACAGAGCGGGTTGATGACCGAG 1494
 Oy 1201 CTGAGGTGAAAAAGCTCTCCGAGAGGGAGAGATCATGTACGCCGGAAGTAGAGAC 1260
 Db 1495 CTGAGGTGAAAAAGCTCTCCGAGAGGGAGAGATCATGTACGCCGGAAGTAGAGAC 1554
 Oy 1261 CTGCTCAGTGTCTGCTGGGTTTGGCCGACGATGATCTCCGAAATCTGTGGGCAATC 1320
 Db 1555 CTGCTCAGTGTCTGCTGGGTTTGGCCGACGATGATCTCCGAAATCTGTGGGCAATC 1614
 Oy 1321 CAGCATACGCCCATGTACAAACAATCAGCCCTGGGAGACAGACAGAGAGAGAGAGAC 1380
 Db 1615 CAGCATACGCCCATGTACAAACAATCAGCCCTGGGAGACAGACAGAGAGAGAGAGAC 1674
 Oy 1381 AAGAAAAAGAAAAACACAGCATGAGAACACAGTAATGAAATAAACCATAAATATTATAG 1440
 Db 1675 AAGAAAAAGAAAAACACAGCATGAGAACACAGTAATGAAATAAACCATAAATATTATAG 1734
 Oy 1441 CCCCTCTGTTCTGCTTACTGAGGCGAGAAATGGTACCAATTTTTCAGTGTGACCTGA 1500
 Db 1735 CCCCTCTGTTCTGCTTACTGAGGCGAGAAATGGTACCAATTTTTCAGTGTGACCTGA 1794
 Oy 1501 CAGCTTCTTTTGCACAAAGCAAGAGAGATTAACACTGTTCAAACCCGGGGAGTTGG 1560
 Db 1795 CAGCTTCTTTTGCACAAAGCAAGAGATTAACACTGTTCAAACCCGGGGAGTTGG 1854
 Oy 1561 CTGTGTTAAAGAAAGACATTAATGCTTTAGACAGCTGTAAAAAAA 1607
 Db 1855 CTGTGTTAAAGAAAGACATTAATGCTTTAGACAGCTGTAAAAAAA 1901

RESULT 18
 US-09-652-121-7293/c
 ; Sequence 7293, Application US/09652121
 ; GENERAL INFORMATION:
 ; APPLICANT: Disleffano, Peter
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
 ; FILE REFERENCE: 1600.1188-001
 ; CURRENT APPLICATION NUMBER: US/09/652,121
 ; PRIOR FILING DATE: 2000-08-30
 ; PRIOR FILING DATE: 1999-08-30
 ; NUMBER OF SEQ ID NOS: 7615
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7293
 ; LENGTH: 1925
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-652-121-7293

Query Match 85.1%; Score 1377; DB 25; Length 1925;
 Best Local Similarity 99.8%; Pred. No. 1.9e-253;
 Matches 1597; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Oy 1 GGCACATTTTGGGATGTTCTTCTCCAGGCTTGGCGTGAATCCAGTGTACCA 60
 Db 1627 GGCACATTTTGGGATGTTCTTCTCCAGGCTTGGCGTGAATCCAGTGTACCA 1568
 Oy 61 GTGTGAAGAAATCCAGTGAACAACGACTGCTCTCCCGAGTTATTGTGAATGGAC 120
 Db 1567 GTGTGAAGAAATCCAGTGAACAACGACTGCTCTCCCGAGTTATTGTGAATGGAC 1508
 Oy 121 GGTGACGTTCAACAGATGTGTGAGAAAGATGAGAGCAAGTGGCGGATCATGTA 180
 Db 1507 GGTGACGTTCAACAGATGTGTGAGAAAGATGAGAGCAAGTGGCGGATCATGTA 1448
 Oy 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCTGTCCGGGTACCAAGTCTT 240
 Db 1447 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCTGTCCGGGTACCAAGTCTT 1388
 Oy 241 CTGCTCCCCAGGAACTGAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 300

Db 1387 CTGCTCCCGAAGGAACTGAACCTCAGTTTGCATCAGTGTGCAACACCCCTCTTTGTA 1328
 Oy 301 CGGGCCAAAGGCCCAAGAAAAGGGAATTTCTGCTCGGCCCTTAGGCCAGGGCTCCGCCAC 360
 Db 1327 CGGGCCAAAGGCCCAAGAAAAGGGAATTTCTGCTCGGCCCTTAGGCCAGGGCTCCGCCAC 1268
 Oy 361 CACCACTCTGTCTCTCAAAATTTAGCCCTCTCTGCGCACACTGTCTGAAGCTGAAGAGATG 420
 Db 1267 CACCACTCTGTCTCTCAAAATTTAGCCCTCTCTGCGCACACTGTCTGAAGCTGAAGAGATG 1208
 Oy 421 CCACCCCTCTCTGCAATTTGTTCTTCCAGCCCTCGGCCCAACCCCCCACTCTCTGAGTGA 480
 Db 1207 CCACCCCTCTCTGCAATTTGTTCTTCCAGCCCTCGGCCCAACCCCCCACTCTCTGAGTGA 1148
 Oy 481 GTTTCTTGGGTGCTCTTTTATTTCTGGGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
 Db 1147 GTTTCTTGGGTGCTCTTTTATTTCTGGGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1088
 Oy 541 CCTGTCAAAATTAATGAAGAGCTCGGTAAAGCATTTGAAATTAATTCAGCTGACTGAAT 600
 Db 1087 CCTGTCAAAATTAATGAAGAGCTCGGTAAAGCATTTGAAATTAATTCAGCTGACTGAAT 1028
 Oy 601 TTTTCAGTATGTACTTGAAGAGAGAGTGAAGTGAAGTTCACCCCATGCTGTGTAAAC 660
 Db 1027 TTTTCAGTATGTACTTGAAGAGAGAGTGAAGTGAAGTTCACCCCATGCTGTGTAAAC 968
 Oy 661 CGGAGTCAGAGGCGCAGGCGGAGAGTCACTCTTAGAAGTCACTGAGTGGGATCTGACC 720
 Db 967 CGGAGTCAGAGGCGCAGGCGGAGAGTCACTCTTAGAAGTCACTGAGTGGGATCTGACC 908
 Oy 721 TTTTGAAGCCCTCAGTGTCCATTCATCCCTGATGGGGCATAGTTTGAAGTGCAGA 780
 Db 907 TTTTGAAGCCCTCAGTGTCCATTCATCCCTGATGGGGCATAGTTTGAAGTGCAGA 848
 Oy 781 GTGAGAGTACGTTTCTTGAAGGCGTGGAGGCGGAGTCCCACTCAAGGCGCTCGCTG 840
 Db 847 GTGAGAGTACGTTTCTTGAAGGCGTGGAGGCGGAGTCCCACTCAAGGCGCTCGCTG 788
 Oy 841 ACATTCAAACTTCATGCTCTGAAAAACATTTCTGACAGCAAAATTTGGCTGTTCCGCC 900
 Db 787 ACATTCAAACTTCATGCTCTGAAAAACATTTCTGACAGCAAAATTTGGCTGTTCCGCC 728
 Oy 901 CTGAGTTGGGCTCTAGTACTGAGACTGATGATGATGATGATGATGATGATGATGATGAT 960
 Db 727 CTGAGTTGGGCTCTAGTACTGAGACTGATGATGATGATGATGATGATGATGATGATGAT 668
 Oy 961 CGCTCTGAAAAGTGTGAAGAAAATTTCTCAAGTCTCTCTGACAGAGACTGGCGCGG 1020
 Db 667 CGCTCTGAAAAGTGTGAAGAAAATTTCTCAAGTCTCTCTGACAGAGACTGGCGCGG 608
 Oy 1021 ACGCGAAGAGCAACGGGCGCTGCACAAAGCGGGCGCTGTGGGTGAGATGCCATGTA 1080
 Db 607 ACGCGAAGAGCAACGGGCGCTGCACAAAGCGGGCGCTGTGGGTGAGATGCCATGTA 548
 Oy 1081 CGGCGAGGCGCTCTGTGTGGTGGCTGCTGACAGCAAGGCGGAGAGCAAGCACTTGC 1140
 Db 547 CGGCGAGGCGCTCTGTGTGGTGGCTGCTGACAGCAAGGCGGAGAGCAAGCACTTGC 489
 Oy 1141 ACGAACACCCCGGAAACTCTGCGAGACACCTGTGTACAGAGCGGGTTGATGACCGAG 1200
 Db 488 ACGAACACCCCGGAAACTCTGCGAGACACCTGTGTACAGAGCGGGTTGATGACCGAG 429
 Oy 1201 CTGAGGTGAAAAAGCTCTCCGAGAAAGGAGAGATATATGAGCCCGGAAGTAGAGAC 1260
 Db 428 CTGAGGTGAAAAAGCTCTCCGAGAAAGGAGAGATATATGAGCCCGGAAGTAGAGAC 369
 Oy 1261 CTGCTCAGTGTGCTGTTGGTTTGGCGGACCATATCTCCGAATCTGTGTGGGATC 1320
 Db 368 CTGCTCAGTGTGCTGTTGGTTTGGCGGACCATATCTCCGAATCTGTGTGGGATC 309
 Oy 1321 CAGCATACGGCCATGTACAAACAATCAGCCCTGGGACAGACAGAGAGAGAGAGAC 1380
 Db 308 CAGCATACGGCCATGTACAAACAATCAGCCCTGGGACAGACAGAGAGAGAGAGAC 249

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Oy 1141 ACGAACCCGCCGAAATGCTGCGAGACACCGTGTACAGAGCGGGTGTGACCCGAG 1200
    |||
Db 1435 ACGAACACCCGCCGAAATGCTGCGAGACACCGTGTACAGAGCGGGTGTGACCCGAG 1494
Oy 1201 CTGAGGTAGAAAAGCTCTCCGAGAGAGGAGAGATCATGTACGCCCGGAATGAGAC 1260
    |||
Db 1495 CTGAGGTAGAAAAGCTCTCCGAGAGAGGAGAGATCATGTACGCCCGGAATGAGAC 1554
Oy 1261 CTCGTCACATGCTGCTTGGGTTGGCCGAGCATGATCTCCGAATCGTTGGGGCATC 1320
    |||
Db 1555 CTCGTCACATGCTGCTTGGGTTGGCCGAGCATGATCTCCGAATCTGGTTGGGGCATC 1614
Oy 1321 CAGCATAGGCGCAATGTACACAATTCAGCCCTGGGACAGACAGAGAGAGAGAC 1380
    |||
Db 1615 CAGCATAGGCGCAATGTACACAATTCAGCCCTGGGACAGACAGAGAGAGAGAC 1674
Oy 1381 AGAGAAAAGAAAACACAGCATGAGACACAGTAATGAATAAACCTAAATATTTAG 1440
    |||
Db 1675 AGAGAAAAGAAAACACAGCATGAGACACAGTAATGAATAAACCTAAATATTTAG 1734
Oy 1441 CCCCTCTTCTGCTGCTTACTGCGCCAGGAAATGGTACCAATTTTTCAGTGTGACTTGA 1500
    |||
Db 1735 CCCCTCTTCTGCTGCTTACTGCGCCAGGAAATGGTACCAATTTTTCAGTGTGACTTGA 1794
Oy 1501 CAGCTTCTTTGCCAACAAGCAAGAGAAATTTAACTGTTTCAACCCGGGGAGTTGG 1560
    |||
Db 1795 CAGCTTCTTTGCCAACAAGCAAGAGAAATTTAACTGTTTCAACCCGGGGAGTTGG 1854
Oy 1561 CTGCTTTAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAA 1607
    |||
Db 1855 CTGCTTTAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAA 1901

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RESULT 17
US-09-808-383-4454
; Sequence 4454, Application US/09808383
; GENERAL INFORMATION:
; APPLICANT: Gearling, David P.
; APPLICANT: Holzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: 1600.1046-002
; CURRENT APPLICATION NUMBER: US/09/808,383
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 09/397,022
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: US 60/100,465
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: US 60/106,443
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: US 60/107,257
; PRIOR FILING DATE: 1998-11-15
; PRIOR APPLICATION NUMBER: US 60/126,906
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/132,099
; NUMBER OF SEQ ID NOS: 5775
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4454
; LENGTH: 1918
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-808-383-4454

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Query Match      85.5%; Score 1384; DB 31; Length 1918;
Best Local Similarity 99.8%; Pred. No. 8,8e-257;
Matches 1604; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Oy 1 GGCACACTTTTTCGCGATGCTTCTGCTTCAGGCTTGGCGTCAAAATCCATGCTTACCA 60
    |||
Db 296 GGCACACTTTTTCGCGATGCTTCTGCTTCAGGCTTGGCGTCAAAATCCATGCTTACCA 355
Oy 61 GTGTGAAGATTCGAGCTGAAACAGACATGCTCTCCCGAGTTCATTGTGAATTTGCAC 120

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    |||
Db 356 GTGTGAAGATTCGAGCTGAAACAAACGACTGCTCTCCCGAGTTCATTGTGAATTTGAC 415
Oy 121 GGTGAAGCTTCAACATGTTGTGAAAGAAGTATGAGACAAATGCCGGATTCATGTA 180
    |||
Db 416 GGTGAAGCTTCAACATGTTGTGAAAGAAGTATGAGACAAATGCCGGATTCATGTA 475
Oy 181 CCGCAATCTCTGTGATCATCATGAGCGGCTGTCTCATGCTCTGCGGGTATCCATCTT 240
    |||
Db 476 CCGCAATCTCTGTGATCATCATGAGCGGCTGTCTCATGCTCTGCGGGTATCCATCTT 535
Oy 241 CTGCTCCCGAGGAAATGAACTGAACTGAGTTGCAATGAGTGTGCAACACCTTTTGTAA 300
    |||
Db 536 CTGCTCCCGAGGAAATGAACTGAACTGAGTTGCAATGAGTGTGCAACACCTTTTGTAA 595
Oy 301 CGGGCCAAAGGCCCAAGAAAAGGGAAATTTCTGCTGCGCTTACGACCAAGGCTCCGAC 360
    |||
Db 596 CGGGCCAAAGGCCCAAGAAAAGGGAAATTTCTGCTGCGCTTACGACCAAGGCTCCGAC 655
Oy 361 CACCATCTGTTTCTCAATTTACCTCTTCTGCGACACTGCTGAAGTGAAGAGATG 420
    |||
Db 656 CACCATCTGTTTCTCAATTTACCTCTTCTGCGACACTGCTGAAGTGAAGAGATG 715
Oy 421 CCAACCCCTCTCATTTGTTCTTCCAGCCCTGCCCCCAACCCCTCCCTAGTGA 480
    |||
Db 716 CCAACCCCTCTCATTTGTTCTTCCAGCCCTGCCCCCAACCCCTCCCTAGTGA 775
Oy 481 GTTCTTCTGCGGCTGCTTTTATTTGCGGTAGGAGCGGAGTCCGTGTTCTTTGTT 540
    |||
Db 776 GTTCTTCTGCGGCTGCTTTTATTTGCGGTAGGAGCGGAGTCCGTGTTCTTTGTT 835
Oy 541 CCTGTCAATATATGAAGACGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGACTGAAT 600
    |||
Db 836 CCTGTCAATATATGAAGACGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGACTGAAT 895
Oy 601 TTTCACTATGACTTGAAGAGAGAGTGAAGTGAAGTTCACCCCATGCTGTGTATAC 660
    |||
Db 896 TTTCACTATGACTTGAAGAGAGAGTGAAGTGAAGTTCACCCCATGCTGTGTATAC 955
Oy 661 CGGAGTCAAGGCGCAGGCTGTGAGAGTCACTTGAAGTCACTGAGTGGGCACTGCC 720
    |||
Db 956 CGGAGTCAAGGCGCAGGCTGTGAGAGTCACTTGAAGTCACTGAGTGGGCACTGCC 1015
Oy 721 TTTTGAAGCCTCCAGTCCATTCATCCCTGATGAGGGGATGTTGAGATGACGACA 780
    |||
Db 1016 TTTTGAAGCCTCCAGTCCATTCATCCCTGATGAGGGGATGTTGAGATGACGACA 1075
Oy 781 GTGAGATGACGTTTCTTGAAGGCTGAGGCGCACTTCCACTCAAGGCTCCCTCGCTTG 840
    |||
Db 1076 GTGAGATGACGTTTCTTGAAGGCTGAGGCGCACTTCCACTCAAGGCTCCCTCGCTTG 1135
Oy 841 ACATTCAAACTCATGCTGCTGAAGAAACCATTTCTGACGACGAGAAATTTGCTGTTCCGCC 900
    |||
Db 1136 ACATTCAAACTCATGCTGCTGAAGAAACCATTTCTGACGACGAGAAATTTGCTGTTCCGCC 1195
Oy 901 CTGAGTTGGGCTAGTACTGAGACTCAATGACTGGAGTTAGACTGGGGCTCGGGCT 960
    |||
Db 1196 CTGAGTTGGGCTAGTACTGAGACTCAATGACTGGAGTTAGACTGGGGCTCGGGCT 1255
Oy 961 CGCTCTGAAGAGTGTTAAGAAATCTTCTCAGTTCCTTTGACAGAGACTGCGCGGG 1020
    |||
Db 1256 CGCTCTGAAGAGTGTTAAGAAATCTTCTCAGTTCCTTTGACAGAGACTGCGCGGG 1315
Oy 1021 ACGGAAGAGCAAGGCGGCTGCAACAAAGCGGCGCTGCTGCTGTGAGTGGCATGTA 1080
    |||
Db 1316 ACGGAAGAGCAAGGCGGCTGCAACAAAGCGGCGCTGCTGCTGTGAGTGGCATGTA 1375
Oy 1081 CGCGCAGCGCTTCTGCTGTTGGCTGTGACGACGACAGGCGCAGACAGCAACCTTGC 1140
    |||
Db 1376 CGCGCAGCGCTTCTGCTGTTGGCTGTGACGACGACAGGCGCAGACAGCAACCTTGC 1434
Oy 1141 ACGAACACCGCCGAAACTGCTGCGAGACACGCTGTACAGAGCGGGTTGATGACGAG 1200
    |||

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Oy	1081	GCGGAGGGCGCTTCCTCCGCGTGTGGCGCTGCTGCAACGCAACAGCGGCGACGACAGCACTTGC	1140
Db	1438	CGCGAGGCGCTTCTCGTGTGTGGCGGTGCGAGCAGACGGCGGACGACACACAC	1141
Oy	1141	ACGAACACCCCGCCGAACCTGCTGGAGAGACACCGTGTACAGAGCGGGGTGATGACCGAG	1200
Db	1497	ACGAACACCCCGCCGAACCTGCTGGAGAGACACCGTGTACAGAGCGGGGTGATGACCGAG	1556
Oy	1201	CTGAGCTGAAAAACGCTCTCCGAGAGGGGAGGAGATATGTACGCCCGAAGTAGAC	1260
Db	1557	CTGAGGTGAAAAACGCTCTCCGAGAGGGGAGGAGATATGTACGCCCGAAGTAGAGAC	1616
Oy	1261	CTCGTCAGTGTGCTTGGGTTTTGGCCGCGACGCATATCCTCCGAATCGGTGGGCATC	1320
Db	1617	CTCGTCAGTGTGCTTGGGTTTTGGCCGCGACGCATATCCTCCGAATCTGGTGGGCATC	1676
Oy	1321	CAGCATACGCCCAATGTGCACACAAATACGCTGGGCGACACGACGAGAGGGAGAGAC	1380
Db	1677	CAGCATACGCCCAATGTGCACACAAATACGCTGGGCGACACGAGAGGGAGAGAC	1736
Oy	1381	AGAGAAAAAGAAAAACACAGCATGAGAACACAGTAAATGATTAATCCATTAATATTTAG	1440
Db	1737	AGAGAAAAAGAAAAACACAGCATGAGAACACAGTAAATGATTAATCCATTAATATTTAG	1796
Oy	1441	CCCTCGTGTCTGTGCTTACTGTGCCACGGAATGTACCAATTTTTCACTGTGTGACTTGA	1500
Db	1797	CCCTCGTGTGTGTGCTTACTGTGCCAGGAAAAAGTACCAATTTTTCACTGTGTGACTTGA	1856
Oy	1501	CAGCTTCTTTGGCACAGAGAGAGATTTTACACGTGTTCAAACCCGGGGGAGTTGG	1560
Db	1857	CAGCTTCTTTGGCACAGAGAGAGATTTTACACGTGTTCAAACCCGGGGGAGTTGG	1916
Oy	1561	CTGTGTTAAAGAAAGACATTAATGTCTTTAGACAGTGTAAAAAATAAAAA	1611
Db	1917	CTGTGTTAAAGAAAGACATTAATGTCTTTAGACAGTGTAAAAAATAAAAA	1967

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RESULT 16
US-09-397-022-4454
: Sequence 4454, Application US/09397022
: GENERAL INFORMATION:
: APPLICANT: Gearing, David P.
: APPLICANT: Holtzman, Douglas A.
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
: TITLE OF INVENTION: HUMAN FETAL SKIN LIBRARY
: FILE REFERENCE: MLN98-46PM
: CURRENT APPLICATION NUMBER: US/09/397,022
: PRIOR FILING DATE: 1993-09-15
: PRIOR APPLICATION NUMBER: 60/100,465
: PRIOR FILING DATE: 1998-09-15
: PRIOR APPLICATION NUMBER: 60/106,443
: PRIOR FILING DATE: 1998-10-30
: PRIOR APPLICATION NUMBER: 60/107,257
: PRIOR FILING DATE: 1998-11-05
: PRIOR APPLICATION NUMBER: 60/126,906
: PRIOR FILING DATE: 1999-03-30
: PRIOR APPLICATION NUMBER: 60/132,099
: PRIOR FILING DATE: 1999-04-30
: NUMBER OF SEQ ID NOS: 5775
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 4454
: LENGTH: 1918
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-397-022-4454

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Query Match	85.5%;	Score 1384;	DB 17;	Length 1918;
Best Local Similarity	99.8%;	Pred. No. 8.8e-257;		
Matches 1604; Conservative	0;	Mismatches 2;	Indels 1;	Gaps 1.

Qy 1 GGAACATTTTTCGGATGTCCTTGCCAGGCTTTGGCGCAAAATCCAGTGTACCA 60
|||||
Db 296 GGCACATTTTTCGGATGTCCTTGCCAGGCTTTGGCGTCAAAATCCAGTGTACCA 355

QY	61	GTGTGAAGAAATTTCACAGCTGAAACAAGACTGCTCCCTCCCGCAGTTCAATTGTGAATTGAC	120
Db	356	GTGTGAAGAAATTTCACAGCTGAAACAAGACTGCTCCCTCCCGCAGTTCAATTGTGAATTGAC	415
QY	121	GGTGAACGTTCAAGACATGTGTCAAGAAAGAATGATGAGCAAAAGTCCGGGATCATGTA	180
Db	416	GGTGAACGTTCAAGACATGTGTCAAGAAAGAATGATGAGCAAAAGTCCGGGATCATGTA	475
QY	181	CCGCAAGTCCCTGTGATATATACGGGCGCTGTCTCATATGCGCTTGC CGGGATACAGTCC	240
Db	476	CCGCAAGTCCCTGTGATATATACGGGCGCTGTCTCATATGCGCTTGC CGGGATACAGTCC	535
QY	241	CTGTCTCCCGAGGAAACATGAAGTCAAGTTTGGATCATAGCGCGCAAAACCCCTTTGTAA	300
Db	536	CTGTCTCCCGAGGAAACATGAAGTCAAGTTTGGATCATAGCGCGCAAAACCCCTTTGTAA	595
QY	301	CGGGCCAGGCCCAAGAAAGGGGAAGTTGTGCTCGGCGCTCAGGCCAGAGCGCTCCGCAC	360
Db	596	CGGGCCAGGCCCAAGAAAGGGGAAGTTGTGCTCGGCGCTCAGGCCAGAGCGCTCCGCAC	655
QY	361	CACCAATCCGTTTCCCAATTAATGAGCCCTTCTCGGCACACTGCTGAAAGTGAAGAATG	420
Db	656	CACCAATCCGTTTCCCAATTAATGAGCCCTTCTCGGCACACTGCTGAAAGTGAAGAATG	715
QY	421	CCAGCCCTCTCGCATTTGTTCTTCAGACCCCTCGGCCCAACCCCAACCTCCCTGAGTA	480
Db	716	CCAGCCCTCTCGCATTTGTTCTTCAGACCCCTCGGCCCAACCCCAACCTCCCTGAGTA	775
QY	481	GTTTCTTCTGGGAGTGCCTTTTATTTCTGGATAGGAGCGGGAGTCCGTGTCTTCTTGT	540
Db	776	GTTTCTTCTGGGAGTGCCTTTTATTTCTGGATAGGAGCGGGAGTCCGTGTCTTCTTGT	835
QY	541	CCCTGTCAAAATATGAAGAAGAGCTGGTAAAGCATTCGAAATAATCACCCTGACATGAT	600
Db	836	CCCTGTCAAAATATGAAGAAGAGCTGGTAAAGCATTCGAAATAATCACCCTGACATGAT	895
QY	601	TTTTCAGTATGTACTTGAAGAAGAGAGTGGATGAAGAATTCACCCCATGCTGTGTAA	660
Db	896	TTTTCAGTATGTACTTGAAGAAGAGAGTGGATGAAGAATTCACCCCATGCTGTGTAA	955
QY	661	CGAGTCAAGGCCACGGGCTGGGAGAGTGTAGTCCTTAABATCATAGTGGGCACTCTGCC	720
Db	956	CGAGTCAAGGCCACGGGCTGGGAGAGTGTAGTCCTTAABATCATAGTGGGCACTCTGCC	1015
QY	721	TTTTGTAAAGCCTTCAGATGTCCATTCCTCATCCCTGATAGGGGGATAGTTGAGATGAC	780
Db	1016	TTTTGTAAAGCCTTCAGATGTCCATTCCTCATCCCTGATAGGGGGATAGTTGAGATGAC	1075
QY	781	GTGAGAGAGAGCTTTCTTGAAGGCTGGAGGGCCAGTTCCCATCAAGGCTCCCTGCTTG	840
Db	1076	GTGAGAGAGAGCTTTCTTGAAGGCTGGAGGGCCAGTTCCCATCAAGGCTCCCTGCTTG	1135
QY	841	ACATTCAAACTTATGCTCTCTGAAAACCAATTCTCTGACACACAATTTGGCTGTTCCGGC	900
Db	1136	ACATTCAAACTTATGCTCTCTGAAAACCAATTCTCTGACACACAATTTGGCTGTTCCGGC	1195
QY	901	CTGAGTTGGGCTCTAGTGAAGTCAAGACTCAATGACTGAGGACTTAGAGTGGGCTCGGCT	960
Db	1196	CTGAGTTGGGCTCTAGTGAAGTCAAGACTCAATGACTGAGGACTTAGAGTGGGCTCGGCT	1255
QY	961	CGCTCTGAAGAAGTCTTAAAGAAATTTCTCAAGTTCTCTCTGACAGAGCACTGGGCGGG	1020
Db	1256	CGCTCTGAAGAAGTCTTAAAGAAATTTCTCAAGTTCTCTCTGACAGAGCACTGGGCGGG	1315
QY	1021	ACCGGAAGACAAACGGGCGCTGCACAAACGGGCGCTGTCCGATGGTGAGTGCACATGTA	1080
Db	1316	ACCGGAAGACAAACGGGCGCTGCACAAACGGGCGCTGTCCGATGGTGAGTGCACATGTA	1375
QY	1081	CGCGAGGGCGCTTCTGTGATGGTGGGGTGTCTGACGGAAGAGCGGCACACAGCACTTGC	1140
Db	1376	CGCGAGGGCGCTTCTGTGATGGTGGGGTGTCTGACGGAAGAGCGGCACACAGCACTTGC	1434

QY 1081 CGCGAGGCGCTTCTGTTGTTGGCTGCTGAGGAGGCGGAGCAGACCTTGC 1140
 1360 CGCGAGGCGCTTCTGTTGTTGGCTGCTGAGGAGGCGGAGCAGACCTTGC 1418
 QY 1141 AGGACACCGGCGGAACTGCTGCGAGGAGCAGCCTGTCAGAGCGGTTGATACCGAG 1200
 1419 AGGACACCGGCGGAACTGCTGCGAGGAGCAGCCTGTCAGAGGAGGTTGATACCGAG 1478
 QY 1201 CTGAGGTAGAAAACGCTCTCGAGAGAGGAGGAGATCATGTACGCCGGAAGTAGGAC 1260
 1479 CTGAGGTAGAAAACGCTCTCGAGAGAGGAGGAGATCATGTACGCCGGAAGTAGGAC 1538
 QY 1261 CTGCTCAGTCTGCTGTTGGGTTGGCGGAGCAGCAGTATCTCCGATCTGTTGGGCTC 1320
 1539 CTGCTCAGTCTGCTGTTGGGTTGGCGGAGCAGCAGTATCTCCGATCTGTTGGGCTC 1598
 QY 1321 CAGCATACGGGCGCAATGTCACAAATCATAGCCCTGGGAGAGCAGCAGAGAGAGAGAC 1380
 1599 CAGCATACGGGCGCAATGTCACAAATCATAGCCCTGGGAGAGCAGCAGAGAGAGAGAC 1658
 QY 1381 AGAGAAAAGAAAACACAGCATGAGAACAGATTAATGAATAAACCATTAATATTTAG 1440
 1659 AGAGAAAAGAAAACACAGCATGAGAACAGATTAATGAATAAACCATTAATATTTAG 1718
 QY 1441 CCCCTCTGTTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
 1719 CCCCTCTGTTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1778
 QY 1501 CAGCTTCTTTTGGCAGAGAGAGAGAGATTTAACTTTTCAAAACCCGGGAGTTGG 1560
 1779 CAGCTTCTTTTGGCAGAGAGAGAGATTTAACTTTTCAAAACCCGGGAGTTGG 1838
 QY 1561 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAATTTTTTTT 1619
 1839 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAATTTTTTTT 1897

RESULT 13

US-09-970-966-214
 : Sequence 214, Application US/09970966
 : GENERAL INFORMATION:
 : APPLICANT: Stolk, John A.
 : APPLICANT: Molesh, David Alan
 : APPLICANT: Filing, Steven P.
 : APPLICANT: Xu, Jianshun
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 : TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 : FILE REFERENCE: 210121.4846
 : CURRENT APPLICATION NUMBER: US/09/970,966
 : CURRENT FILING DATE: 2001-10-02
 : NUMBER OF SEQ ID NOS: 215
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 214
 : LENGTH: 1897
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-09-970-966-214

Query Match 86.2% Score 1396: DB 36: Length 1897:
 Best Local Similarity 99.8% Pred. No. 4.4e-259:
 Matches 1616: Conservative 0: Mismatches 2: Indels 1: Gaps 1:

QY 1 GCGAATCTTTTTCGAGATTTCTTCTGCTGAGGCTTTGCGCTGCAAAATTCAGTGTCTACA 60
 280 GCGAATCTTTTTCGAGATTTCTTCTGCTGAGGCTTTGCGCTGCAAAATTCAGTGTCTACA 339
 QY 61 GTGTGAAGATTTTCAGCTGACACAGCATGCTCTCCCGGAGTTCATTTGATTTGAC 120
 340 GTGTGAAGATTTTCAGCTGACACAGCATGCTCTCCCGGAGTTCATTTGATTTGAC 399
 QY 121 GGTGAAGCTTCAAGCATGTGTGAGAAAGATGATGAGCAAAATGCGGAGATCATGTA 180
 400 GGTGAAGCTTCAAGCATGTGTGAGAAAGATGATGAGCAAAATGCGGAGATCATGTA 459

QY 181 CGGCAAGTCTTGTGATCATGAGGCGCTGTCATGCGCTTGCAGGAGTCTT 240
 460 CGGCAAGTCTTGTGATCATGAGGCGCTGTCATGCGCTTGCAGGAGTCTT 519
 QY 241 CTGCTCCCGAGGAAATCTGAACTGATTTGATCATGCTGTCGAAACACCTCTTTTAA 300
 520 CTGCTCCCGAGGAAATCTGAACTGATTTGATCATGCTGTCGAAACACCTCTTTTAA 579
 QY 301 CGGCGCAAGGCGGCAAGAAAGGGAAGTTGCGCTCGGCGCTCAAGGCGAGGCTCCGAC 360
 580 CGGCGCAAGGCGGCAAGAAAGGGAAGTTGCGCTCGGCGCTCAAGGCGAGGCTCCGAC 639
 QY 361 CACCATCTGTTCTCCTCAATTAATGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
 640 CACCATCTGTTCTCCTCAATTAATGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 699
 QY 421 CCAACCCCT 480
 700 CCAACCCCT 759
 QY 481 GTTCT 540
 760 GTTCT 819
 QY 541 CCTGTGCAATTAATGAAGAGCTCGTAAAGCATTTGATTAATTAATTAATTAATTAAT 600
 820 CCTGTGCAATTAATGAAGAGCTCGTAAAGCATTTGATTAATTAATTAATTAATTAAT 879
 QY 601 TTTTCAATTAATGAAGAGCTCGTAAAGCATTTGATTAATTAATTAATTAATTAAT 660
 880 TTTTCAATTAATGAAGAGCTCGTAAAGCATTTGATTAATTAATTAATTAATTAAT 939
 QY 661 CGGAGTCAAGGCGGAGGCTGAGAGTCAATGCTTGAAGTCAATGCTTGAAGTCAATGCT 720
 940 CGGAGTCAAGGCGGAGGCTGAGAGTCAATGCTTGAAGTCAATGCTTGAAGTCAATGCT 999
 QY 721 TTTTGAAGGCTTCAATGCTTGAAGTCAATGCTTGAAGTCAATGCTTGAAGTCAATGCT 780
 1000 TTTTGAAGGCTTCAATGCTTGAAGTCAATGCTTGAAGTCAATGCTTGAAGTCAATGCT 1059
 QY 781 GTGAGAGTCAATGCTTGAAGTCAATGCTTGAAGTCAATGCTTGAAGTCAATGCTTGA 840
 1060 GTGAGAGTCAATGCTTGAAGTCAATGCTTGAAGTCAATGCTTGAAGTCAATGCTTGA 1119
 QY 841 ACATTCAAATCTCATGCTCTGAAACCATTTCTGTGAGAGAAATGCTGCTTCTGCGC 900
 1120 ACATTCAAATCTCATGCTCTGAAACCATTTCTGTGAGAGAAATGCTGCTTCTGCGC 1179
 QY 901 CTGAGTTGGGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 960
 1180 CTGAGTTGGGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 1239
 QY 961 CGCTCTGAAGAGTCTTGAAGAAATCTTCTGAGTCTTCTGAGAGAGTCTGCGGCG 1020
 1240 CGCTCTGAAGAGTCTTGAAGAAATCTTCTGAGTCTTCTGAGAGAGTCTGCGGCG 1299
 QY 1021 ACGGAG 1080
 1300 ACGGAG 1359
 QY 1081 CGCGAGGCGCTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 1140
 1360 CGCGAGGCGCTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 1418
 QY 1141 ACGAACACCGGCGGAACTGCTGCGAGGAGCAGCCTGTATACAGGAGGTTGATACCGAG 1200
 1419 ACGAACACCGGCGGAACTGCTGCGAGGAGCAGCCTGTATACAGGAGGTTGATACCGAG 1478
 QY 1201 CTGAGGTAGAAAACGCTCTCGAGAGAGGAGGAGATCATGTACGCCGGAAGTAGGAC 1260
 1479 CTGAGGTAGAAAACGCTCTCGAGAGAGGAGGAGATCATGTACGCCGGAAGTAGGAC 1538

Qy	1	GGCAACTTTTGGCGATTGTTCTTGCTTCCAGCGCTTGGCGTGGAAATCCAGTGTACCA	60
Db	280	GGCACTTTTGGCGATTGTTCTTGCTTCCAGCGCTTGGCGTGGAAATCCAGTGTACCA	33
Qy	61	GGTGAATAATTCACAGCTGAACCAACGACTGCTCTCCCGAGTTTCATTGTGAATTGCAC	12
Db	340	GTGTAAATAATTCAGCTGAACCAACGACTGCTCTCCCGAGTTTCATTGTGAATTGCAC	39
Qy	121	GGTGAAGCTTGAACAGATGTGTCTGAAGAAAGATGTGACCAAGTCCGGGATCATGTGA	18
Db	400	GGTGAAGCTTGAACAGATGTGTCTGAAGAAAGATGTGACCAAGTCCGGGATCATGTGA	45
Qy	181	CCGGAAGCTCTGTGCATCATATCAGCGGCTGTCTCATTCGCTGTGGCGGTACAGTCTT	24
Db	460	CCGGAAGCTCTGTGCATCATATCAGCGGCTGTCTCATTCGCTGTGGCGGTACAGTCTT	51
Qy	241	CTGCTCCCGAAGGAAATCTGAATCAGTTTGGACATCCACTGTCTGCACACCCCTTTGTAA	30
Db	520	CTGCTCCCGAAGGAAATCTGAATCAGTTTGGACATCCACTGTCTGCACACCCCTTTGTAA	57
Qy	301	CGGGCCAAAGGCCCAAGAAAAGGGGAAGTTCTGCTGGGCTCAGAGCCAGGCTCCGAC	36
Db	580	CGGGCCAAAGGCCCAAGAAAAGGGGAAGTTCTGCTGGGCTCAGAGCCAGGCTCCGAC	63
Qy	361	CACCATCTGTTCCTCAAAATAGCCCTCTTCTCGGCACATCTGTAGCTGAAGAGATG	42
Db	640	CACCATCTGTTCCTCAAAATAGCCCTCTTCTCGGCACATCTGTAGCTGAAGAGATG	69
Qy	421	CCACCCCTCTCTCATTTGTTCTTCCAGCCCTCGCCCAACCCCCACCTCTCGTAGGA	48
Db	700	CCACCCCTCTCTCATTTGTTCTTCCAGCCCTCGCCCAACCCCCACCTCTCGTAGGA	75
Qy	481	GTTTCTCTCTGGGTCGCTTTAATTCGGGTAGGGAAGCGGAGATCCGTGCTCTTTGTT	54
Db	760	GTTTCTCTCTGGGTCGCTTTAATTCGGGTAGGGAAGCGGAGATCCGTGCTCTTTGTT	81
Qy	541	CCGTGTCAAAATAATGAAGAAGCTCGTAAAGCATTTCAATAAATTCAGCTGTGCTAAT	60
Db	820	CCGTGTCAAAATAATGAAGAAGCTCGTAAAGCATTTCAATAAATTCAGCTGTGCTAAT	87
Qy	601	TTTTCAATATGTCTGAAGGAAGGAGGTGAGATGAAGTTACCCCATGTCTGTGTAC	66
Db	880	TTTTCAATATGTCTGAAGGAAGGAGGTGAGATGAAGTTACCCCATGTCTGTGTAC	93
Qy	661	CGGAGTCAAGGCCAGCGTGGCAGATCTAGTCTTGAAGATCATCTGAGGTGGGATCGCC	72
Db	940	CGGAGTCAAGGCCAGCGTGGCAGATCTAGTCTTGAAGATCATCTGAGGTGGGATCGCC	99
Qy	721	TTTTGAAAGGCTCCAGTGTCCATTTCCATCCCTGATGGGGCATATGTTGAGACTGCAG	78
Db	1000	TTTTGAAAGGCTCCAGTGTCCATTTCCATCCCTGATGGGGCATATGTTGAGACTGCAG	105
Qy	781	GTGAGAGTGAAGTTTCTTGAAGGCTGAGAGGCCAGTCCCACTCAAGGCTCCCTCGCTTG	84
Db	1060	GTGAGAGTGAAGTTTCTTGAAGGCTGAGAGGCCAGTCCCACTCAAGGCTCCCTCGCTTG	111
Qy	841	ACATTCAAACTTCAATGCTCTCGAAACCAATCTTCTGCAAGCAATTTGGCTGTGTCGCG	90
Db	1120	ACATTCAAACTTCAATGCTCTCGAAACCAATCTTCTGCAAGCAATTTGGCTGTGTCGCG	117
Qy	901	CTGAGTTGGGCTCTAGTACTCGAGATCTCAATATAGCTGGGACCTTAGACTGGGCTCGGCT	96
Db	1180	CTGAGTTGGGCTCTAGTACTCGAGATCTCAATATAGCTGGGACCTTAGACTGGGCTCGGCT	123
Qy	961	CGCTCTGAAAAGTCTTTAAGAAATCTTCTCAATCTCTTGCAGAGACTGTGGCCGCGG	102
Db	1240	CGCTCTGAAAAGTCTTTAAGAAATCTTCTCAATCTCTTGCAGAGACTGTGGCCGCGG	129
Qy	1021	ACGGGAAGAGCAAGGGCGCTGCAACAAGGGGCGGTGCGGTGTGTGAGTGTGCGCATGA	108
Db	1300	ACGGGAAGAGCAAGGGCGCTGCAACAAGGGGCGGTGCGGTGTGTGAGTGTGCGCATGA	135

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Db 1015 CTGAGATGACGTTTCTTAGAGGCTGAGAGGCGCAGTCCCATCAAGGCTCCCTGCTTG 1074
Oy 841 ACATTTCAACTTCATGCTCCTGAAACCAATTCCTGACAGAAATGGCTGGTTGGCC 900
Db 1075 ACATTTCAACTTCATGCTCCTGAAACCAATTCCTGACAGAAATGGCTGGTTGGCC 1134
Oy 901 CTGAGTTGGGCTTAGTACTGAGACTCAATGACTGGAGCTTAGAGCTGGGGCTGGCCCT 960
Db 1135 CTGAGTTGGGCTTAGTACTGAGACTCAATGACTGGAGCTTAGAGCTGGGGCTGGCCCT 1194
Oy 961 CGCTCTGAAAGTGTCTTAAGAAATCTTCTCAGTTCTCTTTCGAGAGACTGGCCGGG 1020
Db 1195 CGCTCTGAAAGTGTCTTAAGAAATCTTCTCAGTTCTCTTTCGAGAGACTGGCCGGG 1254
Oy 1021 ACCGCAAGACCAACGGGGCTGACAAAGGGGGCTGCTGCTGGTGGAGTGGCATGTA 1080
Db 1255 ACCGCAAGACCAACGGGGCTGACAAAGGGGGCTGCTGCTGGTGGAGTGGCATGTA 1314
Oy 1081 CGCGAGGCGCTTCTGCTGGTGGCTGCTGACGACAGGCGGACAGCACACCTTGC 1140
Db 1315 CGCGAGGCGCTTCTGCTGGTGGCTGCTGACGACAGGCGGACAGCACACCTTGC 1373
Oy 1141 ACCAACACCCCGGAACTGCTGCGAGACACCCGTACAGAGAGGGGTTGATACCGAG 1200
Db 1374 ACCAACACCCCGGAACTGCTGCGAGACACCCGTACAGAGAGGGGTTGATACCGAG 1433
Oy 1201 CTGAGGTAGAAAGTCTCCGAGAGGGAGAGATCATGTACGCCCGGAAGTAGGAC 1260
Db 1434 CTGAGGTAGAAAGTCTCCGAGAGGGAGAGATCATGTACGCCCGGAAGTAGGAC 1493
Oy 1261 CTGCTCAAGTCTGCTGGGCTTGGCCGACGACATGATCTCCGGAATGGTGGCATC 1320
Db 1494 CTGCTCAAGTCTGCTGGGCTTGGCCGACGACATGATCTCCGGAATGGTGGCATC 1553
Oy 1321 CAGCATACGGCCATGTCACAAACATCAGCCCTGGGCAACACAGAGAGAGAGAGAC 1380
Db 1554 CAGCATACGGCCATGTCACAAACATCAGCCCTGGGCAACACAGAGAGAGAGAGAC 1613
Oy 1381 AGAGAAAAAGAAAAACACAGCATGAGAACACAGTAATGAATAAACATTAATTTAG 1440
Db 1614 AGAGAAAAAGAAAAACACAGCATGAGAACACAGTAATGAATAAACATTAATTTAG 1673
Oy 1441 CCCCTCTGCTGCTGCTTACTGCGCAAGAAATGTTACCAATTTTTCAGTGGACTTGA 1500
Db 1674 CCCCTCTGCTGCTGCTTACTGCGCAAGAAATGTTACCAATTTTTCAGTGGACTTGA 1733
Oy 1501 CAGCTTCTTTTGGCCACAGCAAGAGAGATTTTAACTGTTTCAACCCGGGGAGTTGG 1560
Db 1734 CAGCTTCTTTTGGCCACAGCAAGAGAGATTTTAACTGTTTCAACCCGGGGAGTTGG 1793
Oy 1561 CTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTGT 1599
Db 1794 CTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTGT 1832

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RESULT 11
PCT-US01-45395-214
; Sequence 214, Application PC/TUS0145395
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Xu, Jlangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Filing, Steven P.
; APPLICANT: Molesh, David Alan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.48401PC
; CURRENT APPLICATION NUMBER: PCT/US01/45395
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214

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; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-45395-214

Query Match
Best local similarity 99.8%; Pred. No. 4,4e-259;
Matches 1616; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Oy 1 GGCACATTTTGGCGGATTTGTTCTTCTTCCAGGCTTTGGCGCTGCAATGACGTACCA 60
Db 280 GGCACATTTTGGCGGATTTGTTCTTCTTCCAGGCTTTGGCGCTGCAATGACGTACCA 339
Oy 61 GGTGTAAGTAATTCAGCTGAAACAGACTGCTCCCTCCCGAGTTCTATTGTAATTCAC 120
Db 340 GGTGTAAGTAATTCAGCTGAAACAGACTGCTCCCTCCCGAGTTCTATTGTAATTCAC 399
Oy 121 GGTGTAAGTAATTCAGCTGAAACAGACTGCTCCCTCCCGAGTTCTATTGTAATTCAC 180
Db 400 GGTGTAAGTAATTCAGCTGAAACAGACTGCTCCCTCCCGAGTTCTATTGTAATTCAC 459
Oy 181 CGGCAAGTCTGATGATCATGAGGCGCTGCTCATGCTCTGCGGATACAGTCTT 240
Db 460 CGGCAAGTCTGATGATCATGAGGCGCTGCTCATGCTCTGCGGATACAGTCTT 519
Oy 241 CTGCTCCCGAGGAGAACTGAACTAGTTGATCATGCTGCTGCAACACCTCTTTGTAA 300
Db 520 CTGCTCCCGAGGAGAACTGAACTAGTTGATCATGCTGCTGCAACACCTCTTTGTAA 579
Oy 301 CGGCGCAAGGCGCCAGAAAGGGAGTTTCTGCGGCGCCGACAGGCGGCTCCGAC 360
Db 580 CGGCGCAAGGCGCCAGAAAGGGAGTTTCTGCGGCGCCGACAGGCGGCTCCGAC 639
Oy 361 CACCATCTGTTCTCAATTAAGCCCTCTTCTGCGACACTGCTGAGCTGAAGAGATG 420
Db 640 CACCATCTGTTCTCAATTAAGCCCTCTTCTGCGACACTGCTGAGCTGAAGAGATG 699
Oy 421 CCAACCCCTCTGCAATTTCTTCCAGGCTTGGCCCAACCCCGACCTCCCTGAGTGA 480
Db 700 CCAACCCCTCTGCAATTTCTTCCAGGCTTGGCCCAACCCCGACCTCCCTGAGTGA 759
Oy 481 GTTCTCTGCGGATGCTTTTATCTGGGTAGGAGCGGAGTCCGTCTCTTTGTT 540
Db 760 GTTCTCTGCGGATGCTTTTATCTGGGTAGGAGCGGAGTCCGTCTCTTTGTT 819
Oy 541 CCTGTGCAATTAATGAAGAGCTCGTAAAGCATTTGTGAATTAATTCACCCGACTGAT 600
Db 820 CCTGTGCAATTAATGAAGAGCTCGTAAAGCATTTGTGAATTAATTCACCCGACTGAT 879
Oy 601 TTTGAGTATGACTTGAAGAGAGAGTGAAGTGAAGTTCAACCCCATGCTGTGTAC 660
Db 880 TTTGAGTATGACTTGAAGAGAGAGTGAAGTGAAGTTCAACCCCATGCTGTGTAC 939
Oy 661 CGGAGTCAAGGCCAGGCTGCGAGAGTCACTTGAAGTCACTGAGAGTGGCATCTGCC 720
Db 940 CGGAGTCAAGGCCAGGCTGCGAGAGTCACTTGAAGTCACTGAGAGTGGCATCTGCC 999
Oy 721 TTTTGTAAAGCTCTCAGTGTTCATTCATCCGTGATGGGGGCAATGTTGAGACTGACA 780
Db 1000 TTTTGTAAAGCTCTCAGTGTTCATTCATCCGTGATGGGGGCAATGTTGAGACTGACA 1059
Oy 781 GTGAGAGTGAAGTTTCTTGAAGGCTGAGAGGCCAGTTCCACATCAAGAGCTCCCTG 840
Db 1060 GTGAGAGTGAAGTTTCTTGAAGGCTGAGAGGCCAGTTCCACATCAAGAGCTCCCTG 1119
Oy 841 ACATTTCAACTTCATGCTCTGAAACCAATTCCTGACAGAAATGGCTGGTTGGCC 900
Db 1120 ACATTTCAACTTCATGCTCTGAAACCAATTCCTGACAGAAATGGCTGGTTGGCC 1179
Oy 901 CTGAGTTGGGCTTAGTACTGAGACTCAATGACTGGAGCTTAGAGCTGGGGCTGGCCCT 960
Db 1180 CTGAGTTGGGCTTAGTACTGAGACTCAATGACTGGAGCTTAGAGCTGGGGCTGGCCCT 1239

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Db 541 CCTGTGCAATTAATGAAGAGCTCGTAAAGCATTTCTGAATTAATTCAGCCTGACTGAAT 600
QY 601 TTTCAGTATGACTTGAAGAGAGGTGAGTGAAGTTCACCCCATTCCTCTGTGTAAAC 660
Db 601 TTTCAGTATGACTTGAAGAGAGGTGAGTGAAGTTCACCCCATTCCTCTGTGTAAAC 660
QY 661 CGGAGTCAAGGCCAGGCTGGCAGAGTCACTTGAAGTCACTGAGAGTGGGATCTGGC 720
Db 661 CGGAGTCAAGGCCAGGCTGGCAGAGTCACTTGAAGTCACTGAGAGTGGGATCTGGC 720
QY 721 TTTTGTAAAGCTCCCACTGCTCAATTCATCCCTGATGGGGCAATGTTGAGACTGCAAG 780
Db 721 TTTTGTAAAGCTCCCACTGCTCAATTCATCCCTGATGGGGCAATGTTGAGACTGCAAG 780
QY 781 GTGAGAGTGAAGTCTTCTTGAAGGCTGAGAGGCGAGTTCACACCAAGGCTCCCTCCCTTG 840
Db 781 GTGAGAGTGAAGTCTTCTTGAAGGCTGAGAGGCGAGTTCACACCAAGGCTCCCTCCCTTG 840
QY 841 ACATTTCAACTTCACTGCTCCTGAAGAACATTCCTGACAGAGAAATGGCTGTTGCGCG 900
Db 841 ACATTTCAACTTCACTGCTCCTGAAGAACATTCCTGACAGAGAAATGGCTGTTGCGCG 900
QY 901 CTGAGTTGGGCTCTAGAGACTGACATGACAGTGGAGCTTAACTGGGCTCGGCT 960
Db 901 CTGAGTTGGGCTCTAGAGACTGACATGACAGTGGAGCTTAACTGGGCTCGGCT 960
QY 961 CGCTCTGAAAGTGTGAAGAAATCTTCTCACTTCTCTGACAGAGAGTGGCGCGG 1020
Db 961 CGCTCTGAAAGTGTGAAGAAATCTTCTCACTTCTCTGACAGAGAGTGGCGCGG 1020
QY 1021 ACCGGAAGAGCAACGGGCGCTGCAAAAGCGGCGCTGTCGGTGGAGTGGCGCATGTA 1080
Db 1021 ACCGGAAGAGCAACGGGCGCTGCAAAAGCGGCGCTGTCGGTGGAGTGGCGCATGTA 1080
QY 1081 CGGCGAGGCGCTTCTGTGGTGGCTGCTGACAGAGAGGCGGCGACACAGCACTTCG 1140
Db 1081 CGGCGAGGCGCTTCTGTGGTGGCTGCTGACAGAGAGGCGGCGACACAGCACTTCG 1140
QY 1141 ACAGAAACCCCGGAAACTGCTGCGAGAACCCGCTGTACAGAGCGGGTGTGATGACCGAG 1200
Db 1141 ACAGAAACCCCGGAAACTGCTGCGAGAACCCGCTGTGTACAGAGCGGGTGTGATGACCGAG 1200
QY 1201 CTGAGGTAGAAAAGCTCTCCGAGAGGAGAGAGATATGAGCCCGGAAAGTAGAGAC 1260
Db 1201 CTGAGGTAGAAAAGCTCTCCGAGAGGAGAGAGATATGAGCCCGGAAAGTAGAGAC 1260
QY 1261 CTGCTCAAGTCTGCTGTTGGGTTGGCCGACGACATGATCCCGAATCTGTTGGGCATC 1320
Db 1261 CTGCTCAAGTCTGCTGTTGGGTTGGCCGACGACATGATCCCGAATCTGTTGGGCATC 1320
QY 1321 CAGCATAGGCCCAATGTCAACAACATCAGCCTGGGAGACACAGAGAGAGAGAGAC 1380
Db 1321 CAGCATAGGCCCAATGTCAACAACATCAGCCTGGGAGACACAGAGAGAGAGAGAC 1380
QY 1381 AGAGAAAGAAAACACAGCATGAGAACACAGTAAATGAATGAATTAATTTAG 1440
Db 1381 AGAGAAAGAAAACACAGCATGAGAACACAGTAAATGAATGAATTAATTTAG 1440
QY 1441 CCCCTCTGTTCTGTCTTACTGGCAGGAATGTACCAATTTTCACTGTTGAGCTTGA 1500
Db 1441 CCCCTCTGTTCTGTCTTACTGGCAGGAATGTACCAATTTTCACTGTTGAGCTTGA 1500
QY 1501 CAGCTTCTTTTGGCAAGCAAGAGAAATTTAACATCTTCAAAACCCGCGGAGTGG 1560
Db 1501 CAGCTTCTTTTGGCAAGCAAGAGAAATTTAACATCTTCAAAACCCGCGGAGTGG 1560
QY 1561 CTGTGTAAAGAACCATTAATGCTTGAAGAGTGTAAAGAAAATTTTAAAAA 1619
Db 1561 CTGTGTAAAGAACCATTAATGCTTGAAGAGTGTAAAGAAAATTTTAAAAA 1619

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RESULT 10
US-10-108-260A-197

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; Sequence 197, Application US/10108260A
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO: 197
; LENGTH: 1832
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-197

Query Match      88.1%; Score 1427; DB 40; Length 1832;
Best Local Similarity 99.9%; Pred. No. 5e-265;
Matches 1597; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GGCACCTTTTTCGGATTTGTTCTTCTCCAGGCTTTGCTGCAAAATCCAGTCTACCA 60
Db 235 GGCAACTTTTTCGGATTTGTTCTTCTCCAGGCTTTGCTGCAAAATCCAGTCTACCA 294
QY 61 GTGTGAAGAAATCCAGCTGAACCAAGACTGCTCCCTCCCGAGTTCAATGTGAATTGAC 120
Db 295 GTGTGAAGAAATCCAGCTGAACCAAGACTGCTCCCTCCCGAGTTCAATGTGAATTGAC 354
QY 121 GGTGAACCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGAGTGGGATCATGTA 180
Db 355 GGTGAACCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGAGTGGGATCATGTA 414
QY 181 CGGCAAGTCTGTGATATCATGAGGCGCTGTCTCATTCGCTTCGCGGGATACAGTCTT 240
Db 415 CGGCAAGTCTGTGATATCATGAGGCGCTGTCTCATTCGCTTCGCGGGATACAGTCTT 474
QY 241 CTGCTCCCGAGGAAACTGAACATGATTGATGAGTGTGCAACACCCCTTTGTAA 300
Db 475 CTGCTCCCGAGGAAACTGAACATGATTGATGAGTGTGCAACACCCCTTTGTAA 534
QY 301 CGGGCCAGGCGCCAAAGAAAGGGAGTTCGCTCGGCTTCAGGCGAGGGCTCGGCAC 360
Db 535 CGGGCCAGGCGCCAAAGAAAGGGAGTTCGCTCGGCTTCAGGCGAGGGCTCGGCAC 594
QY 595 CACCATCCTGTTCCCTCAATTAAGCCCTCTTTCGCGACACTGCTGAAGAGAGATG 420
Db 421 CCACCCCTCCTGCAATGTTCTTCCAGCCCTCGGCCCAACCCCCCACTCCCTGAGTGA 480
QY 481 GTTTCCTTGGGTTGCTCTTATTCCTGGGTAAGGAGCGGAGTCCGTTCTCTTTGTT 540
Db 715 GTTTCCTTGGGTTGCTCTTATTCCTGGGTAAGGAGCGGAGTCCGTTCTCTTTGTT 774
QY 774 CCTGTGCAAAATTAAGAAAGAGCTCGTAAAGCATTTGAAATTAATTCAGCTGAGTAAT 600
Db 775 CCTGTGCAAAATTAAGAAAGAGCTCGTAAAGCATTTGAAATTAATTCAGCTGAGTAAT 834
QY 834 TTTTGAATGATGACTTGAAGAGAGGTTGAAGTAAGTTTCAACCCCATCTGTGTAAAC 660
Db 835 TTTTGAATGATGACTTGAAGAGAGGTTGAAGTAAGTTTCAACCCCATCTGTGTAAAC 894
QY 894 CGGAGTCAAGGCCAGGCTGGCAGAGTCACTTGAAGTCACTGAGAGTGGGATCTGCC 720
Db 895 CGGAGTCAAGGCCAGGCTGGCAGAGTCACTTGAAGTCACTGAGAGTGGGATCTGCC 954
QY 954 TTTTGTAAAGCTTCACTGCTCAATTCATCCCTGATGGGGCATTAATTTGAGACTGCA 780
Db 955 TTTTGTAAAGCTTCACTGCTCAATTCATCCCTGATGGGGCATTAATTTGAGACTGCA 1014
QY 1014 GTGAGATGACGTTTCTTGAAGGCTGAGAGGCGAGTTCCCACTCAAGGCTCCCTGCTTG 840

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421 CCACCCCTCTGCATTTCTTCCAGCCCTGCCCCAACCCACCCTCCCTGATGA 480
421 CCACCCCTCTGCATTTCTTCCAGCCCTGCCCCAACCCACCCTCCCTGATGA 480
481 GTTCTTCTGCGTCTTTTATTTCTGGGTAGGAGCGGGATCCGTCTCTTTTGT 540
481 GTTCTTCTGCGTCTTTTATTTCTGGGTAGGAGCGGGATCCGTCTCTTTTGT 540
541 CCTGCAATATATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGATGA 600
541 CCTGCAATATATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGATGA 600
601 TTTCACTATGACTTGAAGAGAGAGTGAAGTGAATTTCAACCCCATGCTGTATAC 660
601 TTTCACTATGACTTGAAGAGAGAGTGAAGTGAATTTCAACCCCATGCTGTATAC 660
661 CGGAGTCAGGCGGAGCTGGCAGAGTCACTCTTGAAGTCACTGAGTGGGATCTGCC 720
661 CGGAGTCAGGCGGAGCTGGCAGAGTCACTCTTGAAGTCACTGAGTGGGATCTGCC 720
721 TTTTGTAAAGCTTCAGTGTCTCATTCATCCCTGATGGGGCATAGTTTGAAGTCA 780
721 TTTTGTAAAGCTTCAGTGTCTCATTCATCCCTGATGGGGCATAGTTTGAAGTCA 780
781 GTGAGAGTCACTTTTCTTATAGGCTGGAGGCGCAGTTCCCACTCAAGGCTCCCTG 840
781 GTGAGAGTCACTTTTCTTATAGGCTGGAGGCGCAGTTCCCACTCAAGGCTCCCTG 840
841 ACATTCAACTTATGCTCTGAAACCATTTCTGACAGAGAAATGGCTGTTCGCGC 900
841 ACATTCAACTTATGCTCTGAAACCATTTCTGACAGAGAAATGGCTGTTCGCGC 900
901 CTGAGTTGGCTCTAGTACTGAGACTCAATGAGCTTGAAGTGGGCTCGGCT 960
901 CTGAGTTGGCTCTAGTACTGAGACTCAATGAGCTTGAAGTGGGCTCGGCT 960
961 CGGCTTAAAGTCTTAAAGAAATCTTCTCATGTTCTTTCAGAGAGAGTGGCGGG 1020
961 CGGCTTAAAGTCTTAAAGAAATCTTCTCATGTTCTTTCAGAGAGAGTGGCGGG 1020
1021 ACAGGAGAGAGAGAGAGGCGCTGCAAGAGGCGGCTGTGAGTGGAGTGGCATGA 1080
1021 ACAGGAGAGAGAGAGAGGCGCTGCAAGAGGCGGCTGTGAGTGGAGTGGCATGA 1080
1081 CGGCAAGGCTTCTGCTGTGGTGGCTGTGAGTGGAGTGGAGTGGAGTGGAGTGG 1140
1081 CGGCAAGGCTTCTGCTGTGGTGGCTGTGAGTGGAGTGGAGTGGAGTGGAGTGG 1140
1141 ACAGAAACCCGCGAAGCTGCTGAGAGAGAGTGTATGATGATGATGATGATGATG 1200
1141 ACAGAAACCCGCGAAGCTGCTGAGAGAGAGTGTATGATGATGATGATGATGATG 1200
1201 CTGAGGTGAGAAAGAGTCTCGAAGAGGAGGAGTGTATGATGATGATGATGATG 1260
1201 CTGAGGTGAGAAAGAGTCTCGAAGAGGAGGAGTGTATGATGATGATGATGATG 1260
1261 CTGCTCAGTCTGCTGTGGTGGTGGCGGAGCATGATCCGCAATCTGTTGGGATC 1320
1261 CTGCTCAGTCTGCTGTGGTGGTGGCGGAGCATGATCCGCAATCTGTTGGGATC 1320
1321 CAGCATACGCGCAATGTCACAAATCAGCCCTGGGAGAGACAGAGAGAGAGAGAC 1380
1321 CAGCATACGCGCAATGTCACAAATCAGCCCTGGGAGAGACAGAGAGAGAGAGAC 1380
1381 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
1381 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
1441 CCCCTCTGCTGCTTACTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
1441 CCCCTCTGCTGCTTACTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500

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1501 CAGCTCTTTTGCACAGAGAGAGATTTAAGTCTTCAACCCCGGGAGTTGG 1560
1501 CAGCTCTTTTGCACAGAGAGAGATTTAAGTCTTCAACCCCGGGAGTTGG 1560
1561 CTGTGTAAAGAGAGAGATTTAAGTCTTCAACCCCGGGAGTTGG 1619
1561 CTGTGTAAAGAGAGAGATTTAAGTCTTCAACCCCGGGAGTTGG 1619

RESULT 9
US-10-212-677-211
: Sequence 211, Application US/10212677
: GENERAL INFORMATION:
: APPLICANT: Chenault, Ruth A.
: APPLICANT: Xu, Jiangchun
: APPLICANT: Fanger, Gary R.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.484C7
: CURRENT APPLICATION NUMBER: US/10/212.677
: CURRENT FILING DATE: 2002-08-02
: NUMBER OF SEQ ID NOS: 288
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 211
: LENGTH: 1619
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-212-677-211

Query Match          100.0%; Score 1619; DB 42; Length 1619;
Best Local Similarity 100.0%; Pred. No. 7.9e-302;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGCACCTTTTCCGAGATGTTCTTCCAGCTTTCGCTGCAAAATCCAGTGTACCA 60
1 GGCACCTTTTCCGAGATGTTCTTCCAGCTTTCGCTGCAAAATCCAGTGTACCA 60
61 GTGTGAAGAAATCCAGCTGAACAGAGCTCTCCCGAGTTCAATGTGAATTCGAC 120
61 GTGTGAAGAAATCCAGCTGAACAGAGCTCTCTCCCGAGTTCAATGTGAATTCGAC 120
121 GGTGAACGTTCAAGCATGTGTCAAGAAAGAGTGTGAAGCAATGCTCCGGATATGA 180
121 GGTGAACGTTCAAGCATGTGTCAAGAAAGAGTGTGAAGCAATGCTCCGGATATGA 180
181 CGGCAAGTCTGTGCTATCAAGCGGCTGTCTCATGCGCTGTGGCGGTACAGTCTT 240
181 CGGCAAGTCTGTGCTATCAAGCGGCTGTCTCATGCGCTGTGGCGGTACAGTCTT 240
241 CTGCTCCCGAGGAACTGACATGATTTGATGATGATGATGATGATGATGATGATG 300
241 CTGCTCCCGAGGAACTGACATGATTTGATGATGATGATGATGATGATGATGATG 300
301 CGGCGCAAGGCCCAAGAGAGAGAGTGTGCTGCGCTTCAGGCGGAGTCTCCGAC 360
301 CGGCGCAAGGCCCAAGAGAGAGAGTGTGCTGCGCTTCAGGCGGAGTCTCCGAC 360
361 CACCATCTGCTTCTCAAAATGAGCTCTTCTTCGCGACACTGTGAAGTGAAGAGATG 420
361 CACCATCTGCTTCTCAAAATGAGCTCTTCTTCGCGACACTGTGAAGTGAAGAGATG 420
421 CCACCCCTCTGCAATGTTCTTCCAGCCCTGCCCCAACCCCATCTCCCTGATGA 480
421 CCACCCCTCTGCAATGTTCTTCCAGCCCTGCCCCAACCCCATCTCCCTGATGA 480
481 GTTCTTCTGCGTCTTTTATTTCTGGGTAGGAGCGGGATCCGTCTCTTTTGT 540
481 GTTCTTCTGCGTCTTTTATTTCTGGGTAGGAGCGGGATCCGTCTCTTTTGT 540
541 CCTGCAATATATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGATGA 600
541 CCTGCAATATATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGATGA 600

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OY 61 GTGTGAAGATTCCAGCTGACAGACGCTCTCCCGGAGTTTCATTGTGAATTGAC 120
    |||
Db 61 GTGTGAAGATTCCAGCTGACAGACGCTCTCCCGGAGTTTCATTGTGAATTGAC 120
OY 121 GGTGAACGTTTCAAGACATGTGTCAAGAAAGAGTGTGAGCAAAAGTCCGGGATCATGTA 180
    |||
Db 121 GGTGAACGTTTCAAGACATGTGTCAAGAAAGAGTGTGAGCAAAAGTCCGGGATCATGTA 180
OY 181 CCGCAAGTCTGTGATCATCAGCGGCGTCTCATTCGCCCTCCCGGATACCACTCTT 240
    |||
Db 181 CCGCAAGTCTGTGATCATCAGCGGCGTCTCATTCGCCCTCCCGGATACCACTCTT 240
OY 241 CTGTCTCCCGAGGAACTGAATCTAGTTTGCATCAGCTGTGTCAACACCCCTTTGTAA 300
    |||
Db 241 CTGTCTCCCGAGGAACTGAATCTAGTTTGCATCAGCTGTGTCAACACCCCTTTGTAA 300
OY 301 CCGGCGCAAGGCGCCAGAAAGAGGAGTTCCTCGGCGCTCAGGCGAGGCGTCCGAC 360
    |||
Db 301 CCGGCGCAAGGCGCCAGAAAGAGGAGTTCCTCGGCGCTCAGGCGAGGCGTCCGAC 360
OY 361 CACCATCTGTCTCAAAATTAGCCCTTCTCGGACACGCTGTAAGCTGAAGAGAGATG 420
    |||
Db 361 CACCATCTGTCTCAAAATTAGCCCTTCTCGGACACGCTGTAAGCTGAAGAGAGATG 420
OY 421 CCACCCCTCCGCAATTTCTTCCAGCCCTCGCCCAACCCCGCACCTCTGTAGTGA 480
    |||
Db 421 CCACCCCTCCGCAATTTCTTCCAGCCCTCGCCCAACCCCGCACCTCTGTAGTGA 480
OY 481 GTTCTCTGTGGGTCTCTTTATCTGTGGGTAGGAGCGGAGTCCGGTCTCTTTGTT 540
    |||
Db 481 GTTCTCTGTGGGTCTCTTTATCTGTGGGTAGGAGCGGAGTCCGGTCTCTTTGTT 540
OY 541 CCTGTGCAATTAATGAAGAGCTCGTAAAGCATTTCTGAATTAATTCAGCTGACTGAAT 600
    |||
Db 541 CCTGTGCAATTAATGAAGAGCTCGTAAAGCATTTCTGAATTAATTCAGCTGACTGAAT 600
OY 601 TTTGAGTATGACTTGAAGAGAGAGTGTGAAGAAAGTTTCAACCCCATGTCTGTAAAC 660
    |||
Db 601 TTTGAGTATGACTTGAAGAGAGAGTGTGAAGAAAGTTTCAACCCCATGTCTGTAAAC 660
OY 661 CCGAGTCAAGGCCAGCTGCGACAGTCACTTAGAAGTCACTGAGTGGGCACTGTGCC 720
    |||
Db 661 CCGAGTCAAGGCCAGCTGCGACAGTCACTTAGAAGTCACTGAGTGGGCACTGTGCC 720
OY 721 TTTTGAAGCCTCCAGCTCCATTCATTCCTGATGGGGCATAGTTTGAAGCTGACA 780
    |||
Db 721 TTTTGAAGCCTCCAGCTCCATTCATTCCTGATGGGGCATAGTTTGAAGCTGACA 780
OY 781 GTGAGAGTGAAGCTTTTCTTAGGGCTGAGGGCGAGTTCCACTCAAGGCTCCCTGCTTG 840
    |||
Db 781 GTGAGAGTGAAGCTTTTCTTAGGGCTGAGGGCGAGTTCCACTCAAGGCTCCCTGCTTG 840
OY 841 ACATTCAAACTTATCTCTCTGAAAAACATTCCTGACAGACAGAAATTTGGCTGTGCGGC 900
    |||
Db 841 ACATTCAAACTTATCTCTCTGAAAAACATTCCTGACAGACAGAAATTTGGCTGTGCGGC 900
OY 901 CTGAGTTGGGCTCTAGTGAAGTCAAGTCAATGATGAGGACTTGAAGCTGAGGCTGCGCT 960
    |||
Db 901 CTGAGTTGGGCTCTAGTGAAGTCAAGTCAATGATGAGGACTTGAAGCTGAGGCTGCGCT 960
OY 961 CCGTCTGAAAAAGTCTTGAAGAAATCTTCTCAGTTCTCTTTCAGAGAGACTGGGCGGG 1020
    |||
Db 961 CCGTCTGAAAAAGTCTTGAAGAAATCTTCTCAGTTCTCTTTCAGAGAGACTGGGCGGG 1020
OY 1021 AGCGGAAGAGCAAGCGGCGCTCACAAAAGCGGCGCTGTGCGTGTGAGTGGCGCATGTA 1080
    |||
Db 1021 AGCGGAAGAGCAAGCGGCGCTCACAAAAGCGGCGCTGTGCGTGTGAGTGGCGCATGTA 1080
OY 1081 CCGCGAGCGCTTCTCTGAGTGTGGGTGCTGAGAGAGAGCGGCGAGCAGCAGCCTTGC 1140
    |||
Db 1081 CCGCGAGCGCTTCTCTGAGTGTGGGTGCTGAGAGAGAGCGGCGAGCAGCAGCCTTGC 1140
OY 1141 ACGAACAACCGCGCAACTGTCTGCGAGGACACGCTGTACAGAGACGGGTTGATGACCGAG 1200
    |||

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Db 1141 ACGAACAACCGCGCAAACTGTCTGAGAGACACCGTGTACAGAGAGGGGTGATACCGAG 1200
OY 1201 CTGAGGTAGAAAAAGCTCTCCGAGAAAGGAGAGAGATCATGTACGCCCGGAATAGAC 1260
    |||
Db 1201 CTGAGGTAGAAAAAGCTCTCCGAGAAAGGAGAGAGATCATGTACGCCCGGAATAGAC 1260
OY 1261 CTGCTCCAGTCTGCTGTGGGTGGTGGCCGACCAATGATCTCCGAATCTGGTGGGATC 1320
    |||
Db 1261 CTGCTCCAGTCTGCTGTGGGTGGTGGCCGACCAATGATCTCCGAATCTGGTGGGATC 1320
OY 1321 CAGCATAGGCGCAATGTCAACAATACAGCCCTGGGAGACAGAGAGAGAGAGAC 1380
    |||
Db 1321 CAGCATAGGCGCAATGTCAACAATACAGCCCTGGGAGACAGAGAGAGAGAGAC 1380
OY 1381 AGAGAAAAAGAAAAACACAGCATGAGAAACAGTAAATGATTAATTAATTTAG 1440
    |||
Db 1381 AGAGAAAAAGAAAAACACAGCATGAGAAACAGTAAATGATTAATTAATTTAG 1440
OY 1441 CCCCTCTGTCTGTGCTTACTGCGCAGGAAATGTACCAATTTTTCAGTGTGACTTGA 1500
    |||
Db 1441 CCCCTCTGTCTGTGCTTACTGCGCAGGAAATGTACCAATTTTTCAGTGTGACTTGA 1500
OY 1501 CAGCTTCTTTTGCACAAAGAGAGAAATTTAACTGTTTCAAAACCGGGGAGTGG 1560
    |||
Db 1501 CAGCTTCTTTTGCACAAAGAGAGAAATTTAACTGTTTCAAAACCGGGGAGTGG 1560
OY 1561 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAGAAAAA 1619
    |||
Db 1561 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAGAAAAA 1619

RESULT 7
US-09-970-966-211
: Sequence 211, Application US/09970966
: GENERAL INFORMATION:
: APPLICANT: Stolk, John A.
: APPLICANT: Molesb, David Alan
: APPLICANT: Fling, Steven P.
: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.484C6
: CURRENT APPLICATION NUMBER: US/09/970,966
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 211
: LENGTH: 1619
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-970-966-211

Query Match          100.0%; Score 1619; DB 36; Length 1619;
Best Local Similarity 100.0%; Pred. No. 7, 9e-302;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGCACATTTTTCGCGATTTTCTTCTTCAGGCTTTCGCTGCAATTCAGTCTACCA 60
    |||
Db 1 GGCACATTTTTCGCGATTTTCTTCTTCAGGCTTTCGCTGCAATTCAGTCTACCA 60
OY 61 GTGTGAAGATTCCAGCTGTAACAGACGCTCCCGGAGTTTCATTGTGAATTGAC 120
    |||
Db 61 GTGTGAAGATTCCAGCTGTAACAGACGCTCCCGGAGTTTCATTGTGAATTGAC 120
OY 121 GGTGAACGTTTCAAGACATGTGTCAAGAAAGAGTGTGAGCAAAAGTCCGGGATCATGTA 180
    |||
Db 121 GGTGAACGTTTCAAGACATGTGTCAAGAAAGAGTGTGAGCAAAAGTCCGGGATCATGTA 180
OY 181 CCGCAAGTCTGTGATCATCAGCGGCGTCTCATTCGCCCTCCCGGATACCACTCTT 240
    |||
Db 181 CCGCAAGTCTGTGATCATCAGCGGCGTCTCATTCGCCCTCCCGGATACCACTCTT 240

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TYPE: DNA
ORGANISM: Homo sapiens
US-09-825-294-211

Query Match 100.0%; Score 1619; DB 31; Length 1619;
Best Local Similarity 100.0%; Pred. No. 7.9e-302;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACACTTTTCCGAGATGTTCTGCTTCCAGGCTTTGCGGCGCAAAATCCAGTGTACCA 60
DB 1 GGCACACTTTTCCGAGATGTTCTGCTTCCAGGCTTTGCGGCGCAAAATCCAGTGTACCA 60
QY 61 GTGTGAAGATTCACGCTGACACAGCAGCTCTCCGCCGAGTTTCATTTGAAATGAC 120
DB 61 GTGTGAAGATTCACGCTGACACAGCAGCTCTCCGCCGAGTTTCATTTGAAATGAC 120
QY 121 GGTGAACGTTCAAGACATGTCTCAAGAAAGATGATGAGCAAGTGGCGGGATCATGTA 180
DB 121 GGTGAACGTTCAAGACATGTCTCAAGAAAGATGATGAGCAAGTGGCGGGATCATGTA 180
QY 181 CCGCAAGTCTGTCGATCATCAGCGGCTGTCATCGGCTTCCGCGGTTACAGTCCCT 240
DB 181 CCGCAAGTCTGTCGATCATCAGCGGCTGTCATCGGCTTCCGCGGTTACAGTCCCT 240
QY 241 CTGCTCCCAAGGAAACGTAAGTCTGATGATGATGATGATGATGATGATGATGATG 300
DB 241 CTGCTCCCAAGGAAACGTAAGTCTGATGATGATGATGATGATGATGATGATGATG 300
QY 301 CCGGCAAGGCGCCCAAGAAAGGGAAGTTCTGCGGCGCTCAGGCGGCTCCGAC 360
DB 301 CCGGCAAGGCGCCCAAGAAAGGGAAGTTCTGCGGCGCTCAGGCGGCTCCGAC 360
QY 361 CACCATCTGTTCTCAAAATTAAGCCCTCTTCCGACACATGCTGAAGAGATG 420
DB 361 CACCATCTGTTCTCAAAATTAAGCCCTCTTCCGACACATGCTGAAGAGATG 420
QY 421 CCACCCCTCTGCAATGTTCTTCCAGCCCTCCGCCACACCCCTCCCTGAGTGA 480
DB 421 CCACCCCTCTGCAATGTTCTTCCAGCCCTCCGCCACACCCCTCCCTGAGTGA 480
QY 481 GTTCTCTGAGGTCCTTTTATCTGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
DB 481 GTTCTCTGAGGTCCTTTTATCTGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 541 CCTGTCAATATATGAAGAGCTCGTAAAGCATTCGTAATTAATTCAGCTGATGAT 600
DB 541 CCTGTCAATATATGAAGAGCTCGTAAAGCATTCGTAATTAATTCAGCTGATGAT 600
QY 601 TTTTCAGTATGTTCTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
DB 601 TTTTCAGTATGTTCTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 661 CCGAGTCAAGGCGCAGGCTGCGAGATCAGTCCCTTGAAGTCACTAGAGTGGGCACT 720
DB 661 CCGAGTCAAGGCGCAGGCTGCGAGATCAGTCCCTTGAAGTCACTAGAGTGGGCACT 720
QY 721 TTTTAAAGCCTCAAGTGTCCATTCATCCCTGATGAGGAGGAGGAGGAGGAGGAG 780
DB 721 TTTTAAAGCCTCAAGTGTCCATTCATCCCTGATGAGGAGGAGGAGGAGGAGGAG 780
QY 781 GTGAAGAGTACCTTTTCTTAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
DB 781 GTGAAGAGTACCTTTTCTTAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 841 ACATTCAAATTCATGCTCTGTAAGAAACCATTCCTGACAGCAATTTGGCTGTGGGC 900
DB 841 ACATTCAAATTCATGCTCTGTAAGAAACCATTCCTGACAGCAATTTGGCTGTGGGC 900
QY 901 CTGAAGTGGGCTCTAGTGAAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCA 960
DB 901 CTGAAGTGGGCTCTAGTGAAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCA 960
QY 961 CGCTCTGAAGAAAGTGTGAAGAAATCTTCTCAGTTCCTCTGACAGGAGTGGCGCGG 1020

DB 961 CGCTCTGAAGAAAGTGTGAAGAAATCTTCTCAGTTCCTTGCAGAGGAGTGGCGCGG 1020
QY 1021 ACAGGAGAGACACAGGCGCTGCAACAGCGGCGCTGTGCTGCTGAGTGGCAGTGA 1080
DB 1021 ACAGGAGAGACACAGGCGCTGCAACAGCGGCGCTGTGCTGCTGAGTGGCAGTGA 1080
QY 1081 CCGCAGAGCGCTTCTGCTGAGTGGGCTGCTGAGCGGAGGAGGAGGAGGAGGAGGAG 1140
DB 1081 CCGCAGAGCGCTTCTGCTGAGTGGGCTGCTGAGCGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1141 ACAGAACCCGCGCAAACTGCTGAGAGACACCGTGTACAGAGCGGCTTGTATGACGAG 1200
DB 1141 ACAGAACCCGCGCAAACTGCTGAGAGACACCGTGTACAGAGCGGCTTGTATGACGAG 1200
QY 1201 CTGAGGTGAAGAAAGTCTCCGAGAAAGGAGAGAGATCATATACCCCGGAGTGA 1260
DB 1201 CTGAGGTGAAGAAAGTCTCCGAGAAAGGAGAGAGATCATATACCCCGGAGTGA 1260
QY 1261 CTGCTCCAGTCTGCTGAGGTTGGGCGGAGCCATGATCTCCGAAATCTGTTGGGATC 1320
DB 1261 CTGCTCCAGTCTGCTGAGGTTGGGCGGAGCCATGATCTCCGAAATCTGTTGGGATC 1320
QY 1321 CAGCATACGGCAATGTCAACATATCAGCCCTGGGAGACAGAGAGAGAGAGAGAC 1380
DB 1321 CAGCATACGGCAATGTCAACATATCAGCCCTGGGAGACAGAGAGAGAGAGAGAC 1380
QY 1381 AGAGAAAGAAAGAAACAGATGAGAAACAGATGAGAAATTAATTAATTAATTAAT 1440
DB 1381 AGAGAAAGAAAGAAACAGATGAGAAACAGATGAGAAATTAATTAATTAATTAAT 1440
QY 1441 CCCCTCTGCTGCTGCTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
DB 1441 CCCCTCTGCTGCTGCTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
QY 1501 CAGCTTCTTTTCCCAAGAGAGAGATTTAACTGTTTAAACCCGCGGAGTGG 1560
DB 1501 CAGCTTCTTTTCCCAAGAGAGAGATTTAACTGTTTAAACCCGCGGAGTGG 1560
QY 1561 CTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGTAAAGGAGGAGGAGGAGGAG 1619
DB 1561 CTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGTAAAGGAGGAGGAGGAGGAG 1619

RESULT 6
US-09-970-966-205
Sequence 205, Application US/09970966
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Molesch, David Alan
APPLICANT: Fling, Steven P.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C6
CURRENT APPLICATION NUMBER: US/09/970,966
CURRENT FILING DATE: 2001-10-02
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 205
LENGTH: 1619
TYPE: DNA
ORGANISM: Homo sapiens
US-09-970-966-205

Query Match 100.0%; Score 1619; DB 36; Length 1619;
Best Local Similarity 100.0%; Pred. No. 7.9e-302;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACACTTTTCCGAGATGTTCTGCTTCCAGGCTTTGCGGCGCAAAATCCAGTGTACCA 60
DB 1 GGCACACTTTTCCGAGATGTTCTGCTTCCAGGCTTTGCGGCGCAAAATCCAGTGTACCA 60

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: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Filing, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: FILE REFERENCE: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
: CURRENT APPLICATION NUMBER: 210121.484C5
: CURRENT FILING DATE: 2001-04-03
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 205
: LENGTH: 1619
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-825-294-205

Query Match      100.0%; Score 1619; DB 31; Length 1619;
Best Local Similarity 100.0%; Pred. No. 7.9e-302;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGGATGTTCTTCTCCAGGCTTTCGCTGCAAAATCCAGTGTACCA 60
    |||||||
Db 1 GGCACCTTTTGGGATGTTCTTCTCCAGGCTTTCGCTGCAAAATCCAGTGTACCA 60
    |||||||

QY 61 GTGTGAAGATTCAGCTGAACAGACTGCTCCCGGAGTTCATTGTAATTGCAC 120
    |||||||
Db 61 GTGTGAAGATTCAGCTGAACAGACTGCTCCCGGAGTTCATTGTAATTGCAC 120
    |||||||

QY 121 GGTGAACGTTCAAGACATGTGTGAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180
    |||||||
Db 121 GGTGAACGTTCAAGACATGTGTGAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180
    |||||||

QY 181 CGGCAAGTCGTGATATCAGGGGCTGTCATGCGCTCTGCGGGGTACAGTCCCTT 240
    |||||||
Db 181 CGGCAAGTCGTGATATCAGGGGCTGTCATGCGCTCTGCGGGGTACAGTCCCTT 240
    |||||||

QY 241 CTGCTCCCCAGGGAACAGTCACTGATTGTCATGCTGCTGCAACACCCCTTTGTTAA 300
    |||||||
Db 241 CTGCTCCCCAGGGAACAGTCACTGATTGTCATGCTGCTGCAACACCCCTTTGTTAA 300
    |||||||

QY 301 CGGGCCAGAGGCCCAAGAAAGGGAAGTTCTGCTCGGCGCTCAGGCCAGAGGCTCCGAC 360
    |||||||
Db 301 CGGGCCAGAGGCCCAAGAAAGGGAAGTTCTGCTCGGCGCTCAGGCCAGAGGCTCCGAC 360
    |||||||

QY 361 CACCATTCCTGCTCAATTTAGCCCTCTCTCGGCACTGCTGAGCTGAGAGATG 420
    |||||||
Db 361 CACCATTCCTGCTCAATTTAGCCCTCTCTCGGCACTGCTGAGCTGAGAGATG 420
    |||||||

QY 421 CCACCCCTCTGATGTTGTTCTTCAGGCCCTGCCCCCAACCCCCACCTCCCTGAGTGA 480
    |||||||
Db 421 CCACCCCTCTGATGTTGTTCTTCAGGCCCTGCCCCCAACCCCCACCTCCCTGAGTGA 480
    |||||||

QY 481 GTTCTCTCGGGGTCTCTTTATTTCTGGGTAGGAGCGGGAGTCCGTCTCTTTTGT 540
    |||||||
Db 481 GTTCTCTCGGGGTCTCTTTATTTCTGGGTAGGAGCGGGAGTCCGTCTCTTTTGT 540
    |||||||

QY 541 CCTGTCAAAATATGAAGAGCTCGTAAAGCATTTCTGAATTAATTTCAAGCCGATGAAT 600
    |||||||
Db 541 CCTGTCAAAATATGAAGAGCTCGTAAAGCATTTCTGAATTAATTTCAAGCCGATGAAT 600
    |||||||

QY 601 TTTTCAGTATGATGTAAGAGAGAGGTGAGTGAAGTTCACCCCATGCTGTGTAAAC 660
    |||||||
Db 601 TTTTCAGTATGATGTAAGAGAGAGGTGAGTGAAGTTCACCCCATGCTGTGTAAAC 660
    |||||||

QY 661 CGGAGTCAAGGCGGAGGCTGAGAGTCACTGCTTGAAGTCACTGAGTGGGCACTCTCC 720
    |||||||
Db 661 CGGAGTCAAGGCGGAGGCTGAGAGTCACTGCTTGAAGTCACTGAGTGGGCACTCTCC 720
    |||||||

QY 721 TTTTGAAGAGCTCCAGAGTCCATTCATCCATGATGGGGGATGTTGAGACTGCGAGA 780
    |||||||
Db 721 TTTTGAAGAGCTCCAGAGTCCATTCATCCATGATGGGGGATGTTGAGACTGCGAGA 780
    |||||||

QY 781 GTGAGAGTGAAGCTTTTCTTAGGGCTGAGAGGCACTTCCCAAGGCTCCCTCGCTTG 840
    |||||||

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|||
Db 781 GTGAGAGTGAAGCTTTTCTTAGGGCTGAGAGGCGAGTCCCACTCAAGGCTCCCTCGCTTG 840
    |||

QY 841 ACATTCAACTTATGCTCTCTGAAACATTTCTGACAGAGAAATGGCTGTTGGCCG 900
    |||
Db 841 ACATTCAACTTATGCTCTCTGAAACATTTCTGACAGAGAAATGGCTGTTGGCCG 900
    |||

QY 901 CTGAGTGGGCTCTAGTACTCGAGACTCAATGACTGAGACTAGACTGAGGCTCGGCT 960
    |||
Db 901 CTGAGTGGGCTCTAGTACTCGAGACTCAATGACTGAGACTAGACTGAGGCTCGGCT 960
    |||

QY 961 CGCTCTGAAAGTGTCTTGAAGAAATCTTCTCACTTCTCTTGGAGAGACTGGCGCGGG 1020
    |||
Db 961 CGCTCTGAAAGTGTCTTGAAGAAATCTTCTCACTTCTCTTGGAGAGACTGGCGCGGG 1020
    |||

QY 1021 ACGCGAAGACCAACGGGCGCTGCAACAAAGCGGCGCTGTGCTGTGTGAGTGTGCAATGTA 1080
    |||
Db 1021 ACGCGAAGACCAACGGGCGCTGCAACAAAGCGGCGCTGTGCTGTGTGAGTGTGCAATGTA 1080
    |||

QY 1081 CGGCGAGGCGCTTCTGCTGTTGGCGGTGCTGACAGCGACAGCGGCGACAGCAGCCTTGC 1140
    |||
Db 1081 CGGCGAGGCGCTTCTGCTGTTGGCGGTGCTGACAGCGACAGCGGCGACAGCAGCCTTGC 1140
    |||

QY 1141 ACGAACAACCGCGGAAACCTGCTGAGAGACACCGTGTACAGAGCGGGTTGATGACCGAG 1200
    |||
Db 1141 ACGAACAACCGCGGAAACCTGCTGAGAGACACCGTGTACAGAGCGGGTTGATGACCGAG 1200
    |||

QY 1201 CTGAGGTAGAAAAAGTCTCTCGAGAGGAGAGAGATCATGTACGCCCGGGAATGAGAC 1260
    |||
Db 1201 CTGAGGTAGAAAAAGTCTCTCGAGAGGAGAGAGATCATGTACGCCCGGGAATGAGAC 1260
    |||

QY 1261 CTGCTCCAGTCGTGCTGTTGGGTTGGCCGAGCCATGCTCCGAAATCTGTTGGGCTATC 1320
    |||
Db 1261 CTGCTCCAGTCGTGCTGTTGGGTTGGCCGAGCCATGCTCCGAAATCTGTTGGGCTATC 1320
    |||

QY 1321 CAGCATAGGCGCAATGTCTACAGACATGAGCCCTGGGCGAGACAGAGAGGAGAGAGAC 1380
    |||
Db 1321 CAGCATAGGCGCAATGTCTACAGACATGAGCCCTGGGCGAGACAGAGAGGAGAGAGAC 1380
    |||

QY 1381 AGAAGAAAGAAAGAACAGAGATGAGAACAGTAAATGATTAAGCAATTAATTTAG 1440
    |||
Db 1381 AGAAGAAAGAAAGAACAGAGATGAGAACAGTAAATGATTAAGCAATTAATTTAG 1440
    |||

QY 1441 CCCCTGTCTGTGCTTACTGCGCAGGAATGTTACCAATTTTTCAGTGTGACTTGA 1500
    |||
Db 1441 CCCCTGTCTGTGCTTACTGCGCAGGAATGTTACCAATTTTTCAGTGTGACTTGA 1500
    |||

QY 1501 CAGCTTCTTTTGCACAGAGAGAGATTTAACTGTTTCAAAACCCGGGGAGTTGG 1560
    |||
Db 1501 CAGCTTCTTTTGCACAGAGAGAGATTTAACTGTTTCAAAACCCGGGGAGTTGG 1560
    |||

QY 1561 CTGTGTTAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAAGAAAAA 1619
    |||
Db 1561 CTGTGTTAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAAGAAAAA 1619
    |||

RESULT 5
US-09-825-294-211
: Sequence 211, Application US/09825294
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Filing, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: FILE REFERENCE: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
: CURRENT APPLICATION NUMBER: 210121.484C5
: CURRENT FILING DATE: 2001-04-03
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 211
: LENGTH: 1619

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RESULT 3
US-09-713-550-205
: Sequence 205, Application US/09713550
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: FILE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.484C4
: CURRENT APPLICATION NUMBER: US/09/713.550
: CURRENT FILING DATE: 2000-11-14
: NUMBER OF SEQ ID NOS: 205
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 205
: LENGTH: 1619
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-713-550-205

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Query Match	100.0%	Score 1619;	DB 28;	Length 1619;
Best Local Similarity	100.0%	Pred. No. 7.9e-302;		
Matches 1619; Conservative	0;	Mismatches	0;	Indels 0;

QY	1	GGCAACCTTTTGGGGATGTCTTGGTCCAGGCTTTGGGGCGCAATTCAGTGTACCA	60
Db	1	GGCAACCTTTTGGGGATGTCTTGGTCCAGGCTTTGGGGCGCAATTCAGTGTACCA	60
QY	61	GTTGGAAGAAATTCAGCTGAACAACAGACTGCTCTCCGCCGAGTTCATTGTGAATTCAC	120
Db	61	GTTGGAAGAAATTCAGCTGAACAACAGACTGCTCTCCGCCGAGTTCATTGTGAATTCAC	120
QY	121	GGTGAAGCTTCAAGACATGTGTAGAAAGAATGATGAGACAAAGTCCGGGATCATGTGA	180
Db	121	GGTGAAGCTTCAAGACATGTGTAGAAAGAATGATGAGACAAAGTCCGGGATCATGTGA	180
QY	181	CCGGAATCTCTGTGCATCATCAGCGGCGTGTGCATCGGCTCGCGGGTACAGTCCCTT	240
Db	181	CCGGAATCTCTGTGCATCATCAGCGGCGTGTGCATCGGCTCTCGCGGGTACAGTCCCTT	240
QY	241	CTGCTCCCAAGGAACTGAATCTGATTTGCATCAGCTGCTCAACACCCCTCTTTGTAA	300
Db	241	CTGCTCCCAAGGAACTGAATCTGATTTGCATCAGCTGCTCAACACCCCTCTTTGTAA	300
QY	301	CGGGCCCAAGGCCCAAGAAAAGGGGAAGTCTGCTCGGCCCTCAGGCCAAGGGCTCCGAC	360
Db	301	CGGGCCCAAGGCCCAAGAAAAGGGGAAGTCTGCTCGGCCCTCAGGCCAAGGGCTCCGAC	360
QY	361	CACCATCTGTTCCTCAAAATTAGCCCTCTTCTCGGACACTCTGAAGTGAAGAGATG	420
Db	361	CACCATCTGTTCCTCAAAATTAGCCCTCTTCTCGGACACTCTGAAGTGAAGAGATG	420
QY	421	CCACCCCTCTCTCATTTGTTCTTCAGCCCTCGCCCCCAACCCCCACCTCCCTGATGA	480
Db	421	CCACCCCTCTCTCATTTGTTCTTCAGCCCTCGCCCCCAACCCCCACCTCCCTGATGA	480
QY	481	GTTTCTTCTGGGTGCTCTTATTCGTGGGTAGGAGAGCGGGAATCCGCTGTCTCTTTGTT	540
Db	481	GTTTCTTCTGGGTGCTCTTATTCGTGGGTAGGAGAGCGGGAATCCGCTGTCTCTTTGTT	540
QY	541	CGTGTGCAAAATATGAAAGAGCTCGGTAAAGCATTCGTAATTAATTCAGCTGACTGAT	600
Db	541	CGTGTGCAAAATATGAAAGAGCTCGGTAAAGCATTCGTAATTAATTCAGCTGACTGAT	600
QY	601	TTTTCAGTATCTACTTGAAAGAGAGGTGAGTGAAGTTCAACCCCACTGTCTGTGTAAC	660

D	b		TTTCAGTATGACTTGAAGAAGAGGTGGAGTGAAAGTTACACCCTCATGTGTGTAAAC	660
Q	y	661	CAGAGTCAAGGCCAGGCTGGCAGAGTCACTCTTAGAAGTCACTGAGTGGGCATCTGCC	720
D	b	661	CGGAGTCAAGGCCAGGCTGGCAGAGTCACTCTTAGAAGTCACTGAGTGGGCATCTGCC	720
Q	y	721	TTTTGTAAAGCTCCACTGTCTGCATTTCATCCCTCGATGGGGCATGTGTTGAACATCGACA	780
D	b	721	TTTTGTAAAGCTCCACTGTCTGCATTTCATCCCTCGATGGGGCATGTGTTGAACATCGACA	780
Q	y	781	GTAAGATGACGTTTTCTTAAGGCGCTGGAGGGCCAGTTTCCACTCAAGGCTCCCTGCTTG	840
D	b	781	GTAAGATGACGTTTTCTTAAGGCGCTGGAGGGCCAGTTTCCACTCAAGGCTCCCTGCTTG	840
Q	y	841	ACATTCAACTCATAGCTCTCTGAAAACAAATTCCTGACACATAATTTGGTGTTCGGCC	900
D	b	841	ACATTCAACTCATAGCTCTCTGAAAACAAATTCCTGACACATAATTTGGTGTTCGGCC	900
Q	y	901	CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACATGGGACTTAGACTGGGCTGGGCT	960
D	b	901	CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACATGGGACTTAGACTGGGCTGGGCT	960
Q	y	961	CGCTCTAAAAAGTGTCTTAAGAAAATTTCTCACTTCTCTTCCAGAGACTGGCGCGG	1020
D	b	961	CGCTCTAAAAAGTGTCTTAAGAAAATTTCTCACTTCTCTTCCAGAGACTGGCGCGG	1020
Q	y	1021	ACCGGAAGAACACAGGGCGCTGCACAAAGCGGGCGCTGCGGTGGGGAGTGGCGCATTA	1080
D	b	1021	ACCGGAAGAACACAGGGCGCTGCACAAAGCGGGCGCTGCGGTGGGGAGTGGCGCATTA	1080
Q	y	1081	CGCGCAGGCGCTTCTCGTGGTTGGCGTGTCTGACGACAGCGGGGACACACACCTTTC	1140
D	b	1081	CGCGCAGGCGCTTCTCGTGGTTGGCGTGTCTGACGACAGCGGGGACACACACCTTTC	1140
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D	b	1141	ACGAACACCGCCCGAAACTCTGCGAGGACACCGTGTACAGAGGGGTTGATGACACAG	1200
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D	b	1201	CTGAGGTAGAAAAACCTCTCCGAAAGGGGAGGAGATCATTACGCCCGAAGTAGAGAC	1260
Q	y	1261	CTGTCCAGTGTGCTGGGTTTGGCCGACGCATGATCTCCGAATCTGTTGGGCAATC	1320
D	b	1261	CTGTCCAGTGTGCTGGGTTTGGCCGACGCATGATCTCCGAATCTGTTGGGCAATC	1320
Q	y	1321	CAGCATACGGCCATGTCTCAACAACAATCACCCCTGGGCAGACACGAGCAGAGAGGAGAC	1380
D	b	1321	CAGCATACGGCCATGTCTCAACAACAATCACCCCTGGGCAGACACGAGCAGAGAGGAGAC	1380
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D	b	1381	AGAGAAAAGAAAAACACAGCATGAGAACACACTAATGANTAAACATAAATATTTTATG	1440
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D	b	1441	CCCCCTGTTCTGTGTTACTGGCCAGGAAATGTACCAATTTTTCAGTGTGGCATGGA	1500
Q	y	1501	CAGCTTCTTTTGCACACAGACAGAGAAATTTAACACTGTTCCAAACCCGGGGGAGTTGG	1560
D	b	1501	CAGCTTCTTTTGCACACAGACAGAGAAATTTAACACTGTTCCAAACCCGGGGGAGTTGG	1560
Q	y	1561	CTGTGTTAAAGAAAGACCAATTAATGTCTTAAACAGGTGAAAAAAAAAAAAAAAAAAAAA	1619
D	b	1561	CTGTGTTAAAGAAAGACCAATTAATGTCTTAAACAGGTGAAAAAAAAAAAAAAAAAAAAA	1619

RESULT 4
US-09-825-294-205
; Sequence 205, Application US/09825294
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun


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ALIGNMENTS

RESULT 1
PCT-US01-45395-205
Sequence 205, Application PC/TUS0145395

GENERAL INFORMATION:

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: APPLICANT: Corixa Corporation
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: APPLICANT: Molesh, David Alan
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.48401PC
: CURRENT APPLICATION NUMBER: PCT/US01/45395
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 205
: LENGTH: 1619
: TYPE: DNA
: ORGANISM: Homo sapiens
PCT-US01-45395-205

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Query Match 100.0%; Score 1619; DB 1; Length 1619;
Best Local Similarity 100.0%; Pred. No. 7.9e-302;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 24791104 seqs, 12571243825 residues

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2	1619	100.0	1619	1 PCT-US01-45395-211	Sequence 211, App
3	1619	100.0	1619	28 US-09-713-550-205	Sequence 205, App
4	1619	100.0	1619	31 US-09-825-294-205	Sequence 205, App
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8	1619	100.0	1619	42 US-10-212-677-205	Sequence 205, App
9	1619	100.0	1619	42 US-10-212-677-211	Sequence 211, App
10	1427	88.1	1832	40 US-10-108-260A-197	Sequence 197, App
11	1396	86.2	1897	1 PCT-US01-45395-214	Sequence 214, App
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14	1396	86.2	1897	42 US-10-212-677-214	Sequence 214, App
15	1388	85.7	1967	1 PCT-US02-29964-16	Sequence 16, App
16	1384	85.5	1918	17 US-09-397-022-4454	Sequence 4454, App
17	1384	85.5	1918	31 US-09-808-383-4454	Sequence 4454, App
18	1377	85.1	1925	25 US-09-652-121-7293	Sequence 7293, App
19	1377	85.1	1925	25 US-09-652-128-9375	Sequence 9375, App
20	1377	85.1	1925	25 US-09-652-917-3346	Sequence 3346, App
21	1377	85.1	1925	27 US-09-699-997-11085	Sequence 11085, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Fri Nov 8 18:56:58 2002

us-09-970-966-211.rni

Page 16

62

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LOCATION: (107)..(880)
US-09-103-663-10

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Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1150 TGTAAAAAAAAAAAAAAAAAAAA 1172

Search completed: November 7, 2002, 23:16:25
Job time : 304.668 secs

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,966B
; FILING DATE: 01-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K.
; REGISTRATION NUMBER: 26,997
; REFERENCE/DOCKET NUMBER: FHCRI7694
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-8100
; TELEFAX: (206) 224-0779
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1008 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; DESCRIPTION: Clone 19; see Figure 26
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
;
; US-08-252-966B-15
;
; Query Match
; Best Local Similarity 100.0%; Score 23; DB 1; Length 1008;
; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Db 975 TGTAAAAAAAAAAAAAAAAA 997
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; RESULT 43
; US-09-173-300-21
; Sequence 21, Application US/09173300
; Patent No. 6451581
; GENERAL INFORMATION:
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB-1126
; CURRENT APPLICATION NUMBER: US/09/173,300
; CURRENT FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 60/063,423
; EARLIER FILING DATE: 1997 October 28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 21
; LENGTH: 1162
; TYPE: DNA
; ORGANISM: Glycine max
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; US-09-173-300-21
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; Query Match
; Best Local Similarity 100.0%; Score 23; DB 4; Length 1162;
; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Db 1132 TGTAAAAAAAAAAAAAAAAA 1154
;
; RESULT 44
; US-07-869-933-10
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; Sequence 10, Application US/07869933
; Patent No. 5770396
; GENERAL INFORMATION:
; APPLICANT: KINNET, Jean-Pierre
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,933
; FILING DATE: 19970416
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1174 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..880
;
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; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; RESULT 45
; US-09-103-663-10
; Sequence 10, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1174
; TYPE: DNA
; ORGANISM: Homo sapiens

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/575,602
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/032,086
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40,403
REFERENCE/DOCKET NUMBER: CGC 1915/Reg
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "cdna sequence for
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HYPOTHETICAL: NO
US-09-575-602-1

Query Match 1.4%; Score 23; DB 4; Length 772;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 41
US-08-032-393-5
Sequence 5, Application US/08032393
Patent No. 5332660
GENERAL INFORMATION:
APPLICANT: Osamu TAKEDA et al.
TITLE OF INVENTION: Gene of Candida Yeast
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/032,393
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/729,414
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 933 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Candida albicans
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-032-393-5

Query Match 1.4%; Score 23; DB 1; Length 933;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
DB 911 TGTAAAAAAAAAAAAAAAAAAAA 933

RESULT 42
US-08-252-966B-15
Sequence 15, Application US/08252966B
Patent No. 5624818
GENERAL INFORMATION:
APPLICANT: Eisenman, Robert N.
APPLICANT: Hurlin, Peter J.
TITLE OF INVENTION: Regulatory Proteins that Dimerize with
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson, and KindnessPLLC
STREET: 1420 Fifth Ave., Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347

```
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/914,383
;; FILING DATE: 17-JUL-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/814,884
;; FILING DATE: 31-DEC-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/756,211
;; FILING DATE: 05-SEP-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: HAMLET-KING, DIANA
;; REGISTRATION NUMBER: 33,302
;; REFERENCE/DOCKET NUMBER: SCH 1359
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-243-6333
;; TELEFAX: 703-243-6410
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 530 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; US-08-206-185-5
```

```
Query Match 1.4%; Score 23; DB 1; Length 530;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 508 TGTAAAAAAAAAAAAAAAAAAAA 530
```

```
RESULT 37
US-09-433-248A-7
; Sequence 7, Application US/09433248A
; Patent No. 6355462
; GENERAL INFORMATION:
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Disease Resistance Factors
; FILE REFERENCE: B1252 US NA
; CURRENT APPLICATION NUMBER: US/09/433,248A
; CURRENT FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,242
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Trillium aestivum
; US-09-433-248A-7
```

```
Query Match 1.4%; Score 23; DB 4; Length 588;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 563 TGTAAAAAAAAAAAAAAAAAAAA 585
```

```
RESULT 38
US-09-385-982-262/c
; Sequence 262, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
```

```
;; TITLE OF INVENTION: PRODUCTS: II
;; FILE REFERENCE: CCDNA-260XX
;; CURRENT APPLICATION NUMBER: US/09/385,982
;; CURRENT FILING DATE: 1999-08-30
;; EARLIER APPLICATION NUMBER: 09/328,111
;; EARLIER FILING DATE: 1999-06-08
;; EARLIER APPLICATION NUMBER: 60/117,393
;; EARLIER FILING DATE: 1999-01-27
;; EARLIER APPLICATION NUMBER: 60/098,639
;; EARLIER FILING DATE: 1998-08-31
;; NUMBER OF SEQ ID NOS: 544
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 262
;; LENGTH: 593
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)..(593)
;; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-262
```

```
Query Match 1.4%; Score 23; DB 4; Length 593;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 75 TGTAAAAAAAAAAAAAAAAAAAA 53
```

```
RESULT 39
5212073-1
; Patent No. 5212073
; APPLICANT: ROLINS, BARRETT,STILES, CHARLES,WONG, GORDON G.
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
; NUMBER OF SEQUENCES: 1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/351,008
; FILING DATE:12-MAY-1989
; SEQ ID NO:1:
; LENGTH: 752
5212073-1
```

```
Query Match 1.4%; Score 23; DB 6; Length 752;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 730 TGTAAAAAAAAAAAAAAAAAAAA 752
```

```
RESULT 40
US-09-575-602-1
; Sequence 1, Application US/09575602
; Patent No. 6392123
; GENERAL INFORMATION:
; APPLICANT: Crossland, Lyle D
; APPLICANT: Harper, Stacy M
; TITLE OF INVENTION: Method of Hybrid Seed Production Using
; TITLE OF INVENTION: Conditional Female Sterility
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: No. 6392123artis Corporation - Patent & Trademark
; ADDRESSEE: Dept.
; STREET: P.O. Box 12257
; CITY: Research Triangle Park
; STATE: NCNY
; COUNTRY: USA
; ZIP: 22057
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

Db 34 TGTAAAAAAAAAAAAAAAAAAAA 12

RESULT 34

US-09-186-188B-29/C
Sequence 29, Application US/09186188B
Patent No. 6455672
GENERAL INFORMATION:
APPLICANT: Benfey et al.
TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses
FILE REFERENCE: 5914-074-999
CURRENT APPLICATION NUMBER: US/09/186,188B
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 08/842,445
PRIOR FILING DATE: 1997-04-24
PRIOR APPLICATION NUMBER: 08/538,617
PRIOR FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 79
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 502
TYPE: DNA
ORGANISM: Plant
US-09-186-188B-29

Query Match 1.4%; Score 23; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 34 TGTAAAAAAAAAAAAAAAAAAAA 12

RESULT 35

US-08-462-894-5
Sequence 5, Application US/08462894
Patent No. 5723312
GENERAL INFORMATION:
APPLICANT: NOESKE-JUNGBLUT, CHRISTIANE
APPLICANT: HAENDLER, BERNHARD
APPLICANT: KRAETZSCHMAR, JOERN
APPLICANT: SCHLEUNING, WOLF-DIETER
APPLICANT: ALAGON, ALEJANDRO
APPLICANT: POSSANI, LOURIVAL
APPLICANT: CUEVAS-AGUIRRE, DELIA
TITLE OF INVENTION: COLLAGEN-INDUCED PLATELET AGGREGATION
TITLE OF INVENTION: INHIBITOR
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,894
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,185
FILING DATE: 07-MAR-1994
APPLICATION NUMBER: US 08/116,889
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/EP92/02052
FILING DATE: 04-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/914,383

FILING DATE: 17-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/814,884

FILING DATE: 31-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/756,211

FILING DATE: 05-SEP-1991

ATTORNEY/AGENT INFORMATION:

NAME: HAMLET-KING, DIANA

REGISTRATION NUMBER: 33,302

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 530 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-462-894-5

Query Match 1.4%; Score 23; DB 1; Length 530;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 508 TGTAAAAAAAAAAAAAAAAAAAA 530

RESULT 36

US-08-206-185-5
Sequence 5, Application US/08206185
Patent No. 5756454
GENERAL INFORMATION:
APPLICANT: NOESKE-JUNGBLUT, CHRISTIANE
APPLICANT: HAENDLER, BERNHARD
APPLICANT: KRAETZSCHMAR, JOERN
APPLICANT: SCHLEUNING, WOLF-DIETER
APPLICANT: ALAGON, ALEJANDRO
APPLICANT: POSSANI, LOURIVAL
APPLICANT: CUEVAS-AGUIRRE, DELIA
TITLE OF INVENTION: COLLAGEN-INDUCED PLATELET AGGREGATION
TITLE OF INVENTION: INHIBITOR
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,185
FILING DATE: 07-MAR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,889
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: WO PCT/EP92/02052
FILING DATE: 04-SEP-1992

```
;; CURRENT APPLICATION NUMBER: US/09/439,313
;; CURRENT FILING DATE: 1999-11-12
;; NUMBER OF SEQ ID NOS: 575
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 353
;; LENGTH: 436
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-439-313-353

Query Match          1.4%; Score 23; DB 4; Length 436;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 29 TGTAAAAAAAAAAAAAAAAAAAAA 7

RESULT 30
US-09-352-616A-353/C
; Sequence 353, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiaqichun
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.4278
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 353
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-353

Query Match          1.4%; Score 23; DB 4; Length 436;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 29 TGTAAAAAAAAAAAAAAAAAAAAA 7

RESULT 31
US-09-372-422A-35
; Sequence 35, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Bartheu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)...(257)
```

```
US-09-372-422A-35

Query Match          1.4%; Score 23; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 406 TGTAAAAAAAAAAAAAAAAAAAAA 428

RESULT 32
US-09-186-276B-29/C
; Sequence 29, Application US/09186276B
; Patent No. 6388173
; GENERAL INFORMATION:
; APPLICANT: Benfey, Phillip
; APPLICANT: Dilaurenzio, Laura
; APPLICANT: Wysocka-Diller, Joanna
; APPLICANT: Malamy, Jocelyn E.
; APPLICANT: Pysch, Leonard
; APPLICANT: Helariutta, Yrjo
; TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses Thereof
; FILE REFERENCE: 5914-075-999
; CURRENT APPLICATION NUMBER: US/09/186,276B
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 08/842,445
; PRIOR FILING DATE: 1997-04-24
; PRIOR APPLICATION NUMBER: 08/638,617
; PRIOR FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Oryza sp.
US-09-186-276B-29

Query Match          1.4%; Score 23; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 34 TGTAAAAAAAAAAAAAAAAAAAAA 12

RESULT 33
US-08-842-445-29/C
; Sequence 29, Application US/08842445A
; Patent No. 6441270
; GENERAL INFORMATION:
; APPLICANT: Benfey et al.
; TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 5914-056-999
; CURRENT APPLICATION NUMBER: US/08/842,445A
; CURRENT FILING DATE: 1997-04-24
; EARLIER APPLICATION NUMBER: 08/638,617
; EARLIER FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Plant
US-08-842-445-29

Query Match          1.4%; Score 23; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
```

APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqi
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352, 616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 357
LENGTH: 393
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-357

Query Match 1.4%; Score 23; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAA 1619
DB 34 TGTAAAAA 12

RESULT 27
US-09-014-969-5
Sequence 5, Application US/09014969
Patent No. 5965397
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Racine, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vlki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 413 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-014-969-5

Query Match 1.4%; Score 23; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAA 1619
DB 387 TGTAAAAA 409

RESULT 28
US-09-605-785-353/C
Sequence 353, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darlick
APPLICANT: Li, Samuel

APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16

CURRENT APPLICATION NUMBER: US/09/605,785

CURRENT FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 835

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 353

LENGTH: 436

TYPE: DNA

ORGANISM: Homo sapien

US-09-605-785-353

Query Match 1.4%; Score 23; DB 4; Length 436;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAA 1619

DB 29 TGTAAAAA 7

RESULT 29

US-09-439-313-353/C

Sequence 353, Application US/09439313

Patent No. 6329505

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Soik, John

APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
|||||

Db 43 TGTAAAAAAAAAAAAAAAAAAAA 21

RESULT 23
US-08-361-441B-14/C
Sequence 14, Application US/08361441B
Patent No. 6077948
GENERAL INFORMATION:
APPLICANT: Russell, Mary E.
APPLICANT: Utans, Ulrike
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
NUMBER OF SEQUENCES: 43
CURRENT FILING DATE: 2000-06-27
ADDRESS: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,441B
FILING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/171,385
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-361-441B-14

Query Match 1.4%; Score 23; DB 3; Length 350;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
|||||

Db 43 TGTAAAAAAAAAAAAAAAAAAAA 21

RESULT 24
US-09-605-785-357/C
Sequence 357, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitchem, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 357
LENGTH: 393
TYPE: DNA
ORGANISM: Homo sapien
US-09-605-785-357

Query Match 1.4%; Score 23; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
|||||

Db 34 TGTAAAAAAAAAAAAAAAAAAAA 12

RESULT 25
US-09-439-313-357/C
Sequence 357, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitchem, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 357
LENGTH: 393
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-357

Query Match 1.4%; Score 23; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
|||||

Db 34 TGTAAAAAAAAAAAAAAAAAAAA 12

RESULT 26
US-09-352-616A-357/C
Sequence 357, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:

REGISTRATION NUMBER: 34, 819
REFERENCE/DOCKET NUMBER: 05433/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-361-441B-20

Query Match 1.4%; Score 23; DB 3; Length 345;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
DB 23 TGTAAAAAAAAAAAAAAAAAAAA 1

RESULT 21
US-08-104-072B-2
Sequence 2, Application US/08104072B
Patent No. 5639948
GENERAL INFORMATION:
APPLICANT: Michiels, Frank
APPLICANT: Morioka, Shinji
APPLICANT: Scherlinck, Trees
APPLICANT: Komari, Toshiko
TITLE OF INVENTION: Stamen-specific Promoters from Rice
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5639948west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/104, 072B
FILING DATE: 05-AUG-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 9200272
FILING DATE: 06-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91403352.7
FILING DATE: 10-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91402590.3
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91400318.1
FILING DATE: 08-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchuk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076, 93USMO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: rice
TISSUE TYPE: anther
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..322
OTHER INFORMATION: /product="cDNA T23"
FEATURE:
NAME/KEY: misc.feature
LOCATION: 333..347
OTHER INFORMATION: /product="cloning adaptor
US-08-104-072B-2

Query Match 1.4%; Score 23; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
DB 284 TGTAAAAAAAAAAAAAAAAAAAA 306

RESULT 22
US-08-171-385-14/C
Sequence 14, Application US/08171385
Patent No. 5527884
GENERAL INFORMATION:
APPLICANT: Mary E. Russell
APPLICANT: Urike Utans
TITLE OF INVENTION: Mediators of Chronic Allograft
TITLE OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171, 385
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34, 819
REFERENCE/DOCKET NUMBER: 05433/006001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 350
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-171-385-14

Query Match 1.4%; Score 23; DB 1; Length 350;
Best Local Similarity 100.0%; Pred. No. 0.67;

US-08-171-385-27

Query Match 1.4%; Score 23; DB 1; Length 340;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
|||||
DB 40 TGTAAAAAAAAAAAAAAAAAAAA 18

RESULT 18

US-08-361-441B-27/c
Sequence 27, Application US/08361441B
Patent No. 6077948

GENERAL INFORMATION:
APPLICANT: Russell, Mary E.
APPLICANT: Utans, Ulrike
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,441B
FILING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/171,385
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-361-441B-27

Query Match 1.4%; Score 23; DB 3; Length 340;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
|||||
DB 40 TGTAAAAAAAAAAAAAAAAAAAA 18

RESULT 19

US-08-171-385-20/c
Sequence 20, Application US/08171385
Patent No. 5527884

GENERAL INFORMATION:
APPLICANT: Mary E. Russell
APPLICANT: Ulrike Utans
TITLE OF INVENTION: Mediators of Chronic Allograft
REJECTION
NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts

COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,385
FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/006001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 345
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-171-385-20

Query Match 1.4%; Score 23; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
|||||
DB 23 TGTAAAAAAAAAAAAAAAAAAAA 1

RESULT 20

US-08-361-441B-20/c
Sequence 20, Application US/08361441B
Patent No. 6077948

GENERAL INFORMATION:
APPLICANT: Russell, Mary E.
APPLICANT: Utans, Ulrike
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,441B
FILING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/171,385
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.

```

; Patent No. 5527884
; GENERAL INFORMATION:
; APPLICANT: Mary E. Russell
; APPLICANT: Ulrike Utans
; TITLE OF INVENTION: Mediators of Chronic Allograft
; TITLE OF INVENTION: Rejection
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 555X
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171.385
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/006001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-171-385-22

Query Match 1.4%; Score 23; DB 1; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
DB 24 TGTAAAAAAAAAAAAAAAAAAAA 2

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; APPLICATION NUMBER: US/08/361,441B
; FILING DATE: 21-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/171.385
; FILING DATE: 21-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-361-441B-22

Query Match 1.4%; Score 23; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
DB 24 TGTAAAAAAAAAAAAAAAAAAAA 2

RESULT 17
US-08-171-385-27/c
; Sequence 27, Application US/08171385
; Patent No. 5527884
; GENERAL INFORMATION:
; APPLICANT: Mary E. Russell
; APPLICANT: Ulrike Utans
; TITLE OF INVENTION: Mediators of Chronic Allograft
; TITLE OF INVENTION: Rejection
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 555X
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171.385
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/006001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

```

TITLE OF INVENTION: Neuronal PAS Domain Protein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,310A
FILING DATE: 21-JAN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UTSD:1226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4184 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-785-310A-4

Query Match 1.5%; Score 24; DB 2; Length 4184;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAACAAAAA 1619
|||||
DB 4138 GTGTAACAAAAA 4161

RESULT 12
US-09-128-155-17/c
Sequence 17, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 176373
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(176373)
OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

Query Match 1.5%; Score 24; DB 3; Length 176373;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAACAAAAA 1619
|||||
DB 68491 GTGTAACAAAAA 68468

RESULT 13
US-09-306-290-11/c
Sequence 11, Application US/09306290
Patent No. 6221635
GENERAL INFORMATION:
APPLICANT: Rovera, Giovanni
TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE
FILE REFERENCE: 09924-10
CURRENT APPLICATION NUMBER: US/09/306,290
CURRENT FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer RGP
US-09-306-290-11

Query Match 1.4%; Score 23; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA 1619
|||||
DB 23 TGTAAAAA 1

RESULT 14
US-09-306-290-16/c
Sequence 16, Application US/09306290
Patent No. 6221635
GENERAL INFORMATION:
APPLICANT: Rovera, Giovanni
TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE
FILE REFERENCE: 09924-10
CURRENT APPLICATION NUMBER: US/09/306,290
CURRENT FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PrimerRGP
US-09-306-290-16

Query Match 1.4%; Score 23; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA 1619
|||||
DB 23 TGTAAAAA 1

RESULT 15
US-08-171-385-22/c
Sequence 22, Application US/08171385

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,188B
FILING DATE: 01-MAR-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, David W.
REGISTRATION NUMBER: 36107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 3073 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1111
US-08-206-188B-31

Query Match 1.5%; Score 24; DB 3; Length 3073;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1596 GTGTAAAAAAAAAAAAAAAAAAAA 1619
|||||
DB 1520 GTGTAAAAAAAAAAAAAAAAAAAA 1543

RESULT 9
PCT-US91-02714-30
Sequence 30, Application PC/TUS9102714
GENERAL INFORMATION:
APPLICANT: Wiegler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02714
FILING DATE: 19910419
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 27805/30197

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 3073 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1111
PCT-US91-02714-30

Query Match 1.5%; Score 24; DB 5; Length 3073;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1596 GTGTAAAAAAAAAAAAAAAAAAAA 1619
|||||
DB 1520 GTGTAAAAAAAAAAAAAAAAAAAA 1543

RESULT 10
US-09-511-625B-67
Sequence 67, Application US/09511625B
Patent No. 6368828
GENERAL INFORMATION:
APPLICANT: Laroche, William J.
APPLICANT: Patel, Bhavlin H.
APPLICANT: Pierce, Jacalyn H.
TITLE OF INVENTION: ATTENUATED AND DOMINANT NEGATIVE VARIANTS
TITLE OF INVENTION: CDNAS OF STAT6: STAT6D AND STAT6C
FILE REFERENCE: 14014.030001
CURRENT APPLICATION NUMBER: US/09/511,625B
CURRENT FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: PCT/US98/17821
PRIOR FILING DATE: 1998-08-27
PRIOR APPLICATION NUMBER: 60/070,397
PRIOR FILING DATE: 1998-01-05
PRIOR APPLICATION NUMBER: 60/056,075
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 67
LENGTH: 3375
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial Sequence: /No. 6368828e -
NAME/KEY: CDS
LOCATION: (115)...(2655)
US-09-511-625B-67

Query Match 1.5%; Score 24; DB 4; Length 3375;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1596 GTGTAAAAAAAAAAAAAAAAAAAA 1619
|||||
DB 3321 GTGTAAAAAAAAAAAAAAAAAAAA 3344

RESULT 11
US-08-785-310A-4
Sequence 4, Application US/08785310A
Patent No. 5840532
GENERAL INFORMATION:
APPLICANT: McKnight, Steven L.
APPLICANT: Russell, David W.

Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1596 GTGTAACAAAAA 1619
Db 1520 GTGTAACAAAAA 1543

RESULT 6
US-08-474-379C-31

Sequence 31, Application US/08474379C
Patent No. 5977305

GENERAL INFORMATION:

APPLICANT: Wigler, Michael H.

APPLICANT: Colicelli, John J.

TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive/6300 Sears Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,379C

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/511,715

FILING DATE: 20-APR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/206,188

FILING DATE: 01-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/688,352

FILING DATE: 19-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Clough, David W.

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 27866/32771

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 3073 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1109

US-08-474-379C-31

Query Match 1.5%; Score 24; DB 2; Length 3073;
Best Local Similarity 100.0%; Pred. No. 0.21;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1596 GTGTAACAAAAA 1619
Db 1520 GTGTAACAAAAA 1543

RESULT 7
US-09-146-249A-31

Sequence 31, Application US/09146249A
Patent No. 6069240

GENERAL INFORMATION:

APPLICANT: Wigler, Michael H.

APPLICANT: Colicelli, John J.

TITLE OF INVENTION: Cloning by Complementation and Related

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/146,249A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/511,715

FILING DATE: 20-APR-1990

ATTORNEY/AGENT INFORMATION:

NAME: Clough, David W.

REGISTRATION NUMBER: 36,107

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312-474-0448

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 3073 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1111

US-09-146-249A-31

Query Match 1.5%; Score 24; DB 3; Length 3073;
Best Local Similarity 100.0%; Pred. No. 0.21;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1596 GTGTAACAAAAA 1619
Db 1520 GTGTAACAAAAA 1543

RESULT 8
US-08-206-188B-31

Sequence 31, Application US/08206188B

Patent No. 6100025

GENERAL INFORMATION:

APPLICANT: Wigler, Michael H.

APPLICANT: Colicelli, John J.

TITLE OF INVENTION: Cloning by Complementation and Related

NUMBER OF SEQUENCES: 84

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068.140A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: NO. 6281409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C70237
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5017
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1046 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Ribes nigrum
STRAIN: Ben Alder
US-09-068-140A-5

Query Match 1.5%: Score 24; DB 4; Length 1046;

Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAAAAA 1619
DB 1015 GTGTAAAAA 1038

RESULT 3
US-09-413-574-1
Sequence 1, Application US/09413574
Patent No. 6235972
GENERAL INFORMATION:
APPLICANT: Mahajan, Pramod B.
APPLICANT: Tagliani, Laura
TITLE OF INVENTION: Maize Rad23 Genes and Uses Thereof
FILE REFERENCE: 0964
CURRENT APPLICATION NUMBER: US/09/413.574
CURRENT FILING DATE: 1999-10-06
EARLIER APPLICATION NUMBER: 60/109,728
EARLIER FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1522
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (58) ... (1272)
US-09-413-574-1

Query Match 1.5%: Score 24; DB 4; Length 1522;

Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAAAAA 1619
DB 1456 GTGTAAAAA 1479

RESULT 4

5168051-9
Patent No. 5168051
APPLICANT: DERYNCK, RIK M.A.; GOEDDEL, DAVID V.
TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/389,929
FILING DATE: 04-AUG-1989
SEQ ID NO: 9
LENGTH: 2671
5168051-9

Query Match 1.5%: Score 24; DB 6; Length 2671;

Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAAAAA 1619
DB 2577 GTGTAAAAA 2600

RESULT 5
US-07-688-352C-31
Sequence 31, Application US/07688352C
Patent No. 5527896
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/688,352C
FILING DATE: 19910419
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 27805/30197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 3073 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 3...1111
US-07-688-352C-31

Query Match 1.5%: Score 24; DB 1; Length 3073;

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:00:33 ; Search time 60.6676 Seconds
(without alignments)
8184.096 Million cell updates/sec

Title: US-09-970-966-211

Perfect score: 1619
Sequence: 1 ggcacatttcgcgaltgt.....aaaaaaaaaaaaaaaa 1619

Scoring table: OLIGO_NUC

Gapop 60.0, Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size: 10

Total number of hits satisfying chosen parameters: 153595

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Issued Patents: NA: *
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	24	1.5	1046	4	US-09-068-140A-5
3	24	1.5	1532	4	US-09-413-574-1
4	24	1.5	2671	6	5168051-9
5	24	1.5	3073	1	US-07-688-352C-31
6	24	1.5	3073	2	US-08-474-379C-31
7	24	1.5	3073	3	US-09-146-249A-31
8	24	1.5	3073	3	US-08-206-188B-31
9	24	1.5	3073	5	PCT-US91-02714-30
10	24	1.5	3375	4	US-09-511-625B-67
11	24	1.5	4184	2	US-08-785-310A-4
12	24	1.5	17673	3	US-09-128-155-17
13	24	1.4	40	4	US-09-306-290-11
14	24	1.4	40	4	US-09-306-290-11
15	24	1.4	321	1	US-08-171-385-22
16	24	1.4	321	1	US-08-361-441B-22
17	24	1.4	340	1	US-08-171-385-27
18	24	1.4	340	1	US-08-361-441B-27
19	24	1.4	345	1	US-08-171-385-20
20	24	1.4	345	1	US-08-104-072B-2
21	24	1.4	347	1	US-08-171-385-14
22	24	1.4	350	3	US-08-361-441B-14
23	24	1.4	350	3	US-09-605-785-357
24	24	1.4	393	4	US-09-439-313-357
25	24	1.4	393	4	US-09-352-616A-357
26	24	1.4	393	4	US-09-014-969-5
27	24	1.4	413	2	US-09-014-969-5

C 28	23	1.4	436	4	US-09-605-785-353	Sequence 353, App
C 29	23	1.4	436	4	US-09-439-313-353	Sequence 353, App
C 30	23	1.4	436	4	US-09-352-616A-353	Sequence 353, App
C 31	23	1.4	442	4	US-09-372-422A-35	Sequence 35, App
C 32	23	1.4	502	4	US-09-186-276B-29	Sequence 29, App
C 33	23	1.4	502	4	US-08-842-445-29	Sequence 29, App
C 34	23	1.4	502	4	US-09-186-188B-29	Sequence 29, App
C 35	23	1.4	530	1	US-08-462-894-5	Sequence 5, App
C 36	23	1.4	530	1	US-08-206-185-5	Sequence 5, App
C 37	23	1.4	588	4	US-09-433-248A-7	Sequence 7, App
C 38	23	1.4	593	4	US-09-385-982-262	Sequence 262, App
C 39	23	1.4	752	6	5212073-1	Patent No. 5212073
C 40	23	1.4	772	4	US-09-575-602-1	Sequence 1, App
C 41	23	1.4	933	1	US-08-032-393-5	Sequence 5, App
C 42	23	1.4	1008	1	US-08-252-966B-15	Sequence 15, App
C 43	23	1.4	1162	4	US-09-173-300-21	Sequence 21, App
C 44	23	1.4	1174	1	US-07-869-933-10	Sequence 10, App
C 45	23	1.4	1174	4	US-09-103-663-10	Sequence 10, App

ALIGNMENTS

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RESULT 1
US-09-248-335-59
; Sequence 59, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEF, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CI-1128-A
; CURRENT APPLICATION NUMBER: US/09/248,335
; EARLIER FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 08/924,759
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 59
; LENGTH: 967
; TYPE: DNA
; ORGANISM: maize
US-09-248-335-59

Query Match
Best Local Similarity 100.0% Score 24; DB 3; Length 967;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAAGAAAAAAGAAAAA 1619
DB 943 GTGTAAGAAAAAAGAAAAA 966

RESULT 2
US-09-068-140A-5
; Sequence 5, Application US/09068140A
; Patent No. 6281409
; GENERAL INFORMATION:
; APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor
; APPLICANT: and Rex Michael Brennan
; TITLE OF INVENTION: Blackcurrant Promoters and Genes
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: Smithline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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562

; PRIOR APPLICATION NUMBER: 60/089907
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089908
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089947
 ; PRIOR FILING DATE: 1998-06-19
 ; PRIOR APPLICATION NUMBER: 60/089948
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 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182

; PRIOR FILING DATE: 1998-07-09
 Query Match 15%; Score 24; DB 10; Length 1337;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1596 GTGTAAAAAAAAAAAAAAAAAAAA 1619
 ||||||||||||||||||
 Db 1298 GTGTAAAAAAAAAAAAAAAAAAAA 1321

Search completed: November 8, 2002, 02:06:56
 Job time : 101.36 secs

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;; PRIOR FILING DATE: 1998-07-02
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Query Match 1.5%; Score 24; DB 10; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1596 GTGTAAAAAAAAAAAAAAAAAAAA 1619
Db 1298 GTGTAAAAAAAAAAAAAAAAAAAA 1321
;
RESULT 45
US-09-990-442-286
; Sequence 286, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaud, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumes, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR APPLICATION NUMBER: 60/084600
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; PRIOR APPLICATION NUMBER: 60/087106
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;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087609
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;; PRIOR APPLICATION NUMBER: 60/087827
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;; PRIOR FILING DATE: 1998-06-18

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;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478

;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 24; DB 10; Length 1337;
Best Local Similarity 100.0%; Pred.No. 0.67;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1596 GTGTAAAAAAAAAAAAAAAAAAAA 1619
Db 1298 GTGTAAAAAAAAAAAAAAAAAAAA 1321

RESULT 44
US-09-991-073-286
Sequence 286, Application US/09991073
Patent NO. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC15
CURRENT APPLICATION NUMBER: US/09/991,073
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/090862
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
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 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 24; DB 10; Length 1337;
 Best Local Similarity 100.0%; Pred No. 0.67; 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0;

Ox 1596 GTGTAAAAA 1619
 Db 1298 CTGTAAAAA 1321

RESULT 43
 US-09-989-732-286
 Sequence 286, Application US/09989732
 Patent No. US20020123463A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Bolstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavich, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumes, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730pic57
 CURRENT FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13
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 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
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PRIOR FILING DATE: 1998-06-25
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PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
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PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 24; DB 10; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAAAAA 1619
Db 1298 GTGTAAAAA 1321

RESULT 42
US-09-969-731-286
Sequence 286, Application US/09989731
Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geriltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
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PRIOR APPLICATION NUMBER: 60/091519
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PRIOR APPLICATION NUMBER: 60/091626
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 24; DB 10; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1596 GTGTAAAAA 1619
Db 1298 GTGTAAAAA 1321

RESULT 41
US-09-989-727-286
Sequence 286, Application US/09989727
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC56
CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 24; DB 10; Length 1337;
Best Local Similarity 100.0%; Pred. NO. 0.67;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GGTGTAATAAAAAAAAAAAAAA 1619
DB 1298 GGTGTAATAAAAAAAAAAAAAA 1321

RESULT 40
US-09-989-279-286
Sequence 286, Application US/09989279
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.

PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 24; DB 10; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1298 GTGTAAAAA 1321

RESULT 39
US-09-989-723-286
Sequence 286, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1062
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC63
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 PRIOR APPLICATION NUMBER: 60/089907
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089908
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089947
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089948
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089952
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/090246
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090252
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090254
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090349

PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090355
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090429
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090431
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090435
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090444
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090445
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090472
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090535
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090540
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090542
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090676
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090678
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090690
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090694
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090695
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090696
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090862
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 1.58; Score 24; DB 9; Length 1337;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1596 GTGTAAAAA 1619
 Db 1298 GTGTAAAAA 1321

RESULT 38
 US-09-989-722-286
 ; Sequence 286, Application us/09989722
 ; Patent No. US20020072067A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.

RESULT 33
US-09-925-300-384
; Sequence 384, Application US/09925300

QY	1596	GTGTA	AAAAAAAAAAAAAAAA	1619
Db	1015	GTGTA	AAAAAAAAAAAAAAAA	1038

```

APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Krickler, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2029 (PARA-018PRV)
CURRENT APPLICATION NUMBER: US/09/770,791
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,480
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: fastseq for windows version 4.0
SEQ ID NO 315
LENGTH: 373
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-770-791-315

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Query Match          1.5%  Score 24;  DB 10;  Length 373;
Best Local Similarity 100.0%;  Pred. No. 0.72;
Matches 24;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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OY 1596 GTGTAATAAAAAAAAAAAAAA 1619
DB 24 GTGTAATAAAAAAAAAAAAAA 1

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RESULT 29
US-09-924-035A-439/c
Sequence 439, Application US/09924035A
Patent No. US20020142319A1
GENERAL INFORMATION:
APPLICANT: Grlach, Jtn
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2011US
CURRENT APPLICATION NUMBER: US/09/924,035A
CURRENT FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: US 60/148,784
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 900
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 439
LENGTH: 419
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-924-035A-439

```

```

Query Match          1.5%  Score 24;  DB 10;  Length 419;
Best Local Similarity 100.0%;  Pred. No. 0.72;
Matches 24;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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OY 1596 GTGTAATAAAAAAAAAAAAAA 1619
DB 45 GTGTAATAAAAAAAAAAAAAA 22

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RESULT 30
US-10-062-254-125
Sequence 125, Application US/10062254
Patent No. US2002013882A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Edgar B
APPLICANT: Cahoon, Rebecca E
APPLICANT: Falco, Saverio Carl
APPLICANT: Fang, Yiwen
APPLICANT: Hanke, Sabine S.
APPLICANT: Lee, Jian-Ming

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APPLICANT: Li, Zhongsen
APPLICANT: Miao, Guo-Hua
APPLICANT: Morgante, Michele
APPLICANT: Niu, Xiping
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
APPLICANT: Zheng, Peizhong
APPLICANT: Zhu, Qun
TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/062,254
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/630,346
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/146511
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/156006
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/156899
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/157287
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/169767
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/171054
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/172958
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/171515
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: 60/173535
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 375
SOFTWARE: Microsoft Office 97
SEQ ID NO 125
LENGTH: 766
TYPE: DNA
ORGANISM: Placramia pentandra
US-10-062-254-125

```

```

Query Match          1.5%  Score 24;  DB 12;  Length 766;
Best Local Similarity 100.0%;  Pred. No. 0.69;
Matches 24;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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OY 1596 GTGTAATAAAAAAAAAAAAAA 1619
DB 734 GTGTAATAAAAAAAAAAAAAA 757

```

```

RESULT 31
US-09-925-300-627
Sequence 627, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruden,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 627
LENGTH: 871
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature

```

OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-584

Query Match
Best Local Similarity 1.5%; Score 25; DB 10; Length 2968;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1595 AGGTGTAACAAAAA 1619
DB 2886 AGGTGTAACAAAAA 2910

RESULT 25

US-09-770-696-104
Sequence 104, Application US/09770696
Patent No. US2001004940A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jörn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Ledford, Brooke L.
APPLICANT: Moessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Krickler, Majja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2031US (PARA-020PRV)
CURRENT APPLICATION NUMBER: US/09/770,696
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,278
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 911
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 104
LENGTH: 208
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-770-696-104

Query Match
Best Local Similarity 1.5%; Score 24; DB 10; Length 208;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAAAAA 1619
DB 169 GTGTAAAAA 192

RESULT 26

US-09-920-300A-58
Sequence 58, Application US/09920300A
Patent No. US20020136728A1
GENERAL INFORMATION:
APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121,547
CURRENT APPLICATION NUMBER: US/09/920,300A

CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 58
LENGTH: 258
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 258
OTHER INFORMATION: n = A,T,C or G
US-09-920-300A-58

Query Match
Best Local Similarity 1.5%; Score 24; DB 10; Length 258;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAAAAA 1619
DB 228 GTGTAAAAA 251

RESULT 27

US-10-033-528-58
Sequence 58, Application US/10033528
Patent No. US20020131971A1
GENERAL INFORMATION:
APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121,547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 58
LENGTH: 258
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 258
OTHER INFORMATION: n = A,T,C or G
US-10-033-528-58

Query Match
Best Local Similarity 1.5%; Score 24; DB 12; Length 258;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAAAAA 1619
DB 228 GTGTAAAAA 251

RESULT 28

US-09-770-791-315/C
Sequence 315, Application US/09770791
Patent No. US20020062014A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jörn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Matthews, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Moessner, Jeffrey P.

```

1 FILE REFERENCE: 16511.006/37-21(10298)C
2
3 CURRENT APPLICATION NUMBER: US/09/960,352
4
5 CURRENT FILING DATE: 2001-09-24
6
7 NUMBER OF SEQ ID NOS: 15112
8
9 SEQ ID NO 9079
10
11 LENGTH: 152
12
13 TYPE: DNA
14
15 ORGANISM: Bos taurus
16
17 OTHER INFORMATION: Clone ID: 39-LIB3058-009-Q1-K1-B12
18
19 US-09-360-352-9079

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Query Match	1.58;	Score 25;	DB 10;	Length 152;
Best Local Similarity	100.0%;	Pred. No. 0.29;		
Matches 25; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

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Qy 1595 AGTGTAACAAAAAAAAAAAAAAAA 1619
      |||||
Db 52 AGTGTAACAAAAAAAAAAAAAAAA 28
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Query Match      1.5%; Score 25; DB 10; Length 363;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

```

OY 1595 AGTGTAACAAAAAAGAAAAA 1615
      |||||
Db 27 AGTGTAACAAAAAAGAAAAA 3

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```

RESULT 22
US-09-867-701-5174/c
: Sequence 5174, Application US/09867701
: Patent No. US20020132237A1
: GENERAL INFORMATION:
: APPLICANT: Aglate, Paul A.
: APPLICANT: Jones, Robert
: APPLICANT: Haddock, Susan L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.497
: CURRENT APPLICATION NUMBER: US/09/867,701
: CURRENT FILING DATE: 2001-05-29
: NUMBER OF SEQ ID NOS: 10912
: SOFTWARE: FASTSeq for Windows Version 4.0
: SEQ ID NO 5174
: LENGTH: 395
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-867-701-5174

```

Query Match	1.5%;	Score 25;	DB 10;	length 395
Best Local Similarity	100.0%;	Pred. No.	0.28;	

	Matches	25;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1595	AGTGTAAAAAAAAAAAAAAAAAAAAA	1619							
Db	27	AGTGTAAAAAAAAAAAAAAAAAAAAA	3							

```

US-09-919-580-143/c
? RESULT 23
? Sequence 143, Application US/09919580
? Patent NO. US20020110832A1
? GENERAL INFORMATION:
? APPLICANT: Pyle, Ruth
? APPLICANT: Xu, Jiangchun
? APPLICANT: Seerist, Heather
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
? FILE REFERENCE: 210121.552
? CURRENT APPLICATION NUMBER: US/09/919,580
? CURRENT FILING DATE: 2001-07-30
? NUMBER OF SEQ ID NOS: 934
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO: 143
? LENGTH: 568
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 62, 74, 231, 357, 405, 499, 510, 532, 564
? OTHER INFORMATION: n = A,T,C or G
US-09-919-580-143

```

Query Match	1.58;	Score 25;	DB 10;	Length 568;
Best Local Similarity	100.0%;	Pred. No. 0.27;		
Matches 25; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY 1595 AGTGTAAAAAAGAAAAAAGAAAAA 1615
    ||| ||| ||| ||| ||| ||| ||| |||
Db 35 AGTGTAAAAAAGAAAAAAGAAAAA 11
```

```

RESULT 24
US-09-925-301-584
: Sequence 584, Application US/09925301
: Patent No. US20020052308A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA106
: CURRENT APPLICATION NUMBER: US/09/925, 301
: CURRENT FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05882
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124, 270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 1694
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 584
: LENGTH: 2968
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (454)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (1437)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (2961)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (2964)

```


NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7826
LENGTH: 381
TYPE: DNA
ORGANISM: Homo sapien
US-09-867-701-7826

Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e-42;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 959 CTCGCTGTAAGAAAGCTTAGAAATCTTCTCAGTCTCTCTGACAGAGACTGGCCG 1018
DB 116 CTCGCTGTAAGAAAGCTTAGAAATCTTCTCAGTCTCTCTGACAGAGACTGGCCG 175
QY 1019 GGACGGAAGACAGACGGGCGCTGCACAAAGCGGCGCTGCGGTGGAGTGGCATG 1078
DB 176 GGACGGAAGACAGACGGGCGCTGCACAAAGCGGCGCTGCGGTGGAGTGGCATG 235
QY 1079 TACGC 1083
DB 236 TACGC 240

RESULT 17

US-09-867-701-4251
Sequence 4251, Application US/09867701
Patent No. US20020132237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4251
LENGTH: 430
TYPE: DNA
ORGANISM: Homo sapien
US-09-867-701-4251

Query Match
Best Local Similarity 100.0%; Pred. No. 2e-40;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 CTCGATGTCCTTCAGACCCCTGCGCCCAACCCCACTCCCTGAGTGGTTCTCTG 490
DB 182 CTCGATGTCCTTCAGACCCCTGCGCCCAACCCCACTCCCTGAGTGGTTCTCTG 241
QY 491 GGTGCTCTTTATCTGGGTAGGAGCGGAGTCCGTCTCTTGTCTCTGTCGCAA 550
DB 242 GGTGCTCTTTATCTGGGTAGGAGCGGAGTCCGTCTCTTGTCTCTGTCGCAA 301

RESULT 18

US-09-867-701-2375
Sequence 2375, Application US/09867701
Patent No. US20020132237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2375
LENGTH: 558
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1)...(358)
OTHER INFORMATION: n = A,T,C or G
US-09-867-701-2375

Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-37;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1138 TGCAGAACACCCGCCGAACCTGCGAGAGACCGGTACAGGAGCGGTGAGACC 1197
DB 142 TGCAGAACACCCGCCGAACCTGCGAGAGACCGGTGAGAGCGGTGAGACC 201
QY 1198 GAGCTGAGGTGAGAAACGTCCTCGAGAGGAGGAGATCATGTACGCC 1249
DB 202 GAGCTGAGGTGAGAAACGTCCTCGAGAGGAGGAGATCATGTACGCC 253

RESULT 19

US-09-834-975-825
Sequence 825, Application US/09834975
Patent No. US20020110815A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Van Hulle, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
FILE REFERENCE: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MRI-0163
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 825
LENGTH: 1368
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1)...(1368)
OTHER INFORMATION: n = A,T,C or G
US-09-834-975-825

Query Match
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1593 ACAGGTGTAAGAAAAA 1619
DB 459 ACAGGTGTAAGAAAAA 485

RESULT 20

US-09-960-352-9079/C
Sequence 9079, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Ningbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NOCTIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

OY 1525 GAGATTAACTGTTTCAAAACCCGGGAGATTGGCTGTGTTAAAGAACCATTTAA 1384
 |||||||
 DB 75 GAGATTAACTGTTTCAAAACCCGGGAGATTGGCTGTGTTAAAGAACCATTTAA 16
 OY 1585 TGCCTTACAGACTGT 1599
 |||||||
 DB 15 TGCCTTACAGACTGT 1

RESULT 13

US-09-867-701-8894/c
 ; Sequence 8894, Application US/09867701
 ; Patent No. US20020132237A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aglate, Paul A.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jones, Robert
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.497
 ; CURRENT APPLICATION NUMBER: US/09/867,701
 ; CURRENT FILING DATE: 2001-05-29
 ; NUMBER OF SEQ ID NOS: 10912
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8894
 ; LENGTH: 201
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-867-701-8894

Query Match 10.3%; Score 166; DB 10; Length 201;
 Best Local Similarity 100.0%; Pred. No. 2.3e-59;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1223 AGAAGGGAGAGAGATCATGTAGCGCCGGAAGTAGAGACCTGTCAGTGTGCTGGTT 1282
 |||||||
 DB 181 AGAAGGGAGAGAGATCATGTAGCGCCGGAAGTAGAGACCTGTCAGTGTGCTGGTT 122
 OY 1283 TGGCCGCGACCATATCTCTCGAATCTGTGGGCAATCCAGTATAGGCAATGTACAA 1342
 |||||||
 DB 121 TGGCCGCGACCATATCTCTCGAATCTGTGGGCAATCCAGTATAGGCAATGTACAA 62
 OY 1343 CAATCAGCCCTGGGCGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1388
 |||||||
 DB 61 CAATCAGCCCTGGGCGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 16

RESULT 14

US-09-867-701-1532
 ; Sequence 1532, Application US/09867701
 ; Patent No. US20020132237A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aglate, Paul A.
 ; APPLICANT: Jones, Robert
 ; APPLICANT: Harlocker, Susan L.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.497
 ; CURRENT APPLICATION NUMBER: US/09/867,701
 ; CURRENT FILING DATE: 2001-05-29
 ; NUMBER OF SEQ ID NOS: 10912
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1532
 ; LENGTH: 390
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(390)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-867-701-1532

Query Match 9.5%; Score 154; DB 10; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.9e-54;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1358 AGACACGAGCAG 1417
 |||||||
 DB 147 AGACACGAGCAG 206
 OY 1418 GATTAAGCATTAAATTTTATAGCCCTGTGCTGTACTGAGCAAGAAATGTAC 1477
 |||||||
 DB 207 GATTAAGCATTAAATTTTATAGCCCTGTGCTGTACTGAGCAAGAAATGTAC 266
 OY 1478 CAATTTTCAGTGTGAGACTTGACAGCTTCTTTT 1511
 |||||||
 DB 267 CAATTTTCAGTGTGAGACTTGACAGCTTCTTTT 300

RESULT 15

US-09-825-294-213
 ; Sequence 213, Application US/09825294
 ; Patent No. US20020004491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Fling, Steven P.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; FILE REFERENCE: 210121.484C5
 ; CURRENT APPLICATION NUMBER: US/09/825,294
 ; CURRENT FILING DATE: 2001-04-03
 ; NUMBER OF SEQ ID NOS: 215
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 213
 ; LENGTH: 480
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-825-294-213

Query Match 9.0%; Score 146; DB 10; Length 480;
 Best Local Similarity 99.5%; Pred. No. 3.8e-51;
 Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCGCACTTTTGGCGGATTTCTTCTCCAGGCTTTGGGCTCAATCCAGTGTACCA 60
 |||||||
 DB 280 GCGCACTTTTGGCGGATTTCTTCTCCAGGCTTTGGGCTCAATCCAGTGTACCA 339
 OY 61 GTGTGAAGATTTCCAGCTGAACAACGACTCTCTCCCGAGTTCATTGTGAATTGCAC 120
 |||||||
 DB 340 GTGTGAAGATTTCCAGCTGAACAACGACTCTCTCCCGAGTTCATTGTGAATTGCAC 399
 OY 121 GGTGAAGCTTAAAGCATGTGTCAAGAAAGTAGATGAGCAAGTGGCGGATCATGA 180
 |||||||
 DB 400 GGTGAAGCTTAAAGCATGTGTCAAGAAAGTAGATGAGCAAGTGGCGGATCATGA 459
 OY 181 CCGCAAGTCTGTGCAT 197
 |||||||
 DB 460 CCGCAAGTCTGTGCAT 476

RESULT 16

US-09-867-701-7826
 ; Sequence 7826, Application US/09867701
 ; Patent No. US20020132237A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aglate, Paul A.
 ; APPLICANT: Jones, Robert
 ; APPLICANT: Harlocker, Susan L.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.497
 ; CURRENT APPLICATION NUMBER: US/09/867,701
 ; CURRENT FILING DATE: 2001-05-29

QY 241 CTGCTCCCGAGGAACTGAACTGAGTTCATGAGTGTGCAACACCCCTTTGTAA 300
 |||||||
 Db 251 CTGCTCCCGAGGAACTGAACTGAGTTCATGAGTGTGCAACACCCCTTTGTAA 310
 |||||||
 QY 301 CGGGCCAGG 310
 |||||||
 Db 311 CGGGCCAGG 320

RESULT 10

US-09-867-701-2409/c
 ; Sequence 2409, Application US/09867701
 ; Patent No. US20020132237A1

GENERAL INFORMATION:

APPLICANT: Aglate, Paul A.
 APPLICANT: Jones, Robert
 APPLICANT: Harlocker, Susan L.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 FILE REFERENCE: 210121.497
 CURRENT APPLICATION NUMBER: US/09/867,701
 CURRENT FILING DATE: 2001-05-29
 NUMBER OF SEQ ID NOS: 10912
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 2409
 LENGTH: 349
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-867-701-2409

Query Match
 Best Local Similarity 100.0%; Pred. No. 1.7e-117;
 Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1292 CCATGATCTCGGATCTGTTGGCATCCAGCATGCGGCAATGTCACAAATCAGCC 1351
 |||||||
 Db 310 CCATGATCTCGGATCTGTTGGCATCCAGCATGCGGCAATGTCACAAATCAGCC 251
 |||||||
 QY 1352 CTGGGCGACAGCAGCAGGAGGAGAGACAGAGAAAAAGAAAAACACAGATGAGAACCA 1411
 |||||||
 Db 250 CTGGGCGACAGCAGCAGGAGGAGAGACAGAGAAAAAGAAAAACACAGATGAGAACCA 191
 |||||||
 QY 1412 GTAATGTAATAAACCATTAATATTATTCACCCCTGCTCTGCTTACTGCGGAGAA 1471
 |||||||
 Db 190 GTAATGTAATAAACCATTAATATTATTCACCCCTGCTCTGCTTACTGCGGAGAA 131
 |||||||
 QY 1472 TGGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCACAAGCAGAGAAAT 1531
 |||||||
 Db 130 TGGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCACAAGCAGAGAAAT 71
 |||||||
 QY 1532 TAACACTGTTTCAACCCGGGGAGTTGGCTGTAAAGAAAGCATTAAATGCTTTA 1591
 |||||||
 Db 70 TAACACTGTTTCAACCCGGGGAGTTGGCTGTAAAGAAAGCATTAAATGCTTTA 11
 |||||||
 QY 1592 GACAGTG 1598
 |||||||
 Db 10 GACAGTG 4

RESULT 11

US-09-825-294-212
 ; Sequence 212, Application US/09825294
 ; Patent No. US20020004491A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
 APPLICANT: Stock, John A.
 APPLICANT: Algate, Paul A.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 FILE REFERENCE: 210121.484C5
 CURRENT APPLICATION NUMBER: US/09/825,294
 CURRENT FILING DATE: 2001-04-03

NUMBER OF SEQ ID NOS: 215
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 212
 ; LENGTH: 1010
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-825-294-212

Query Match
 Best Local Similarity 100.0%; Pred. No. 1.1e-102;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 AGGCTTCCGCTGCAATTCACAGTGTGAAGAAATTCACAGTGAACAGCTG 90
 |||||||
 Db 258 AGGCTTCCGCTGCAATTCACAGTGTGAAGAAATTCACAGTGAACAGCTG 317
 |||||||
 QY 91 CTCTCCCGGAGTTCAATTTGAAATTCAGGTTGAAAGTTCAAGATGTGCAGAAAG 150
 |||||||
 Db 318 CTCTCCCGGAGTTCAATTTGAAATTCAGGTTGAAAGTTCAAGATGTGCAGAAAG 377
 |||||||
 QY 151 AGTATGAGCAAGATCCCGGATCATGTACCCCAAGTCTGTGATCATCAGCGGCTG 210
 |||||||
 Db 378 AGTATGAGCAAGATCCCGGATCATGTACCCCAAGTCTGTGATCATCAGCGGCTG 437
 |||||||
 QY 211 TCTCATGCTCTGCGGAGTACAGTCTTCTGCTCCAGGAAATGAACTGATTG 270
 |||||||
 Db 438 TCTCATGCTCTGCGGAGTACAGTCTTCTGCTCCAGGAAATGAACTGATTG 497
 |||||||
 QY 271 CATCAGCTGTGCAACACCCCTTTGTAC 301
 |||||||
 Db 498 CATCAGCTGTGCAACACCCCTTTGTAC 528

RESULT 12

US-09-867-701-4240/c
 ; Sequence 4240, Application US/09867701
 ; Patent No. US20020132237A1

GENERAL INFORMATION:

APPLICANT: Aglate, Paul A.
 APPLICANT: Jones, Robert
 APPLICANT: Harlocker, Susan L.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 FILE REFERENCE: 210121.497
 CURRENT APPLICATION NUMBER: US/09/867,701
 CURRENT FILING DATE: 2001-05-29
 NUMBER OF SEQ ID NOS: 10912
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 4240
 LENGTH: 409
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-867-701-4240

Query Match
 Best Local Similarity 99.7%; Pred. No. 9e-100;
 Matches 314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1285 GCCGAGCCATGATCTCTCGAATCTGTTGGCATCCAGCATACGGCCATGTACAAACA 1344
 |||||||
 Db 315 GCCGAGCCATGATCTCTCGAATCTGTTGGCATCCAGCATACGGCCATGTACAAACA 256
 |||||||
 QY 1345 ATCAGCCCTGGGAGACACGAGGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGA 1404
 |||||||
 Db 255 ATCAGCCCTGGGAGACACGAGGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGA 196
 |||||||
 QY 1405 GAACACAGTAATGAATAAACCATTAATATTATAGCCCTGCTGTGCTTACTGCG 1464
 |||||||
 Db 195 GAACACAGTAATGAATAAACCATTAATATTATAGCCCTGCTGTGCTTACTGCG 136
 |||||||
 QY 1465 CAGGAATGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCACAAGCAAGA 1524
 |||||||
 Db 135 CAGGAATGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCACAAGCAAGA 76

```

APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Filing, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.4845
CURRENT APPLICATION NUMBER: US/09/825.294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 199
LENGTH: 369
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(369)
OTHER INFORMATION: n = A,T,C or G
US-09-825-294-199

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```

Query Match          19.5%; Score 315; DB 10; Length 369;
Best Local Similarity 100.0%; Pred. No. 8.7e-121;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 30 CAGGCTTTGGCGTGCAGAAATCCAGTGTACCAAGTGTGAAGAAATTCAGCTGAACAGAGCT 89
    |||||||
DB 30 CAGGCTTTGGCGTGCAGAAATCCAGTGTACCAAGTGTGAAGAAATTCAGCTGAACAGAGCT 89
OY 90 GCTCTCTCCCGAGTTCATGTGTAATGACAGGGTGAACGTTCAAGACATGTGCAGAAAG 149
    |||||||
DB 90 GCTCTCTCCCGAGTTCATGTGTAATGACAGGGTGAACGTTCAAGACATGTGCAGAAAG 149
OY 150 AAGTATGAGACAAAGTCCGGGATGATGATACCGCAAGTCTTGATCATCATCGCGGCT 209
    |||||||
DB 150 AAGTATGAGACAAAGTCCGGGATGATGATACCGCAAGTCTTGATCATCATCGCGGCT 209
OY 210 GTCTATATGCTCTGCGGGTACAGTCTTCTGCTCCCGAGGAAACTGAATCAAGTTT 269
    |||||||
DB 210 GTCTATATGCTCTGCGGGTACAGTCTTCTGCTCCCGAGGAAACTGAATCAAGTTT 269
OY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGCGCAAGGCCCAAGAAAGGGGAGTT 329
    |||||||
DB 270 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGCGCAAGGCCCAAGAAAGGGGAGTT 329
OY 330 CTGCTCTGGCGCTCA 344
    |||||||
DB 330 CTGCTCTGGCGCTCA 344

```

RESULT 8

```

US-09-867-701-1516/c
Sequence 1516, Application US/09867701
Patent No. US2002013237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867.701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1516
LENGTH: 373
TYPE: DNA
ORGANISM: Homo sapien
US-09-867-701-1516

```

```

Query Match          19.5%; Score 315; DB 10; Length 373;
Best Local Similarity 100.0%; Pred. No. 8.7e-121;

```

```

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1285 GCCGAGCCATGATCTCTCCGATCTGTTGGGCAATCCAGCATACGGCAATGTCACAA 1344
    |||||||
DB 315 GCCGAGCCATGATCTCTCCGATCTGTTGGGCAATCCAGCATACGGCAATGTCACAA 256
OY 1345 ATCAGCCCTGGGCGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1404
    |||||||
DB 255 ATCAGCCCTGGGCGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 196
OY 1405 GAGCACTAAATGAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1464
    |||||||
DB 195 GAGCACTAAATGAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 136
OY 1465 CAGGAATGTATCAATTTTTCAGTGTGAGCTGACAGCTCTTTTCCACAAGACA 1524
    |||||||
DB 135 CAGGAATGTATCAATTTTTCAGTGTGAGCTGACAGCTCTTTTCCACAAGACA 76
OY 1525 GAGAAATTAACACTGTTTCAACCCCGGGAGTGGCTGTGTTAAAGAACATTAA 1584
    |||||||
DB 75 GAGAAATTAACACTGTTTCAACCCCGGGAGTGGCTGTGTTAAAGAACATTAA 16
OY 1585 TGCTTTAGACAGTGT 1599
    |||||||
DB 15 TGCTTTAGACAGTGT 1

```

RESULT 9

```

US-09-825-294-9
Sequence 9, Application US/09825294
Patent No. US2002004491A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Filing, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.4845
CURRENT APPLICATION NUMBER: US/09/825.294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C or G
US-09-825-294-9

```

```

Query Match          19.1%; Score 310; DB 10; Length 396;
Best Local Similarity 100.0%; Pred. No. 1e-118;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 GGCACTTTTGGCGATTTTCTTCTCCAGGCTTTCGCTGCAAAATCCAGTCTACCA 60
    |||||||
DB 11 GGCACTTTTGGCGATTTTCTTCTCCAGGCTTTCGCTGCAAAATCCAGTCTACCA 70
OY 61 GTGTGAAGATTCAGACTGACAGAGTGTCTCCCGAGTTCATTTGAATTCAC 120
    |||||||
DB 71 GTGTGAAGATTCAGACTGACAGAGTGTCTCCCGAGTTCATTTGAATTCAC 130
OY 121 GGTGAAGTTCAGACATGTGTCAAGAAATGATGAGCAAGTGTGCGGAGTCAATGA 180
    |||||||
DB 131 GGTGAAGTTCAGACATGTGTCAAGAAATGATGAGCAAGTGTGCGGAGTCAATGA 190
OY 181 CCGGAGTCTGTGATCAATCAAGGCTGTCTCAATGCGCTTGGCGGATCAAGTCTT 240
    |||||||
DB 191 CCGGAGTCTGTGATCAATCAAGGCTGTCTCAATGCGCTTGGCGGATCAAGTCTT 250

```


Db 760 GTTCTTCGCGTCCCTTTTATTCGGTAGGAGCGGAGTCCGTTCTTTGTT 819
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 QY 601 TTTCAGTATGATTTGAAGAAGAGAGTGGAGTGAAGTTTACCCCATCTCTGTGTAA 660
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 Db 940 CCGAATCAAGGCGGCGGAGAGTGCCTTAGAAGTACTAGAGTGGAGTGGAGTGGC 999
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 Db 1000 TTTTGAAGCCTCCAGTGTCCATTCATCCCTGATGGGGGAGTATGTTGAGACTGAGA 1059
 QY 781 GTGAGAGTACGTTTCTTAGGGCTGGAGGGCAGTTCCCACTGAAGGCTCCGCTTG 840
 Db 1060 GTGAGAGTACGTTTCTTAGGGCTGGAGGGCAGTTCCCACTGAAGGCTCCGCTTG 1119
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 Db 1120 ACATTCAAATTCATGCTCCTGAAATCCTCTGACAGAGAAATGGCTGTTTCGCG 1179
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 QY 1021 ACGCGAAGAGCAACGGGCGCTGCACAAAGCGGCGCTGCTGGTGGAGTGGCGCATTA 1080
 Db 1300 ACGCGAAGAGCAACGGGCGCTGCACAAAGCGGCGCTGCTGGTGGAGTGGCGCATTA 1359
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 Db 1360 CCGGCGAGGCGCTCTGCTGTTGGCTGCTGAGAGCAAGCGGGGAGCAAGCACTTGC 1418
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 Db 1539 CTGCTCCAGTCTGCTGGGTTGGCGGAGCATGATCCTCCGAAATGTTGGGCAATC 1598
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 QY 1501 CAGCTCTTTTGGCAAGAGAGAGAAATTTAACTGTTTCAAAACCGGGGAGATGG 1560
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 Db 1839 CTGTGTTAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAAGAAAAAAGAAAA 1897

RESULT 4
 US-09-825-294-210
 ; Sequence 210, Application US/09625294
 ; Patent No. US2002000491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Fling, Steven P.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TITILE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.4845
 ; CURRENT FILING DATE: 2001-04-03
 ; NUMBER OF SEQ ID NOS: 215
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 210
 ; LENGTH: 625
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc-feature
 ; LOCATION: (1)...(625)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-825-294-210

Query Match 30.0%; Score 486; DB 10; Length 625;
 Best Local Similarity 99.8%; Pred. No. 2,9e-191;
 Matches 606; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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 QY 1052 GGCCTGTGCTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1111
 Db 61 GGCCTGTGCTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120
 QY 1112 CAGCGAGAGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 1171
 Db 121 CAGCGAGAGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 1179
 QY 1172 CCGTGTACAGAGAGCGGCTTGTATGACCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1231
 Db 180 CCGTGTACAGAGAGCGGCTTGTATGACCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 239
 QY 1232 GAGAGATCATGTACCGCCCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1291
 Db 240 GAGAGATCATGTACCGCCCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 299
 QY 1292 CCAATGATCTCTCCAAATCTGTTGGGATCCAGCATGCGGCAATGTACACAAATCAGCC 1351
 Db 300 CCAATGATCTCTCCAAATCTGTTGGGATCCAGCATGCGGCAATGTACACAAATCAGCC 359
 QY 1352 CTGGGCAAGACAG 1411
 Db 360 CTGGGCAAGACAG 419
 QY 1412 GTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1471
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 Db 480 TGATACCAATTTTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 539
 QY 1532 TAACACGTTTTCAAAACCGGGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1591
 Db 540 TAACACGTTTTCAAAACCGGGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 599
 QY 1592 GACAGTG 1598

Qy	421	CCACCCCTCTCGATGTTCTTCCAGCCCTCGCCCCCAACCCCACTCTCTGAGTGA	480
Db	421	CCACCCCTCTCGATGTTCTTCCAGCCCTCGCCCCCAACCCCACTCTCTGAGTGA	480
Qy	481	GTTTCTTCTGGGTCCTTTTATTTCTGGGTAAAGAGCGGAGTCGCGTCTCTTGT	540
Db	481	GTTTCTTCTGGGTCCTTTTATTTCTGGGTAAAGAGCGGAGTCGCGTCTCTTGT	540
Qy	541	CCCTGCAATTAATGAAGAAGCTCGGTTAAAGCATTTCTGAATTAATTCAGCTGCAAT	600
Db	541	CCCTGCAATTAATGAAGAAGCTCGGTTAAAGCATTTCTGAATTAATTCAGCTGCAAT	600
Qy	601	TTTTCAATATGTAATTAAGGAAGAGAGTGAATGAATTCACCCCATGCTGTAAAC	660
Db	601	TTTTCAATATGTAATTAAGGAAGAGAGTGAATGAATTCACCCCATGCTGTAAAC	660
Qy	661	CGGAGTAAAGGCCAAGCTGGCAGAGTCAAGTCTTGAAGATCACTGAGAGTGGGATCTGCC	720
Db	661	CGGAGTAAAGGCCAAGCTGGCAGAGTCAAGTCTTGAAGATCACTGAGAGTGGGATCTGCC	720
Qy	721	TTTTGTAAAGCCCTCAGATGCTCATTCCTCAATCCCTGAATGGGGCAATGTTTAAGCTGACA	780
Db	721	TTTTGTAAAGCCCTCAGATGCTCATTCCTCAATCCCTGAATGGGGCAATGTTTAAGCTGACA	780
Qy	781	GTCAGACTGACGTTTTCTTAAAGGCTGGAAGGCCAGTTCCCACTCAAGGCTCCCTGCTTG	840
Db	781	GTCAGAGTGCAGTTTTCTTAAAGGCTGGAAGGCCAGTTCCCACTCAAGGCTCCCTGCTTG	840
Qy	841	ACATTCAAACTTCATGCTCTCTGAAAAACCATTCCTCTGCAACGAATTGCTGTTCGCGC	900
Db	841	ACATTCAAACTTCATGCTCTCTGAAAAACCATTCCTCTGCAACGAATTGCTGTTCGCGC	900
Qy	901	CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGACTTAAGACTGGGGCTGGGCT	960
Db	901	CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGACTTAAGACTGGGGCTGGGCT	960
Qy	961	CGCTCGAAAAATGCTTAAAGAAATCTTCTCAGTTCTCTTGCAAGAGACTGGCCCGGG	1020
Db	961	CGCTCGAAAAATGCTTAAAGAAATCTTCTCAGTTCTCTTGCAAGAGACTGGCCCGGG	1020
Qy	1021	ACGCGAAGAGCAACGGGCGCTGCACAAAGGGGGGCTGTGGGTGGAGTCCGATGTA	1080
Db	1021	ACGCGAAGAGCAACGGGCGCTGCACAAAGGGGGGCTGTGGGTGGAGTCCGATGTA	1080
Qy	1081	CGCGGAGGGGCTCTCGTGTGTGGCGCTGTGCAGCAAGGGCGGACGACACACTTGC	1140
Db	1081	CGCGGAGGGGCTCTCGTGTGTGGCGCTGTGCAGCAAGGGCGGACGACACACTTGC	1140
Qy	1141	ACGAACACCCGCGCAAACTGCTGCGAGAGAACCGGTACAGAGGCGGGTGAATGACGAG	1200
Db	1141	ACGAACACCCGCGCAAACTGCTGCGAGAGAACCGGTACAGAGGCGGGTGAATGACGAG	1200
Qy	1201	CTGAGGTGAAAAAACGTTCTCGAGAAAGGAGGAGGATCTAGCCCGGAAGTAGAC	1260
Db	1201	CTGAGGTGAAAAAACGTTCTCGAGAAAGGAGGAGGATCTAGCCCGGAAGTAGAC	1260
Qy	1261	CTGCTCAGTGTGCTTGGGTTGGGCGGACGCCATGATCTCTCGAATCTGTTGGGATC	1320
Db	1261	CTGCTCAGTGTGCTTGGGTTGGGCGGACGCCATGATCTCTCGAATCTGTTGGGATC	1320
Qy	1321	CAGCATACGGCCAAATGTCACAACAATCAGCCCTGGGCGACACGAGCAGAGAGGAGAC	1380
Db	1321	CAGCATACGGCCAAATGTCACAACAATCAGCCCTGGGCGACACGAGCAGAGAGGAGAC	1380
Qy	1381	AGAGAAAAAGAAAAACAGCATGAGAACACAGTAAATGAATTAACATTAATAATTTAG	1440
Db	1381	AGAGAAAAAGAAAAACAGCATGAGAACACAGTAAATGAATTAACATTAATAATTTAG	1440
Qy	1441	CCCTCTGTTCTGTGCTTACTTGCGCAGAAAGGTACCAATTTTTCTAGTGTGGACTTGA	1500
Db	1441	CCCTCTGTTCTGTGCTTACTTGCGCAGAAAGGTACCAATTTTTCTAGTGTGGACTTGA	1500

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OY 1501 CAGCTTCCTTTTGCACACAGCAAGAGAAATTTAACAGCTGTTTCAAAACCGGGGAGTTGG 1560
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OY 1561 CTGTGTTAAAGAAAGACCATTAAATGCTTTAGACAGCTGTAAAAA 1619
Db 1561 CTGTGTTAAAGAAAGACCATTAAATGCTTTAGACAGCTGTAAAAA 1619

RESULT 3
US-09-825-294-214
; Sequence 214, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825.294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1897)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214

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Db	241	CTGTCTCTCCCGAGGAACTGAAC	TGACTAGTTTGCATCAGCTGCTGC	AACACCCCTCTTTGAA	300
Oy	301	CGGGCCCAAGGCCCAAGAAAAGG	GGGAAGTTTGCTGACCTCGGGCCTC	AGGCCACAGGGCTCCGGAC	360
Db	301	CGGGCCCAAGGCCCAAGAAAAGG	GGGAAGTTTGCTGACCTCGGGCCTC	AGGCCACAGGGCTCCGGAC	360
Oy	361	CACCATTCGTGTCCTCAAAATTA	AGCCCTCTTCTCGGCACACTGCTGA	AGCTGAAGAGATG	420
Db	361	CACCATTCGTGTCCTCAAAATTA	AGCCCTCTTCTCGGCACACTGCTGA	AGCTGAAGAGATG	420
Oy	421	CGACCCCTCCGTCATGTTGTTCT	TCACAGCCCTCGGCCCAACCCCCAC	CTCCCTGAGTGA	480
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Oy	481	GTTCCTCTGCGGTGTCCTTTTA	TTCCTGSGGTAGGAGCGGGAGTCC	GTCTCTTTTGT	540
Db	481	GTTCCTCTGCGGTGTCCTTTTA	TTCCTGSGGTAGGAGCGGGAGTCC	GTCTCTTTTGT	540
Oy	541	CCGTGCAATTAATTAAGAAAGAG	TCGGGTAAAGCATTCGAAATTAATTA	TAGCCTGACTGAAT	600
Db	541	CCGTGCAATTAATTAAGAAAGAG	TCGGGTAAAGCATTCGAAATTAATTA	TAGCCTGACTGAAT	600
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Db	601	TTTCAGTATGTACTTTAAGAGAA	GGAGGTGAGTGAATTCACCCCATCT	GTGTGTAAAC	660
Oy	661	CGGAGTCAAGGCCACGAGCTGG	CAGAGTCATCCTTTGAAGTAC	TCAGAGAGTGGGCAATCGGC	720
Db	661	CGGAGTCAAGGCCACGAGCTGG	CAGAGTCATCCTTTGAAGTAC	TCAGAGAGTGGGCAATCGGC	720
Oy	721	TTTTGTAAAGCTCTCAGGTGTC	ATTCCTCATCCCTGATGGGGGCAT	AGTTTGAAGTCAAG	780
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Db	781	GTGAGAGTGACGTTTCTTTAG	GGCTGTGAGGGCCACTTCCCACT	CAAGGTCCTCGCTTG	840
Oy	841	ACATTCAAACTTCATGCTCCT	GTGAAAACCAATTCCTGACAG	AGAAATGGCTGGTTTCGCGC	900
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Oy	901	CTGAGTGGGCTCTAGTGA	CTCGAGCTCAATAGTCTAGAC	TCTAGGAGCTCGGGCT	960
Db	901	CTGAGTGGGCTCTAGTGA	CTCGAGCTCAATAGTCTAGAC	TCTAGGAGCTCGGGCT	960
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Db	1081	CGCGAGCGGCTCTCCG	TGCGGTGGGCGGTGCGAC	AGGAGGCGGAGCAACGACTTGC	1140
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Db	1321	CAGCATCGGCCCAATGCTCAACAAATCACCCCTCGGACACGAGCGAGGAGGAGAC	1380
Qy	1381	AGGAAAGAGAAAAACACAGCATGAGAACACAGTAATGATTTAAACATATAATATTAG	1440
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Qy	1501	CAGCTCTTTTGGCACACAGCAGAGAGAAATTTAACACTGTTTCAAAACCCGGGGAGTTGG	1560
Db	1501	CAGCTCTTTTGGCACACAGCAGAGAGAAATTTAACACTGTTTCAAAACCCGGGGAGTTGG	1560
Qy	1561	CTGCTGTTAAAGAAAGACCATTAATATGTTTAGCACTGTAAAAAATTTTTTTTTTTTTTTT	1619
Db	1561	CTGCTGTTAAAGAAAGACCATTAATATGTTTAGCACTGTAAAAAATTTTTTTTTTTTTTTT	1619

RESULT 2

03/09/02 21.1
 ? Sequence 211, Application US/09825294
 ? Patent No. US2002000491A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Xu, Jiangchun
 ? APPLICANT: Stolk, John A.
 ? APPLICANT: Algate, Paul A.
 ? APPLICANT: Fling, Steven P.
 ? TITLE OF INVENTION: COMPOSITIONS AND METHODS
 ? TITLE OF INVENTION: THERAPY AND DIAGNOSIS
 ? FILE REFERENCE: 210121.48405
 ? CURRENT APPLICATION NUMBER: US/09/825,294
 ? CURRENT FILING DATE: 2001-04-03
 ? NUMBER OF SEQ ID NOS: 215
 ? SOFTWARE: FastSeq for Windows Version 3.0.0
 ? SEQ ID NO 211
 ? LENGTH: 1619
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 ? US-09-825-294-211

Query Match	100.0%;	Score 1619;	DB 10;	Length 1619;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1619; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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Qy	61	GTGTAAAGATTTCCAGCTGAAACAACGACTGCTCCTCCCGGAGTCATATTGTAAATTGCAC	120
Db	61	GTGTAAAGATTTCCAGCTGAAACAACGACTGCTCCTCCCGGAGTCATATTGTAAATTGCAC	120
Qy	121	GGTGAACGTTCCAGACATGTGTCAAGAAAGAATGATGGAGCAAAAGTCCCGGATCATGTA	180
Db	121	GGTGAACGTTCCAGACATGTGTCAAGAAAGAATGATGGAGCAAAAGTCCCGGATCATGTA	180
Qy	181	CCGCAAGTCTGTGATCATCAGCGGCCCTGTCTCATGCTCTGCGCGGTACCAAGTCTTT	240
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Qy	361	CACCATCTGTTTCTCAAAATTAGCCCTTTCTCGGCACACTGCTGAAGCTGAAGAGATG	420
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1619	100.0	1619	US-09-825-294-211	Sequence 211, App
3	1396	86.2	1897	US-09-825-294-214	Sequence 214, App
4	486	30.0	625	US-09-825-294-210	Sequence 210, App
5	486	30.0	625	US-09-825-294-210	Sequence 210, App
6	386	23.8	1362	US-09-825-294-208	Sequence 10876, A
7	315	19.5	369	US-09-825-294-199	Sequence 208, App
8	315	19.5	373	US-09-825-294-199	Sequence 199, App
9	310	19.1	349	US-09-825-294-8	Sequence 1516, App
10	307	19.0	349	US-09-825-294-8	Sequence 9, App11
11	271	16.7	1010	US-09-825-294-212	Sequence 2409, App
12	264	16.3	409	US-09-825-294-212	Sequence 212, App
13	156	10.3	201	US-09-867-701-4240	Sequence 4240, App
14	154	9.5	390	US-09-867-701-8894	Sequence 8894, App
15	146	9.0	480	US-09-825-294-1532	Sequence 1532, App
16	125	7.7	381	US-09-825-294-213	Sequence 213, App
17	120	7.4	430	US-09-867-701-7826	Sequence 7826, App
18	112	6.9	558	US-09-867-701-4251	Sequence 4251, App
19	27	1.7	1368	US-09-834-975-825	Sequence 2375, App

C 20	25	1.5	152	10	US-09-960-352-9079	Sequence 9079, App
C 21	25	1.5	363	10	US-09-867-701-4911	Sequence 4911, App
C 22	25	1.5	395	10	US-09-867-701-5174	Sequence 5174, App
C 23	25	1.5	568	10	US-09-919-580-143	Sequence 143, App
C 24	25	1.5	2968	10	US-09-925-301-584	Sequence 584, App
C 25	24	1.5	208	10	US-09-770-696-104	Sequence 104, App
C 26	24	1.5	258	10	US-09-920-300A-58	Sequence 58, App1
C 27	24	1.5	258	10	US-09-920-300A-58	Sequence 58, App1
C 28	24	1.5	258	10	US-09-920-300A-58	Sequence 58, App1
C 29	24	1.5	419	10	US-09-924-035A-439	Sequence 315, App
C 30	24	1.5	766	12	US-10-062-254-125	Sequence 439, App
C 31	24	1.5	871	10	US-09-925-300-627	Sequence 125, App
C 32	24	1.5	939	12	US-10-078-923-89	Sequence 627, App
C 33	24	1.5	1029	10	US-09-925-300-384	Sequence 89, App1
C 34	24	1.5	1046	10	US-09-800-528-5	Sequence 89, App1
C 35	24	1.5	1066	10	US-09-764-870-15	Sequence 5, App11
C 36	24	1.5	1190	10	US-09-410-194-14	Sequence 15, App1
C 37	24	1.5	1337	9	US-09-992-598-286	Sequence 14, App1
C 38	24	1.5	1337	10	US-09-989-722-286	Sequence 286, App
C 39	24	1.5	1337	10	US-09-989-723-286	Sequence 286, App
C 40	24	1.5	1337	10	US-09-989-723-286	Sequence 286, App
C 41	24	1.5	1337	10	US-09-989-723-286	Sequence 286, App
C 42	24	1.5	1337	10	US-09-989-731-286	Sequence 286, App
C 43	24	1.5	1337	10	US-09-989-731-286	Sequence 286, App
C 44	24	1.5	1337	10	US-09-991-073-286	Sequence 286, App
C 45	24	1.5	1337	10	US-09-990-442-286	Sequence 286, App

ALIGNMENTS

RESULT 1
US-09-825-294-205
Sequence 205, Application US/09825294
Patent No. US2002004491A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.484C5
CURRENT APPLICATION NUMBER: US/09/825,294
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 205
LENGTH: 1619
TYPE: DNA
ORGANISM: Homo sapiens
US-09-825-294-205

Query Match	100.0%	Score 1619;	DB 10;	Length 1619;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1619;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
QY 1	GGCACTTTTGGGATTTGTTCTGCTCCAGGCTTTGGCGTCAATTCAGTGTACCA	60		
DB 1	GGCACTTTTGGGATTTGTTCTGCTCCAGGCTTTGGCGTCAATTCAGTGTACCA	60		
QY 61	GTTGGAAGATTCACAGCTGACAGCTGCTCCCGGAGTTCATTGGAATTCAG	120		
DB 61	GTTGGAAGATTCACAGCTGACAGCTGCTCCCGGAGTTCATTGGAATTCAG	120		
QY 121	GGTGAAGCTTCAAGACATGTGTCAAGAAAGTGTGAGCAAAAGTCCGGATCATGTA	180		
DB 121	GGTGAAGCTTCAAGACATGTGTCAAGAAAGTGTGAGCAAAAGTCCGGATCATGTA	180		
QY 181	CCGCAAGTCTGTGATCATCATGCGCGCTGTCTATGCTTCCGCGGATACAGTCTT	240		
DB 181	CCGCAAGTCTGTGATCATCATGCGCGCTGTCTATGCTTCCGCGGATACAGTCTT	240		

182

CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.

XX
SQ Sequence 51 BP: 9 A; 5 C; 10 G; 27 T; 0 other;

Query Match 1.5%; Score 25; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1393 AACACAGCATGAGACACAGTAAT 1417
|||||
DB 51 AACACAGCATGAGACACAGTAAT 27

Search completed: November 7, 2002, 18:15:59
Job time : 343.774 secs

XX Shinkets RA, Leach M;
 XX WPI: 2001-465210/50.
 DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX
 PS Claim 1: Page 3450; 4143pp; English.
 XX The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 CC
 SQ Sequence 50 BP; 11 A; 16 C; 10 G; 13 T; 0 other;
 XX
 XX
 Query Match 1.6%; Score 26; DB 22; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 933 GACTGGACTTACGCTGGGCTCGGC 958
 ID 50 GACTGGACTTACGCTGGGCTCGGC 25
 Db
 RESULT 42
 AAL33985/c
 ID AAL33985 standard; DNA; 50 BP.
 XX
 AC AAL33985:
 XX
 XX 24-JAN-2002 (first entry)
 DT
 XX
 DE Human SNP oligonucleotide #7193.
 DE
 XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 KW
 XX Homo sapiens.
 OS
 XX W0200147944-A2.
 PN
 XX
 XX 05-JUL-2001.
 PD
 XX 28-DEC-2000; 2000WO-US35498.
 PF
 XX 28-DEC-1999; 99US-0173419.
 PR
 XX 27-DEC-2000; 2000US-0173419.
 PR
 XX (CURA-) CURAGEN CORP.
 PA
 XX Shinkets RA, Leach M;
 XX
 XX

DR WPI: 2001-465210/50.
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX
 PS Claim 1: Page 3451; 4143pp; English.
 XX The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 CC
 SQ Sequence 50 BP; 14 A; 13 C; 17 G; 6 T; 0 other;
 XX
 XX
 Query Match 1.6%; Score 26; DB 22; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1285 GCCGACCATGATCCTCCGAATCTG 1310
 ID 26 GCCGACCATGATCCTCCGAATCTG 1
 Db
 RESULT 43
 AAL33986/c
 ID AAL33986 standard; DNA; 50 BP.
 XX
 AC AAL33986:
 XX
 XX 24-JAN-2002 (first entry)
 DT
 XX
 DE Human SNP oligonucleotide #7194.
 DE
 XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 KW
 XX Homo sapiens.
 OS
 XX W0200147944-A2.
 PN
 XX
 XX 05-JUL-2001.
 PD
 XX 28-DEC-2000; 2000WO-US35498.
 PF
 XX 28-DEC-1999; 99US-0173419.
 PR
 XX 27-DEC-2000; 2000US-0173419.
 PR
 XX (CURA-) CURAGEN CORP.
 PA
 XX Shinkets RA, Leach M;
 XX
 XX WPI: 2001-465210/50.
 DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 XX

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX
XX
PT New oligonucleotide libraries comprising oligonucleotides which
selectively hybridize to mRNAs transcribed from a transcription unit of
a genome, useful for detecting tissue-, pathology-, and
developmental-specific genes
XX
XX
PS Example 1; SEQ ID 14725; 47pp; English.
XX
XX
CC The present invention describes oligonucleotide libraries for detecting
messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
biological sample, in expression profiling studies, in qualitatively or
quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
condition; to detect developmental specific genes; and to detect RNA
transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN72253 to ABN95589 represent
oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 17 A; 17 C; 15 G; 11 T; 0 other;

Query Match
Best Local Similarity 3.7%; Score 60; DB 24; Length 60;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 864 AACCATTCCTGTCAGCAGAAATGGCTGTTGCGCCCTGACTTGGCTTACTGCTCG 923
DB 60 AAACCATTCCTGTCAGCAGAAATGGCTGTTGCGCCCTGACTTGGCTTACTGCTCG 1
|||||
AC AAS60824;
XX
XX
DT 29-JAN-2002 (first entry)
XX
DE Human cancer agent-sensitive marker #326.
XX
XX
KW Human: cancer cell marker; TAXOL; cytoskeletal; tumour; carcinoma;
KW squamous cell carcinoma; sarcoma; fibrosarcoma; leukemia;
KW lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
KW Hodgkin's disease; glioma; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200179556-A2.
XX
XX
PD 25-OCT-2001.
XX
XX
PF 13-APR-2001; 2001WO-US12132.
XX
XX
PR 14-APR-2000; 2000US-197538P.
XX
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX
XX
PI Lillie J, Brown JL, Bolt A, Van Huffel C;
XX WPI; 2001-602933/68.
XX
XX
PT Novel nucleic acid, used as a marker to determine the effectiveness of
using TAXOL to treat cancer cell growth in individuals -
XX
XX
PS Claim 1; Page 339-340; 527pp; English.
XX
XX
CC The invention relates to 1046 novel nucleic acids which are used as
markers for determining the sensitivity of a cancer cell to the
CC anticancer agent TAXOL. Cancer cells can be treated with TAXOL when
CC they are shown to express one of the 242 sensitivity markers or the
CC cells are shown not to express one of the 804 resistance markers.
CC The methods can be used to determine the effectiveness of TAXOL
in the treatment of cancer cell growth in an individual. The markers
CC can be used as targets in developing anti-cancer agents such as
chemotherapeutic compounds. The markers can also be used as targets in
CC developing treatments for cancer, particularly those cancers which
display resistance to agents and exhibit expression of the markers. The
CC anticancer agents developed by the novel method can be used to treat
cancer. Probes based on the markers can be used to detect transcripts or
CC genomic sequences corresponding to the markers, in the identification of
cells or tissues which mis-express the protein. Cancers which may
CC be targeted include carcinoma (e.g. squamous cell carcinoma),
CC sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic leukaemia),
CC lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's disease and
CC tumours (e.g. glioma). The present sequence is one of the 1046
novel cancer cell markers.
XX
SQ Sequence 1368 BP; 517 A; 312 C; 321 G; 213 T; 5 other;

Query Match
Best Local Similarity 1.7%; Score 27; DB 22; Length 1368;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1593 ACACTGTAAATAAAAAAAAAAAAAA 1619
DB 459 ACACTGTAAATAAAAAAAAAAAAAA 485
|||||
AC AAL33984/C
ID AAL33984 standard; DNA; 50 BP.
XX
XX
AC AAL33984;
XX
XX
DT 24-JAN-2002 (first entry)
XX
XX
DE Human SNP oligonucleotide #7192.
XX
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytoskeletal;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200147944-A2.
XX
XX
PD 05-JUL-2001.
XX
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
XX
PR 28-DEC-1999; 99US-0173419.
XX
XX
PR 27-DEC-2000; 2000US-0173419.
XX
XX
PA (CURA-) CURAGEN CORP.

Algate PA, Harlocker SL, Jones R;
 WPI: 2002-122075/16.
 Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide

Claim 1; SEQ ID 4251; 489pp; English.

The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumor polypeptide encoded by a polynucleotide (III) having a CDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II), (II) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumor protein comprising contacting T cells with (III) or (II). (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumor polypeptides and proteins in tumor cells; and to isolate a full length gene from a suitable library e.g., a tumor CDNA library using well known techniques.

Sequence 430 BP: 92 A; 121 C; 108 G; 109 T; 0 other;

Query Match 7.4%; Score 120; DB 24; Length 430;
 Best Local Similarity 100.0%; Pred. NO. 1.4e-38;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 431 CTGATGTTCTTCCAGCCGCGCCCAACCCCAACCTCCCTGAGTATTTCTG 490
 Db 182 CTGATGTTCTTCCAGCCGCGCCCAACCCCAACCTCCCTGAGTATTTCTG 241
 Oy 491 GGTGCTCTTTATCTGGTAGGAGCGGAGTCCGTTCTCTTTCTGTCGCAAA 550
 Db 242 GGTGCTCTTTATCTGGTAGGAGCGGAGTCCGTTCTCTTTCTGTCGCAAA 301

RESULT 38

ABL79397 standard; CDNA: 558 BP.

ABL79397;

17-MAY-2002 (first entry)

Human ovarian cancer related CDNA clone SEQ ID NO:2375.

Human; ovarian cancer; ovarian tumor; cytostatic; gene; ss.

Homo sapiens.

WO200192581-A2.

06-DEC-2001.

29-MAY-2001; 2001WO-US17756.

26-MAY-2000; 2000US-207484P.

(CORI-) CORIXA CORP.

Algate PA, Harlocker SL, Jones R;

WPI: 2002-122075/16.

Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide

Claim 1; SEQ ID 2375; 489pp; English.

The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumor polypeptide encoded by a polynucleotide (III) having a CDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II), (II) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumor protein comprising contacting T cells with (III) or (II). (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumor polypeptides and proteins in tumor cells; and to isolate a full length gene from a suitable library e.g., a tumor CDNA library using well known techniques.

Sequence 558 BP: 147 A; 133 C; 166 G; 106 T; 6 other;

Query Match 6.9%; Score 112; DB 24; Length 558;
 Best Local Similarity 100.0%; Pred. NO. 2.2e-35;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1138 TGCACGAACACCCCGCAACCTCGGAGACACCGTACAGAGCGGTTGATGACC 1197
 Db 142 TGCACGAACACCCCGCAACCTCGGAGACACCGTACAGAGCGGTTGATGACC 201
 Oy 1198 GAGCTGAGTGAAGAAAGTCTCCGAGAGGAGGAGGATCATGTAGCCCC 1249
 Db 202 GAGCTGAGTGAAGAAAGTCTCCGAGAGGAGGAGGATCATGTAGCCCC 253

RESULT 39

ABN41977/C standard; DNA: 60 BP.

ABN41977;

15-JUL-2002 (first entry)

Human spliced transcript detection oligonucleotide SEQ ID NO:14725.

Human; mouse; rat; splice transcript; detection; RNA transcript;

splice variant; transcriptome; oligonucleotide library; ss.

Homo sapiens.

WO200210449-A2.

07-FEB-2002.

20-JUL-2001; 2001WO-1B01903.

28-JUL-2000; 2000US-221607P.

02-MAY-2001; 2001US-287724P.

(COMP-) COMPUGEN INC.

XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
PT prevention and/or treatment of cancer, especially ovarian cancer.
XX
XX
PS Claim 1a; Page 127; 131pp; English.

CC The invention relates to ovarian tumour polynucleotides and polypeptides
CC that may be utilised in cancer therapy, for example in a vaccine or
CC gene therapy. Polypeptides and polynucleotides of the invention are
CC useful for detecting a cancer in a patient, for stimulating and/or
CC expanding T-cells specific for a tumour protein, and for inhibiting the
CC development of a cancer in a patient. They are also useful for
CC stimulating an immune response in a patient, and for treating a cancer in
CC a patient and for determining the presence of a cancer in a patient.
CC The isolated polynucleotides of the invention are useful for their
CC ability to selectively form duplex molecules with complementary stretches
CC of the entire desired gene or gene fragments, and for designing and
CC preparing ribozyme molecules for inhibiting expression of tumour
CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
CC invention are also useful in recombinant DNA molecules to direct
CC expression of a polypeptide in appropriate host cells. The current
CC sequence represents the ovarian carcinoma BE336607 nucleotide sequence.

XX
SQ Sequence 480 BP; 86 A; 154 C; 153 G; 87 T; 0 other;

Query Match 9.0%; Score 146; DB 24; Length 480;
Best Local Similarity 99.5%; Pred. No. 5e-49;
Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCACATTTTGGGATGTTCTGCTTCCAGGCTTGGCGCAAAATCCAGTGTACCA 60
DB 280 GGCACATTTTGGGATGTTCTGCTTCCAGGCTTGGCGCAAAATCCAGTGTACCA 339

QY 61 GTGTGAAGATTCACGCTGACGACGCTCTCCGCCGATTCATTTGAAATTGCAC 120
DB 340 GTGTGAAGATTCACGCTGACGACGCTCTCCGCCGATTCATTTGAAATTGCAC 399

QY 121 GGTGAAGCTTCAAGACATGTCAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 180
DB 400 GGTGAAGCTTCAAGACATGTCAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 459

QY 181 CCGCAAGTCTGTGCAT 197
DB 460 CCGCAAGTCTGTGCAT 476

RESULT 36
ABL84848
ID ABL84848 standard; cDNA: 381 BP.

AC ABL84848;
XX
DT 17-MAY-2002 (first entry)
XX
DE Human ovarian cancer related cDNA clone SEQ ID NO:7826.
XX
KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200192581-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US17756.
XX
PR 26-MAY-2000; 2000US-207484P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algatec PA, Harlocker SL, Jones R.
XX
DR WPI; 2002-122075/16.

XX Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing
PT polypeptide.

XX
PS Claim 1; SEQ ID 7826; 489pp; English.

CC The present invention describes a composition (I) comprising: carriers
CC and immunostimulants; and a polypeptide (II) of a ovarian tumor
CC and lymphoma encoded by a polynucleotide (III) having a cDNA sequence
CC (SI) from the 10912 nucleotide sequences as given in ABL77023 to
CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
CC population of (II), or antigen presenting cells that express (II).
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridizes to
CC (SI) can be used for detecting ovarian cancer in a patient's biological
CC sample preferably serum or ovarian tissue. The method comprises
CC contacting a biological sample from a patient with (IV), detecting the
CC amount of polynucleotide hybridizing to (IV) and comparing the amount to
CC a predetermined cutoff value and thereby detecting ovarian cancer in the
CC patient, where the amount of polynucleotide hybridizing to (IV) is
CC detected preferably by polymerase chain reaction (PCR). (I) comprising
CC (III) and/or (II) is useful for stimulating and/or expanding T cells
CC specific for an ovarian tumor protein comprising contacting T cells
CC with (III) or (II). (III) is useful in design and preparation of
CC ribozyme molecules for inhibiting expression of the tumour polypeptides
CC and proteins in tumour cells; and to isolate a full length gene from a
CC suitable library e.g., a tumour cDNA library using well known
CC techniques.

XX
SQ Sequence 381 BP; 85 A; 101 C; 122 G; 73 T; 0 other;

Query Match 7.7%; Score 125; DB 24; Length 381;
Best Local Similarity 100.0%; Pred. No. 1.4e-40;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 959 CTCGCTCTGAAAAGTCTTAAGAAATCTTCTCACTTCTCTTCAGAGACGTGGCGCG 1018
DB 116 CTCGCTCTGAAAAGTCTTAAGAAATCTTCTCTCACTTCTCTTCAGAGACGTGGCGCG 175

QY 1019 GGACGGGAAGACCAAGGGCGCTGCACAAAGCGGGCGCTGCGGTGGAGTGGCGCATG 1078
DB 176 GGACGGGAAGACCAAGGGCGCTGCACAAAGCGGGCGCTGCGGTGGAGTGGCGCATG 235

QY 1079 TACGC 1083
DB 236 TACGC 240

RESULT 37
ABL81273
ID ABL81273 standard; cDNA: 430 BP.

AC ABL81273;
XX
DT 17-MAY-2002 (first entry)
XX
DE Human ovarian cancer related cDNA clone SEQ ID NO:4251.
XX
KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200192581-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US17756.
XX
PR 26-MAY-2000; 2000US-207484P.
XX
PA (CORI-) CORIXA CORP.
XX

PT polypeptide -
 XX
 PS Claim 1: SEQ ID 1532; 489pp; English.
 CC The present invention describes a composition (I) comprising: carriers
 CC and immunostimulants; and a polynucleotide (II) of an ovarian tumor
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
 CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
 CC population of (II), or antigen presenting cells that express (II).
 CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridizes to
 CC (S1) can be used for detecting ovarian cancer in a patient's biological
 CC sample preferably serum or ovarian tissue. The method comprises
 CC contacting a biological sample from a patient with (IV), detecting the
 CC amount of polynucleotide hybridizing to (IV) and comparing the amount to
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the
 CC patient, where the amount of polynucleotide hybridizing to (IV) is
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells
 CC specific for an ovarian tumor protein comprising contacting T cells
 CC with (III) or (II). (III) is useful in design and preparation of
 CC ribozyme molecules for inhibiting expression of the tumor polypeptides
 CC and proteins in tumor cells; and to isolate a full length gene from a
 CC suitable library e.g., a tumor cDNA library using well known
 CC techniques.
 XX
 SQ Sequence 390 BP; 121 A; 82 C; 99 G; 86 T; 2 other:
 Query Match 9.5%; Score 154; DB 24; Length 390;
 Best Local Similarity 100.0%; Pred. No. 3.1e-52;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1358 AGACACGACGAGGAGGAGACAGAGAAAGAAACACAGATGAGACAGTAAT 1417
 Db 147 AGACACGACGAGGAGGAGACAGAGAAAGAAACACAGATGAGACAGTAAT 206
 QY 1418 GAATTAACCATTAATATTAGCCCTCTGTCTGTCTTACTGSCAGGAATGTGAC 1477
 Db 207 GAATTAACCATTAATATTAGCCCTCTGTCTGTCTTACTGSCAGGAATGTGAC 266
 QY 1478 CAATTTTCACTGTGACCTTGACAGCTTCTTT 1511
 Db 267 CAATTTTCACTGTGACCTTGACAGCTTCTTT 300
 RESULT 34
 ABL03283
 ID ABL03283 standard; cDNA; 480 BP.
 XX
 AC ABL03283;
 XX
 DT 05-SEP-2002 (first entry)
 XX
 DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 213.
 XX
 KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
 KW cystostatic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200239885-A2.
 XX
 PD 23-MAY-2002.
 XX
 PF 13-NOV-2001; 2001WO-US45395.
 XX
 PR 14-NOV-2000; 2000US-0713550.
 PR 03-APR-2001; 2001US-0825294.
 PR 02-OCT-2001; 2001US-0970966.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

XX
 DR WPI: 2002-500186/53.
 XX
 PT Novel ovarian cancer polypeptide and polynucleotide, useful for
 PT detecting the presence of ovarian cancer in a patient, and in
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
 PT
 PS Claim 2: Page 196; 197pp; English.
 CC The present invention provides human ovarian cancer associated proteins
 CC and coding sequences. The sequences can be used in the diagnosis and
 CC treatment of ovarian cancers. The present sequence is a coding sequence
 CC of the invention.
 XX
 SQ Sequence 480 BP; 86 A; 154 C; 153 G; 87 T; 0 other:
 Query Match 9.0%; Score 146; DB 24; Length 480;
 Best Local Similarity 99.5%; Pred. No. 5e-49;
 Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGCACATTTTGGGATGTTCTTCTTCAGCTTTCGCTGCAATTCAGTCTACCA 60
 Db 280 GGCACATTTTGGGATGTTCTTCTTCAGCTTTCGCTGCAATTCAGTCTACCA 339
 QY 61 GTGTGAAGAAATTCACGCTGACACGACTGCTCCGCCGAGTTGATGATGAC 120
 Db 340 GTGTGAAGAAATTCACGCTGACACGACTGCTCCGCCGAGTTGATGATGAC 399
 QY 121 GGTGACGCTTCAGACATGTCGTCAGAAAGAGTGGAGCAAGTGGCGGATCATGTA 180
 Db 400 GGTGACGCTTCAGACATGTCGTCAGAAAGAGTGGAGCAAGTGGCGGATCATGTA 459
 QY 181 CCGCAAGTCTCTGCAT 197
 Db 460 CCGCAAGTCTCTGCAT 476
 RESULT 35
 ABL40351
 ID ABL40351 standard; cDNA; 480 BP.
 XX
 AC ABL40351;
 XX
 DT 28-JUN-2002 (first entry)
 XX
 DE Ovarian carcinoma BE33607 nucleotide sequence.
 XX
 KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumor; cancer;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002004491-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 03-APR-2001; 2001US-0825294.
 XX
 PR 10-SEP-1999; 99US-0394374.
 PR 01-MAY-2000; 2000US-0561778.
 PR 15-AUG-2000; 2000US-0640173.
 PR 07-SEP-2000; 2000US-0656668.
 PR 14-NOV-2000; 2000US-0713550.
 XX
 PA (XUJ/) XU J.
 PA (STOL/) STOLK J A.
 PA (ALGA/) ALGATE P A.
 PA (FLIN/) FLING S P.
 XX
 PI Xu J, Stolk JA, Algate PA, Fling SP;
 DR WPI: 2002-171027/22.

CC presence of similar nucleic acid sequences in samples. They may also be
CC used to study the expression and function of secretory proteins/membrane
CC polypeptides and their role in metabolism. The polypeptides may be used
CC as antigens in the production of antibodies against them and in assays to
CC identify modulators (agonists and antagonists) of expression and
CC activity. The antibodies and antagonists may also be used as therapeutic
CC agents to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbent assay
CC (ELISA). Examples of diseases which may be treated include rheumatoid
CC arthritis and diabetes.

CC
XX Sequence 591 BP; 108 A; 198 C; 173 G; 109 T; 3 other;

Query Match 15.4%; Score 250; DB 22; Length 591;
Best Local Similarity 100.0%; Pred. No. 8e-91;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGGATTTGTTCTTCACAGCTTTGGCTGCAATTCAGTGTACCA 60

DB 294 GGCACCTTTTGGGATTTGTTCTTCACAGCTTTGGCTGCAATTCAGTGTACCA 353

QY 61 GTGTGAAGATTCACAGTGAACAGACAGTCTCCCGGATTCATTTGAATTCAC 120

DB 354 GTGTGAAGATTCACAGTGAACAGACAGTCTCCCGGATTCATTTGAATTCAC 413

QY 121 GGTGAAGTTCACAGATGTGTGAGAAAGATGAGCAAAAGTCCCGGATTCATGTA 180

DB 414 GGTGAAGTTCACAGATGTGTGAGAAAGATGAGCAAAAGTCCCGGATTCATGTA 473

QY 181 CCGCAAGTCTGTGATATCAGAGGCGCTGTCTATCCCTCTGCGGGATCCAGTCTT 240

DB 474 CCGCAAGTCTGTGATATCAGAGGCGCTGTCTATCCCTCTGCGGGATCCAGTCTT 533

QY 241 CTGCTCCCA 250

DB 534 CTGCTCCCA 543

DB

RESULT 32
ABL85916/C

ID ABL85916 standard; cDNA; 201 BP.

XX ABL85916;

DT 17-MAY-2002 (first entry)

DE Human ovarian cancer related cDNA clone SEQ ID NO:8894.

KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

OS Homo sapiens.

PN WO200192581-A2.

PD 06-DEC-2001.

PF 29-MAY-2001; 2001WO-US17756.

PR 26-MAY-2000; 2000US-207484P.

PA (CORI-) CORIXA CORP.

PI Algate PA, Harlocker SL, Jones R;

DR WPI; 2002-122075/16.

XX Composition for therapy and diagnosis of ovarian cancer comprising

PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding

PT polypeptide, antibody specific to polypeptide or T cell expressing

PT
XX
PS Claim 1; SEQ ID 8894; 489bp; English.

XX The present invention describes a composition (I) comprising: carriers
CC and immunostimulants; and a polypeptide (II) having a cDNA sequence
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to
CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
CC population of (II), or antigen presenting cells that express (II).
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC (S1) can be used for detecting ovarian cancer in a patient's biological
CC sample preferably serum or ovarian tissue. The method comprises
CC contacting a biological sample from a patient with (IV), detecting the
CC amount of polynucleotide hybridising to (IV) and comparing the amount to
CC a predetermined cutoff value and thereby detecting ovarian cancer in the
CC patient, where the amount of polynucleotide hybridising to (IV) is
CC detected preferably by polymerase chain reaction (PCR). (I) comprising
CC (III) and/or (II) is useful for stimulating and/or expanding T cells
CC specific for an ovarian tumour protein comprising contacting T cells
CC with (III) or (II). (III) is useful in design and preparation of
CC ribozyme molecules for inhibiting expression of the tumour polypeptides
CC and proteins in tumour cells; and to isolate a full length gene from a
CC suitable library e.g., a tumour cDNA library using well known
CC techniques.

CC
XX Sequence 201 BP; 28 A; 61 C; 46 G; 66 T; 0 other;

Query Match 10.3%; Score 166; DB 24; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.2e-57;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1223 AGAAGGGAGAGAGATCATGTACGCCGGAAGTACCTGTCAGTGTGCTGGTT 1282

DB 181 AGAAGGGAGAGAGATCATGTACGCCGGAAGTACCTGTCAGTGTGCTGGTT 122

QY 1283 TGGCCGAGCCATGATCTCCGATCTGTTGGATTCAGCATAGGCCAATGTCACAA 1342

DB 121 TGGCCGAGCCATGATCTCCGATCTGTTGGATTCAGCATAGGCCAATGTCACAA 62

QY 1343 CAATCAGCCCTGGGCGACACGACGAGGAGGAGACAGAGAAAA 1388

DB 61 CAATCAGCCCTGGGCGACACGACGAGGAGGAGAGAGAAAA 16

DB

RESULT 33
ABL78554

ID ABL78554 standard; cDNA; 390 BP.

XX ABL78554;

DT 17-MAY-2002 (first entry)

DE Human ovarian cancer related cDNA clone SEQ ID NO:1532.

KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

OS Homo sapiens.

PN WO200192581-A2.

PD 06-DEC-2001.

PF 29-MAY-2001; 2001WO-US17756.

PR 26-MAY-2000; 2000US-207484P.

PA (CORI-) CORIXA CORP.

PI Algate PA, Harlocker SL, Jones R;

DR WPI; 2002-122075/16.

XX Composition for therapy and diagnosis of ovarian cancer comprising

PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding

PT polypeptide, antibody specific to polypeptide or T cell expressing

QY 211 TCTCATGCGCTCTGCGGGGTACCACTCTTGTCTCCCGAGGAAACTGAATCAGTTTG 270
 |||
 DB 438 TCTCATGCGCTCTGCGGGGTACCACTCTTGTCTCCCGAGGAAACTGAATCAGTTTG 497
 QY 271 CATCAGCTCTGCAACACCCCTCTTTGTAAC 301
 |||
 DB 498 CATCAGCTCTGCAACACCCCTCTTTGTAAC 528

RESULT 30

ABL81262/c
 ID ABL81262 standard; cDNA; 409 BP.

AC ABL81262;

XX 17-MAY-2002 (first entry)

DE Human ovarian cancer related cDNA clone SEQ ID NO:4240.

XX Human: ovarian cancer; ovarian tumour; cytostatic; gene; ss.

XX Homo sapiens.

PN HQ200192581-A2.

XX 06-DEC-2001.

PF 29-MAY-2001; 2001MO-US17756.

PR 26-MAY-2000; 2000US-207484P.

XX (CORI-) CORIYA CORP.

PI Algate PA, Harlocker SL, Jones R;

DR WPI; 2002-122075/16.

PT Composition for therapy and diagnosis of ovarian cancer comprising
 polyprotein of a ovarian tumor polyprotein, polynucleotide encoding
 PT polyprotein, antibody specific to polyprotein or T cell expressing
 PT polyprotein

PS Claim 1; SEQ ID 4240; 489pp; English.

CC The present invention describes a composition (I) comprising: carriers
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
 CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
 CC population of (II), or antigen presenting cells that express (II).
 CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
 CC (S1) can be used for detecting ovarian cancer in a patient's biological
 CC sample preferably serum or ovarian tissue. The method comprises
 CC contacting a biological sample from a patient with (IV), detecting the
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the
 CC patient, where the amount of polynucleotide hybridising to (IV) is
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells
 CC specific for an ovarian tumour protein comprising contacting T cells
 CC with (III) or (II). (III) is useful in design and preparation of
 CC ribozyme molecules for inhibiting expression of the tumour polypeptides
 CC and proteins in tumour cells; and to isolate a full length gene from a
 CC suitable library e.g., a tumour cDNA library using well known
 CC techniques.

XX Sequence 409 BP; 89 A; 106 C; 87 G; 127 T; 0 other;

XX Query Match 16.3%; Score 264; DB 24; Length 409;

XX Best Local Similarity 99.7%; Pred. NO. 2e-96;

XX Matches 314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1285 GCCGACGACATATCTCTCGAATCTGTTGGCATCCAGCATACGCGCAATGTCACAAACA 1344

DB |||
 DB 315 GCCGACGACATATCTCTCGAATCTGTTGGCATCCAGCATACGCGCAATGTCACAAACA 256
 QY 1345 ATCAGCCCTGGGCGACACACGACGAGGAGGAGACACAGAAAAAACAACACATGA 1404
 |||
 DB 255 ATCAGCCCTGGGCGACACACGACGAGGAGGAGACACAGAAAAAACAACACATGA 196
 QY 1405 GAACACAGTAATGAATAAACCATTAATATTAGCCCTCTGTTGCTTACTGCGC 1464
 |||
 DB 195 GAACACAGTAATGAATTAATTAACCATTAATATTAGCCCTCTGTTGCTTACTGCGC 136
 QY 1465 CAGGAATGTTACCAATTTTTCAGTTGAGCTTGACAGCTTCTTTGCGCAACGACAGA 1524
 |||
 DB 135 CAGGAATGTTACCAATTTTTCAGTTGAGCTTGACAGCTTCTTTGCGCAACGACAGA 76
 QY 1525 GAGAAATTTAACACTGTTTCAAAACCGGGGAGTGGCTGTGTTAAGAAAGACCATTA 1584
 |||
 DB 75 GAGAAATTTAACACTGTTTCAAAACCGGGGAGTGGCTGTGTTAAGAAAGACCATTA 16
 QY 1585 TGCTTTAGACAGTGT 1599
 |||
 DB 15 TGCTTTAGACAGTGT 1

RESULT 31

AAF94044
 ID AAF94044 standard; DNA; 591 BP.

AC AAF94044;

DT 23-MAY-2001 (first entry)

XX Primer specific for DNA encoding secretory/membrane protein SEQ ID 478.

XX Human; secretory protein; membrane protein; vaccine; gene therapy;
 XX rheumatoid arthritis; diabetes; PCR primer; ss.

XX Synthetic.

XX EP1067182-A2.

XX 10-JAN-2001.

XX 07-JUL-2000; 2000EP-0114090.

XX 08-JUL-1999; 99JP-0194179.

XX 11-JAN-2000; 2000JP-0118775.

XX 02-MAY-2000; 2000JP-0183766.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

XX WPI; 2001-093989/11.

PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
 PT gene therapy or as candidate target molecules in drug development -

PS Claim 4; SEQ ID 478; 609pp + CD ROM; English.

CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by
 CC AAB88317 - AAB88419. Included in the invention are primers
 CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
 CC cDNA sequences of the invention. The invention also includes methods for
 CC the production of antibodies directed against the proteins, and cDNA
 CC sequences, which can be used in vaccines. The polynucleotide sequences
 CC can be used in gene therapy. The polynucleotide sequences and the
 CC proteins they encode may be used in the prevention, treatment and
 CC diagnosis of diseases associated with inappropriate secretory
 CC protein/membrane protein expression. The nucleic acids and complementary
 CC sequences may also be used as DNA probes in diagnostic assays
 CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the

XX
DR WPI; 2002-171027/22

aa Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
 pt prevention and/or treatment of cancer, especially ovarian cancer
 pt
 xx
 ps Claim 1a; page 41-42; 131pp; English.

XX The invention relates to ovarian tumour polynucleotides and polypeptides
 CC that may be utilised in cancer therapy, for example in a vaccine or
 CC gene therapy. Polypeptides and polynucleotides of the invention are
 CC useful for detecting a cancer in a patient, for stimulating and/or
 CC expanding T-cells specific for a tumour protein, and for inhibiting the
 CC development of a cancer in a patient. They are also useful for
 CC stimulating an immune response in a patient, and for treating a cancer in
 CC a patient and for determining the presence of a cancer in a patient.
 CC The isolated polynucleotides of the invention are useful for their
 CC ability to selectively form duplex molecules with complementary stretches
 CC of the entire desired gene or gene fragments, and for designing and
 CC preparing ribozyme molecules for inhibiting expression of tumour
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
 CC invention are also useful in recombinant DNA molecules to direct
 CC expression of a polypeptide in appropriate host cells. The sequences
 CC given in records ABL48760-ABL48956 represent polynucleotides encoding
 CC ovarian carcinoma proteins.
 XX Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other;

Query Match	19.1%	Score 310;	DB 24;	Length 396;
Best Local Similarity	-100.0%;	Pred. No. 6.7e-115;		
Matches 310; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	GGCACTTTTTCGGGATTTGTTCTTGCTTCCAGGCTTTGGCGGTGAATTCAGTGTACCA	60
Db	11	GGCACTTTTTCGGGATTTGTTCTTGCTTCCAGGCTTTGGCGGTGAATTCAGTGTACCA	70
Qy	61	GTGTGAAGATTTCCACGTGAAACAGACTGCTCTCCCCGAGTTCAATTTGAAATTTGAC	120
Db	71	GTGTGAAGATTTCCACGTGAAACAGACTGCTCTCCCCGAGTTCAATTTGAAATTTGAC	130
Qy	121	GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA	180
Db	131	GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA	190
Qy	181	CGGCAAGTCTCTGCATATATCAGCGGCGCTGTCTCATTCGCCCTCTGCGGGATACAGATCCTT	240
Db	191	CGGCAAGTCTCTGCATATATCAGCGGCGCTGTCTCATTCGCCCTCTGCGGGATACAGATCCTT	250
Qy	241	CTGCTCTCCAGGGAAATGAATCTAGTTTGCATCAGCTGTGTGCAACAACCCCTCTTTTAA	300
Db	251	CTGCTCTCCAGGGAAATGAATCTAGTTTGCATCAGCTGTGTGCAACAACCCCTCTTTTAA	310
Qy	301	CGGGCCAAAG 310	
Db	311	CGGGCCAAAG 320	

RESULT 27	
ABL79431/C	
ID	ABL79431 standard; CDNA; 349 BP.
XX	
AC	ABL79431;
XX	
DT	17-MAY-2002 (first entry)
XX	
DE	Human ovarian cancer related cDNA clone SEQ ID NO:2409.
XX	
KW	Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss
XX	
OS	Homo sapiens.
XX	
PN	W0200192581-A2.
XX	

PD 06-DEC-2001.

PF 29-MAY-2001; 2001WO-US17756

PR 26-MAY-2000; 2000US-207484P

PA (CORI-) CORIXA CORP.

PI Algate PA, Harlocker SL, Jones R;

DR WPI; 2002-122075/16

<p> Composition for therapy and diagnosis of ovarian cancer comprising PR polypeptide of a ovarian tumor polypeptide, polynucleotide encoding PR polypeptide, antibody specific to polypeptide or T cell expressing PR polypeptide - </p>	
--	--

PS Claim 1; SEQ ID 2409; 489pp; English.

The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) having a cDNA sequence polypeptide encoded by a polynucleotide (III) having a cDNA sequence (SI) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II), (I) has cytotoxic activity. An oligonucleotide (IV) that hybridizes to (SI) can be used for detecting ovarian cancer in a patient's biological sample, preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridizing to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridizing to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (II) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (II). (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour cDNA library using well known techniques.

Sequence 349 BP; 79 A; 84 C; 78 G; 108 T; 0 other;

Query Match	19.0%	Score 307	DB 24	Length 349
Best Local Similarity	100.0%	Pred. NO.	1.1e-113	
Matches 307: Conservative	0	Mismatches	0	Indels 0
				Gaps 0

Qy	1292	CCGATGCTCTCCGATCTGTTGGGATCCAGCATATAGGGCATGTGCATCAAAATCACGC	1351
Db	310	CCATGATCTCTCCGATCTGTTGGGATCTCCAGCATATAGGGCATGTGCATCAAAATCACGC	251
Qy	1352	CTGGCGACACACGACGAGGAGGAGAGACAGAAAAAGAAAAACACAGCATGTGAAACACA	1411
Db	250	CTGGCGACAGACAGACGAGGAGGAGAGACAGAAAAAGAAAAACACAGCATGTGAAACACA	191
Qy	1412	GTTAAATGAATTAACCATTAATATTATTAGCCCTCTGTCTGTGCTTACTGTGGCCAGANA	1471
Db	190	GTTAAATGAATTAACCATTAATATTATTAGCCCTCTGTCTGTGCTTACTGTGGCCAGANA	131
Qy	1472	TGGTACCAATTTTTCAGTGTGTGGACTTCACAGCTTTCTTTTGGCCACAAGCAAGAGAAATT	1531
Db	130	TGGTACCAATTTTTCAGTGTGTGGACTTCACAGCTTTCTTTTGGCCACAAGCAAGAGAAATT	71
Qy	1532	TAAACAGTTTCAAAACCCGGGGAGTTGGCTGTGTAAAGAAAGACCATTAAATGCTTTA	1591
Db	70	TAAACAGTTTCAAAACCCGGGGAGTTGGCTGTGTAAAGAAAGACCATTAAATGCTTTA	11
Qy	1592	GACAGTGTG 1598	
Db	10	GACAGTGTG 4	

RESULT 28

PS Claim 5: Page 119, 189pp; English.

XX
CC The present invention provides a number of coding sequences and proteins,
CC the over-expression of which is associated with ovarian carcinoma/cancer.
CC These can be used in the diagnosis, treatment and prevention of ovarian
CC cancer, optionally by gene therapy or in the form of a vaccine. The
CC present sequence is an example of one of these sequences.

XX
SQ Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other;

Query Match 19.1%; Score 310; DB 22; Length 396;
Best Local Similarity 100.0%; Pred. No. 6,7e-115;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACTTTTTCGGATTTCTTCTTCAGAGCTTTCGGTCAAAATCCAGTGTACCA 60
DB 11 GGCACTTTTTCGGATTTCTTCTTCAGAGCTTTCGGTCAAAATCCAGTGTACCA 70
QY 61 GTGTGAAGAAATTCAGCTGACACGACTGCTCTCCCGAGTTCAATGTGAATTGCAC 120
DB 71 GTGTGAAGAAATTCAGCTGACACGACTGCTCTCCCGAGTTCAATGTGAATTGCAC 130
QY 121 GGTGAAGCTTCAAGCATGTGTCAAGAAAGTGTGAGCAAGTCCGGGATCATGTA 180
DB 131 GGTGAAGCTTCAAGCATGTGTCAAGAAAGTGTGAGCAAGTCCGGGATCATGTA 190
QY 181 CCGCAAGTCTGTGTCATCATCAGCGGCTGTCTCATGCGCTCTGCGGGATCACAGTCTT 240
DB 191 CCGCAAGTCTGTGTCATCATCAGCGGCTGTCTCATGCGCTCTGCGGGATCACAGTCTT 250
QY 241 CTGCTCCCGAGGAAACGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 251 CTGCTCCCGAGGAAACGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 310
QY 301 CGGGCCCAAG 310
DB 311 CGGGCCCAAG 320

RESULT 25

ABT03085

ID ABT03085 standard; cDNA; 396 BP.

AC ABT03085;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 9.

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
KW cytosolic; gene; ss.

OS Homo sapiens.

PN WO200239885-A2.

PD 23-MAY-2002.

PF 13-NOV-2001; 2001MO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

DR MPI; 2002-500186/53.

PT Novel ovarian cancer polypeptide and polynucleotide, useful for
PT detecting the presence of ovarian cancer in a patient, and in
PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

PT
XX
XX Example 1; Page 116, 197pp; English.

XX
CC The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention.

XX
SQ Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other;

Query Match 19.1%; Score 310; DB 24; Length 396;
Best Local Similarity 100.0%; Pred. No. 6,7e-115;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACTTTTTCGGATTTCTTCTTCAGAGCTTTCGGTCAAAATCCAGTGTACCA 60
DB 11 GGCACTTTTTCGGATTTCTTCTTCAGAGCTTTCGGTCAAAATCCAGTGTACCA 70
QY 61 GTGTGAAGAAATTCAGCTGACACGACTGCTCTCCCGAGTTCAATGTGAATTGCAC 120
DB 71 GTGTGAAGAAATTCAGCTGACACGACTGCTCTCCCGAGTTCAATGTGAATTGCAC 130
QY 121 GGTGAAGCTTCAAGCATGTGTCAAGAAAGTGTGAGCAAGTCCGGGATCATGTA 180
DB 131 GGTGAAGCTTCAAGCATGTGTCAAGAAAGTGTGAGCAAGTCCGGGATCATGTA 190
QY 181 CCGCAAGTCTGTGTCATCATCAGCGGCTGTCTCATGCGCTCTGCGGGATCACAGTCTT 240
DB 191 CCGCAAGTCTGTGTCATCATCAGCGGCTGTCTCATGCGCTCTGCGGGATCACAGTCTT 250
QY 241 CTGCTCCCGAGGAAACGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 251 CTGCTCCCGAGGAAACGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 310
QY 301 CGGGCCCAAG 310
DB 311 CGGGCCCAAG 320

RESULT 26

ABL48768

ID ABL48768 standard; cDNA; 396 BP.

AC ABL48768;

DT 18-JUN-2002 (first entry)

DE Ovarian carcinoma sequence isolate 21920.

KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
KW ss.

OS Homo sapiens.

PN US200204491-A1.

PD 10-JAN-2002.

PF 03-APR-2001; 2001US-0825294.

PR 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.

PR 15-AUG-2000; 2000US-0640173.

PR 07-SEP-2000; 2000US-0656668.

PR 14-NOV-2000; 2000US-0713550.

PA (XUJ/) XU J.
PA (STOL/) STOLK J A.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PI Xu J, Stolk JA, Algate PA, Fling SP;

Db 30 CAGCGTTTCCGCTGCAATCCAGTGTCTACAGTGTGAAGATTTCACGTGACACAGACT 89
 QY 90 GCTCCCTCCCGCAGTTCATTGTGTAATTCACGCTGACGCTTCAGACATGTGTGACAAG 149
 Db 90 GCTCCCTCCCGCAGTTCATTGTGTAATTCACGCTGACGCTTCAGACATGTGTGACAAG 149
 QY 150 AAGTGTGAGCAAGTCCCGGATCATGTACCGCAAGTCTGTGCAATCATCAGCGGCT 209
 Db 150 AAGTGTGAGCAAGTCCCGGATCATGTACCGCAAGTCTGTGCAATCATCAGCGGCT 209
 QY 210 GTCCTATCCGCTCTGCGGATACAGTCTCTGCTCCCGCAGGAACTGAATCAGTTT 269
 Db 210 GTCCTATCCGCTCTGCGGATACAGTCTCTGCTCCCGCAGGAACTGAATCAGTTT 269
 QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTACGGCCCAAGGCCCAAGAAAGGGAAGT 329
 Db 270 GCATCAGCTGTGCAACACCCCTCTTTGTACGGCCCAAGGCCCAAGAAAGGGAAGT 329
 QY 330 CTGCGTGGGCGCTCA 344
 Db 330 CTGCGTGGGCGCTCA 344

RESULT 23

ABL78538/C

ID ABL78538 standard; cDNA: 373 BP.

AC ABL78538;

17-MAY-2002 (first entry)

Human ovarian cancer related cDNA clone SEQ ID NO:1516.

Human ovarian cancer; ovarian tumour; cytostatic; gene; ss.

Human sapiens.

MO200192581-A2.

06-DEC-2001.

29-MAY-2001; 2001MO-US17756.

26-MAY-2000; 2000US-207484P.

(CORI-) CORIXA CORP.

Algate PA, Harlocker SL, Jones R;

WPI: 2002-122075/16.

Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide -

Claim 1; SEQ ID 1516; 489pp; English.

The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells

CC specific for an ovarian tumour protein comprising contacting T cells with (III) or (II). (III) is useful in design and preparation of CC ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a CC suitable library e.g., a tumour cDNA library using well known techniques.

Sequence 373 BP; 83 A; 96 C; 80 G; 114 T; 0 other:

Query Match 19.5%; Score 315; DB 24; Length 373;

Best Local Similarity 100.0%; Pred. No. 6.6e-117; Mismatches 0; Gaps 0;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1285 GCCGAGCCATATCTCCGATCTGTGTGGCAATCCAGATACGCCAATGTCACACA 1344
 Db 315 GCCGAGCCATATCTCCGATCTGTGTGGCAATCCAGATACGCCAATGTCACACA 256
 QY 1345 ATCAGCCCTGGGCGACGACGACGAGGAGAGACAGAGAAAAAGAAACACGCAATGA 1404
 Db 255 ATCAGCCCTGGGCGACGACGACGAGGAGAGACAGAGAAAAAGAAACACGCAATGA 136
 QY 1405 GAGCAGATTAATGAATTAACCATTAATATTTAGCCCTCTGTCTGTCTTACTGCGC 1464
 Db 195 GAGCAGATTAATGAATTAACCATTAATATTTAGCCCTCTGTCTGTCTTACTGCGC 136
 QY 1465 CAGGAATGGTACCAATTTTTCAGTGTGACCTTGACAGCTTCTTTGCCAAGCAAGA 1524
 Db 135 CAGGAATGGTACCAATTTTTCAGTGTGACCTTGACAGCTTCTTTGCCAAGCAAGA 76
 QY 1525 GAGAAATTTAACACTGTTTCAAAACCGGGGAGTGGCTGTGTTAAGAAAGCAATTAA 1584
 Db 75 GAGAAATTTAACACTGTTTCAAAACCGGGGAGTGGCTGTGTTAAGAAAGCAATTAA 16
 QY 1585 TGCTTTAGACAGTGT 1599
 Db 15 TGCTTTAGACAGTGT 1

RESULT 24

AAF94818

ID AAF94818 standard; cDNA; 396 BP.

AC AAF94818;

23-MAY-2001 (first entry)

Human ovarian cancer associated coding sequence SEQ ID NO: 9.

Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.

Homo sapiens.

MO200118046-A2.

15-MAR-2001.

08-SEP-2000; 2000MO-US24827.

10-SEP-1999; 99US-0394374.

01-MAY-2000; 2000US-0561778.

15-AUG-2000; 2000US-0640173.

07-SEP-2000; 2000US-0656668.

(CORI-) CORIXA CORP.

Xu J, Stolk JA;

WPI: 2001-211395/21.

Isolated polypeptides associated with ovarian carcinomas, and the nucleic acids that encode them, useful for the prevention diagnosis and treatment of ovarian cancers -

AAH50766/c
 ID AAH50766 standard; cDNA: 444 BP.
 AC
 XX
 XX
 AAH50766;
 DT 23-AUG-2001 (first entry)
 DE Human tumour associated cDNA #95.
 DE Human cancer specific gene expression; gene therapy;
 DE age related differential expression; ss.
 OS Homo sapiens.
 OS WO200136685-A2.
 XX
 XX
 PD 25-MAY-2001.
 PF 17-NOV-2000; 2000WO-US31809.
 XX
 XX
 PR 17-NOV-1999; 99US-0166056.
 PR 17-NOV-1999; 99US-0166106.
 XX
 PA (NXYI-) NXYIS NEURO THERAPIES INC.
 PI Kroes RA, Moskal JR, Yamamoto H;
 DR MPI; 2001-355647/37.
 XX
 XX
 PT Novel nucleic acid molecules differentially expressed in brain cancers,
 PT useful for ascertaining propensity of cell for malignant phenotype or
 PT ascertaining suitability of anti-neoplastic drug candidate -
 PS Claim 28; Page 50; 82pp; English.
 XX
 XX
 CC The present invention provides the sequences of 184 cDNA fragments which
 CC are differentially expressed in cancer cell depending on the age of the
 CC patient. They can be used to diagnose and identify treatments for
 CC cancers, particularly brain cancers such as haemangioblastoma, teratoma,
 CC haemangioma, glioblastoma, schwannoma, osteoma and pinealoma. The
 CC present sequence is a cancer-associated cDNA of the invention.
 CC
 XX
 XX
 SQ Sequence 444 BP; 95 A; 113 C; 94 G; 142 T; 0 other;
 Query Match 22.5%; Score 364; DB 22; Length 444;
 Best Local Similarity 99.8%; Pred. No. 1.3e-136; Indels 0; Gaps 0;
 Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1196 CCGAGCTGAGTGAAGAAACGCTCCGAGAGGAGAGATCATGTACGCCGGAAGT 1255
 Db 431 CCGAGCTGAGTGAAGAAACGCTCCGAGAGGAGAGATCATGTACGCCGGAAGT 372
 Oy 1256 AGGACCTGCTCAGTGTGTTGGGTTGGCCGACCATGATCTCCGAATCTGTTGG 1315
 Db 371 AGGACCTGCTCAGTGTGTTGGGTTGGCCGACCATGATCTCCGAATCTGTTGG 312
 Oy 1316 GCATCCAGCATGAGGCAATGTCACCAATCAGCCCTGGCAGACAGGAGGAGGA 1375
 Db 311 GCATCCAGCATGAGGCAATGTCACCAATCAGCCCTGGCAGACAGGAGGAGGA 252
 Oy 1376 GAGACAGAGAAAGAAACACAGCATGAGACACAGTAATGATTAATTAATTAATA 1435
 Db 251 GAGACAGAGAAAGAAACACAGCATGAGACACAGTAATGATTAATTAATTAATA 192
 Oy 1436 TTTAGCCCCCTGTTGCTTACGTGCGAGGAAATGATCAATTTTCACTGTTGA 1495
 Db 191 TTTAGCCCCCTGTTGCTTACGTGCGAGGAAATGATCAATTTTCACTGTTGA 132
 Oy 1496 CTTGACACCTTTTGGCACAAGCAGAGAGATTTTACACTGTTTCAAAACCGGGGA 1555
 Db 131 CTTGACACCTTTTGGCACAAGCAGAGAGATTTTACACTGTTTCAAAACCGGGGA 72
 Oy 1556 GTTGGCTGTGTTAAAGAAACCATTAATGCTTTAGACAGTGTAAAAA 1610

DB 71 GTTGGCTGTGTTAAAGAAACCATTAATGCTTTAGACAGTGTAAAAA 17
 RESULT 20
 ID AAF95007 standard; DNA: 369 BP.
 AC
 XX
 XX
 AAF95007;
 DT 23-MAY-2001 (first entry)
 DE Human ovarian cancer associated coding sequence SEQ ID NO: 199.
 DE Human, ovarian cancer; vaccine; gene therapy; carcinoma; ds.
 OS Homo sapiens.
 OS WO200118046-A2.
 XX
 XX
 PD 15-MAR-2001.
 PF 08-SEP-2000; 2000WO-US24827.
 XX
 XX
 PR 10-SEP-1999; 99US-0394374.
 PR 01-MAY-2000; 2000US-0561778.
 PR 15-AUG-2000; 2000US-0640173.
 PR 07-SEP-2000; 2000US-0656668.
 XX
 PA (CORI-) CORIXA CORP.
 PI Xu J, Stolk JA;
 DR MPI; 2001-211395/21.
 XX
 XX
 PT Isolated polypeptides associated with ovarian carcinomas, and the
 PT nucleic acids that encode them, useful for the prevention diagnosis and
 PT treatment of ovarian cancers -
 PS Claim 18; Page 189; 189pp; English.
 XX
 XX
 CC The present invention provides a number of coding sequences and proteins,
 CC the over-expression of which is associated with ovarian carcinoma/cancer.
 CC These can be used in the diagnosis, treatment and prevention of ovarian
 CC cancer, optionally by gene therapy or in the form of a vaccine. The
 CC present sequence is an example of one of these sequences.
 CC
 XX
 XX
 SQ Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;
 Query Match 19.5%; Score 315; DB 22; Length 369;
 Best Local Similarity 100.0%; Pred. No. 6.6e-117; Indels 0; Gaps 0;
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 30 CAGGCTTGGCGCAAAATCCATGCTACAGTGAAGATTTCCAGCTGAACAGACT 89
 Db 30 CAGGCTTGGCGCAAAATCCATGCTACAGTGAAGATTTCCAGCTGAACAGACT 89
 Oy 90 GCTCTCTCCCGAGTTCATTTGTAATTCACGCTGAACCTTCAAGCATGTCTCAAAAG 149
 Db 90 GCTCTCTCCCGAGTTCATTTGTAATTCACGCTGAACCTTCAAGCATGTCTCAAAAG 149
 Oy 150 AAGTATGAGCAAAAGGCGGATCATGTACCGCAAGTCTGTGATCATCAGGCT 209
 Db 150 AAGTATGAGCAAAAGGCGGATCATGTACCGCAAGTCTGTGATCATCAGGCT 209
 Oy 210 GTCTCATGCTGCTGCGGATACAGTCTTCTGCTCCAGGGAATGAATCACTAGTTT 269
 Db 210 GTCTCATGCTGCTGCGGATACAGTCTTCTGCTCCAGGGAATGAATCACTAGTTT 269
 Oy 270 GCATCAGCTGCTGCAACACCTCTCTTTGTAAGGCGCAAGGCCAAGAAAGGGAAGTT 329
 Db 270 GCATCAGCTGCTGCAACACCTCTCTTTGTAAGGCGCAAGGCCAAGAAAGGGAAGTT 329

CC preparing ribozyme molecules for inhibiting expression of tumour
CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
CC invention are also useful in recombinant DNA molecules to direct
CC expression of a polypeptide in appropriate host cells. The current
CC sequence represents the ovarian carcinoma GPR39 cDNA.
XX
SQ Sequence 1362 BP; 263 A; 435 C; 362 G; 302 T; 0 other;

Query Match	23.8%	Score 386;	DB 24;	Length 1362;
Best Local Similarity	99.8%	Pred. No. 1.7e-145;		
Matches 506; Conservative	0;	Mismatches	0;	Indels 1; Gaps 1;

QY	845	TCAACTTCATGTCCTCGAAAACCATTCCTCGAGAGAAATTGGCTGCTTTCGGCCCTGA	904
Db	1362	TCAACTTCATGTCCTCGAAAACCATTCCTCGAGAGAAATTGGCTGCTTTCGGCCCTGA	1303
QY	905	GTTGGGCTCTAGTACTCGAGACTCAATGACTGGAGCTTAGACTGGGCTCGGCTGCT	964
Db	1302	GTTGGGCTCTAGTACTCGAGACTCAATGACTGGAGCTTAGACTGGGCTCGGCTGCT	1243
QY	965	CTGAAATGCTTTAAGAAATCTTTCACGTTCTTCCTTGCAGAGACTGGCCCGGAGCG	1024
Db	1242	CTGAAATGCTTTAAGAAATCTTTCACGTTCTTCCTTGCAGAGACTGGCCCGGAGAGCG	1183
QY	1025	GAAAGCAACGGGGCGCTGCACAAAGCGGGGCGCTGTGCGTGAGAGTGCGCACTGACGCG	1084
Db	1182	GAAAGCAACGGGGCGCTGCACAAAGCGGGGCGCTGTGCGTGAGAGTGCGCACTGACGCG	1123
QY	1085	CAGGCGCTTCGTTGGTTCGCGTGTGTCAGACGACAGGCGGCAACGACAGCCTTGACGA	1144
Db	1122	CAGGCGCTTCGTTGGTTCGCGTGTGTCAGACGACAGGCGGCAACGACAGCCTTGACGA	1064
QY	1145	ACACCCGCCGAAACTGCTGCGAGAGACACGCTGACAGAGAGCGGTTGATGACCCGACGTA	1204
Db	1063	ACACCCGCCGAAACTGCTGCGAGAGACACGCTGACAGAGAGCGGTTGATGACCCGACGTA	1004
QY	1205	GCTGAAAAACGTCCTCCGAGAAAGGAGAGATCATGTAGCCGCCGGAATGAGACCTCG	1264
Db	1003	GCTGAAAAACGTCCTCCGAGAAAGGAGAGATCATGTAGCCGCCGGAATGAGAGACCTCG	944
QY	1265	TCCAGTCGTCCTTGGTTTGGCCGACGCCATATCTCCGAATCTGGATTGGGACATCCAGC	1324
Db	943	TCCAGTCGTCCTTGGTTTGGCCGACGCCATATCTCCGAATCTGGATTGGGACATCCAGC	884
QY	1325	ATACGGGCATGTCACAAATCAGCC	1351
Db	883	ATACGGGCATGTCACAAATCAGCC	857

XX	RESULT 18
XX	AAE94186/C
XX	ID AAE94186 standard; DNA; 587 BP.
XX	AAE94186;
XX	23-MAY-2001 (first entry)
DE	Primer specific for DNA encoding secretory/membrane protein SEQ ID 620
XX	
KW	Human; secretory protein; membrane protein; vaccine; gene therapy;
KW	Rheumatoid arthritis; diabetes; PCR primer; ss.
XX	
OS	Synthetic.
XX	
PN	EPI067182-A2.
XX	
XX	10-JAN-2001.
XX	
XX	
PF	07-JUL-2000; 2000EP-0114090.
XX	
XX	
PR	08-JUL-1999; 99UP-0194179.
PR	11-JAN-2000; 2000UP-0118775.
XX	
3R	02-MAY-2000; 2000UP-0183766.

XX (HELI-) HELIX RES INST.
PA
XX
XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K,
PI
XX
XX WPT; 2001-093989/11.
XX

Claim 5; SEQ ID 620; 609pp + CD ROM; English.

CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC that encode human secretory or membrane proteins represented by
CC AAB88317 - AAB88419. Included in the invention are primers
CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
CC cDNA sequences of the invention. The invention also includes methods for
CC the production of antibodies directed against the proteins, and cDNA
CC sequences, which can be used in vaccines. The polynucleotide sequences
CC can be used in gene therapy. The polynucleotide sequences and the
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate secretory
CC protein/membrane protein expression. The nucleic acids and complementary
CC sequences may also be used as DNA probes in diagnostic assays
CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC presence of similar nucleic acid sequences in samples. They may also be
CC used to study the expression and function of secretory proteins/membrane
CC polypeptides and their role in metabolism. The polypeptides may be used
CC as antigens in the production of antibodies against them and in assays to
CC identify modulators (agonists and antagonists) of expression and
CC activity. The antibodies (agonists and antagonists) may also be used as therapeutic
CC agents to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbent assay
CC (ELISA)). Examples of diseases which may be treated include rheumatoid
CC arthritis and diabetes.

Sequence 587 BP; 117 A; 162 C; 140 G; 162 T; 6 other.

Query Match	22.68;	Score 366;	DB 22;	Length 587;
Best Local Similarity	99.88;	Pred. No. 2e-137;		
Matches 416;	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps	0

QY	1183	AGCGGGTGTATGACCCGAGCTAGGTACAAAACGTCGCCGAAAGGGGAGGAGMCAATG	124
Db	417	AGCGGGTGTATGACCCGAGCTAGGTAGAAAAGCTCCGAGAAAGGGGAGGAGTCAATG	358
QY	1243	TACGCCCGGAGTAGGACCTGTCACACTGCTGGGTGGGTGGCCGACCACATGATCCG	1302
Db	357	TACGCCCGGAGTAGGACCTGTCACAGTGTGCTGGGTGGGTGGCCGACCACATGATCCTC	298
QY	1303	CGAATTCGTGGTGGGCATCCAGCATACGGCCAAATGTGCACAACAATCAGCCCTGGGCAGACA	1362
Db	297	CGAATTCGTGGTGGGCATCCAGCATACGGCCAAATGTGCACAACAATCAGCCCTGGGCAGACA	238
QY	1363	CGACGAGAGGAGAGACACAGAAAAAGAAAACACAGCATGAGAACACAGTAAATGATTA	1422
Db	237	CGACGAGAGGAGAGAGACACAGAAAAAGAAAACACAGCATGAGAACACAGTAAATGATTA	178
QY	1423	AAACCATAAATATTTTAGCCCTCTTCTGTGCTTACTAGGCGCAGAAATGGTACCATT	1482
Db	177	AAACCATAAATATTTTAGCCCTCTTCTGTGCTTACTAGGCGCAGAAATGGTACCATT	118
QY	1483	TTTTCAGTGTGGACCTGCACGCTTCTTTTGCCACAAGCAAGAGAAATTTAAACTGTT	1542
Db	117	TTTTCAGTGTGGACCTGCACGCTTCTTTTGCCACAAGCAAGAGAAATTTAAACTGTT	58
QY	1543	CAAAACCCGGGGGAGTGGCTGTGTAAABAAGACCATTTAAATGCTTTAGACAGTGT	1599
Db	57	CAAAACCCGGGGGAGTGGCTGTGTAAABAAGACCATTTAAATGCTTTAGACAGTGT	1

RESULT 19

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RESULT 16
ABT03279/C
ID ABT03279 standard; cDNA: 1362 BP.
XX
XX
XX ABT03279;
XX
XX 05-SEP-2002 (first entry)
XX
XX Human ovarian carcinoma associated coding sequence SEQ ID NO: 208.
XX
XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
XX cytostatic; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200239885-A2.
XX
XX 23-MAY-2002.
XX
XX 13-NOV-2001; 2001WO-US45395.
XX
XX 14-NOV-2000; 2000US-0713550.
XX 03-APR-2001; 2001US-0825294.
XX 02-OCT-2001; 2001US-0970966.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Stolck JA, Algate PA, Fling SP, Molesch DA;
XX
XX WPI: 2002-500186/53.
XX
XX Novel ovarian cancer polypeptide and polynucleotide, useful for
XX detecting the presence of ovarian cancer in a patient, and in
XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
XX
XX Claim 2: Page 193; 197pp; English.
XX
XX The present invention provides human ovarian cancer associated proteins
XX and coding sequences. The sequences can be used in the diagnosis and
XX treatment of ovarian cancers. The present sequence is a coding sequence
XX of the invention.
XX
XX Sequence 1362 BP; 263 A; 435 C; 362 G; 302 T; 0 other;
XX
Query Match 23.8%; Score 386; DB 24; Length 1362;
Best Local Similarity 99.8%; Pred. No. 1.7e-145;
Matches 506; Conservative 0; Mismatches 0; Indels 1; Gaps 1:
QY 845 TCAACTTCATGCTCCGAAACCATTCCTGAGAGAGAAATGGGCTTGGCGGCTGA 904
DB 1362 TCAAACTTCATGCTCCGAAACCATTCCTGAGAGAGAAATGGGCTTGGCGGCTGA 1303
QY 905 GTTGGGCTAGTACGACGACGACGACGACGACGACGACGACGACGACGACGACG 964
DB 1302 GTTGGGCTAGTACGACGACGACGACGACGACGACGACGACGACGACGACG 1243
QY 965 CTGAAAAGCTTAAGAAATCTTCTCAGTTCTTCTGAGAGAGACGCGCGGACGC 1024
DB 1242 CTGAAAAGCTTAAGAAATCTTCTCAGTTCTTCTGAGAGAGACGCGCGGACGC 1183
QY 1025 GAAGAGCAAGGGGCGGCGCAAGAGGGGCGGCGGCGGCGGCGGCGGCGGCGG 1084
DB 1182 GAAGAGCAAGGGGCGGCGGCGCAAGAGGGGCGGCGGCGGCGGCGGCGGCGG 1123
QY 1085 CAGCGCTTCTCTGTTGGGCTGCTGACGAGACAGGCGGCGACACACCTTGACGA 1144
DB 1122 CAGCGCTTCTCTGTTGGGCTGCTGACGAGACAGGCGGCGACACACCTTGACGA 1064
QY 1145 ACACCGCGGAAAGTCTGCGAGAGACCGGTACAGAGCGGGTGTATACGAGAGCTGA 1204

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DB 1063 ACACCGCGGAAAGTCTGCGAGAGACCGGTACAGAGAGCGGGTGTATACGAGAGCTGA 1004
QY 1205 GGTAGAAAACGCTCTCGAAGAGGAGAGATCATGTACGCGCGGAGGTAGACCTCG 1264
DB 1003 GGTAGAAAACGCTCTCGAAGAGGAGAGATCATGTACGCGCGGAGGTAGACCTCG 944
QY 1265 TCCAGTCGCTGTTGGGTTGGCGGACGACATGATCCCTCCGAAATCTGTTGGGACATCCAG 1324
DB 943 TCCAGTCGCTGTTGGGTTGGCGGACGACATGATCCCTCCGAAATCTGTTGGGACATCCAG 884
QY 1325 ATACGGCCAAATGTCACACAAATCAGCC 1351
DB 883 ATACGGCCAAATGTCACACAAATCAGCC 857

RESULT 17
ABL40347/C
ID ABL40347 standard; cDNA: 1362 BP.
XX
XX ABL40347;
XX
XX 28-JUN-2002 (first entry)
XX
XX Ovarian carcinoma GPR39 cDNA.
XX
XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1362
XX FT /*tag= a
XX FT /product= "Ovarian carcinoma protein GPR39"
XX
XX US2002004491-A1.
XX
XX 10-JAN-2002.
XX
XX 03-APR-2001; 2001US-0825294.
XX
XX 10-SEP-1999; 99US-039437A.
XX 01-MAY-2000; 2000US-056177B.
XX 15-AUG-2000; 2000US-0640173.
XX 07-SEP-2000; 2000US-0656668.
XX 14-NOV-2000; 2000US-0713550.
XX
XX (XUJ/) XU J.
XX (STOL/) STOLK J A.
XX (ALGA/) ALGATE P A.
XX (FLIN/) FLING S P.
XX
XX Xu J, Stolck JA, Algate PA, Fling SP;
XX
XX WPI: 2002-171027/22.
XX P-PSDB: ABB09416.
XX
XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX prevention and/or treatment of cancer, especially ovarian cancer
XX
XX Claim 1a: Page 123-124; 131pp; English.
XX
XX The invention relates to ovarian tumour polynucleotides and polypeptides
XX that may be utilised in cancer therapy, for example in a vaccine or
XX gene therapy. Polypeptides and polynucleotides of the invention are
XX useful for detecting a cancer in a patient, for stimulating and/or
XX expanding T-cells specific for a tumour protein, and for inhibiting the
XX development of a cancer in a patient. They are also useful for
XX stimulating an immune response in a patient, and for treating a cancer in
XX a patient and for determining the presence of a cancer in a patient.
XX The isolated polynucleotides of the invention are useful for their
XX ability to selectively form duplex molecules with complementary stretches
XX of the entire desired gene or gene fragments, and for designing and

```


CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
 CC presence of similar nucleic acid sequences in samples. They may also be
 CC used to study the expression and function of secretory proteins/membrane
 CC polypeptides and their role in metabolism. The polypeptides may be used
 CC as antigens in the production of antibodies against them and in assays to
 CC identify modulators (agonists and antagonists) of expression and
 CC activity. The antibodies and antagonists may also be used as therapeutic
 CC agents to down regulate expression and activity. The antibodies may also
 CC be used as diagnostic agents for detecting the presence of the
 CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay
 CC (ELISA). Examples of diseases which may be treated include Rheumatoid
 CC arthritis and diabetes.

XX Sequence 1890 BP; 419 A; 528 C; 533 G; 410 T; 0 other;

Query Match 62.6%; Score 1014; DB 22; Length 1890;

Best Local Similarity 99.6%; Pred. No. 0; Mismatches 1594; Conservative 0; Indels 2; Gaps 4;

```

Oy 1 GGCACATTTTGGCGATTTGTTCTTCTTCAGAGGCTTGCCTGCAAAATCCAGTGTACCA 60
Db 294 GGCACATTTTGGCGATTTGTTCTTCTTCAGAGGCTTGCCTGCAAAATCCAGTGTACCA 353
Oy 61 GTGTAAATAATTCACGCTGAACAACGACTGCTCTCCCGCAGTTTCAATTTGAAATGGAC 120
Db 354 GTGTAAATAATTCACGCTGAACAACGACTGCTCTCCCGCAGTTTCAATTTGAAATGGAC 413
Oy 121 GGTGAACGTTGACAGATGTGTGCAAGAAAGATGTGAGCAAAAGTCCCGGAGTCACTA 180
Db 414 GGTGAACGTTGACAGATGTGTGCAAGAAAGATGTGAGCAAAAGTCCCGGAGTCACTA 473
Oy 181 CCGCAAGTCTGTGCATCATAGCGGCTGTCTCATGCGCTCTCCGGGTACACAGTCTT 240
Db 474 CCGCAAGTCTGTGCATCATAGCGGCTGTCTCATGCGCTCTCCGGGTACACAGTCTT 533
Oy 241 CTGCTCCCGCAGGAAACGAACTGATTTGCATGAGTGTCTGCAACACCCCTTTTGTAA 300
Db 534 CTGCTCCCGCAGGAAACGAACTGATTTGCATGAGTGTCTGCAACACCCCTTTTGTAA 593
Oy 301 CGGCGCAAGGCCCAAGAAAGGGAAGTTCGCTCGGCCCTCAGGCGAGGCTCCGCGAC 360
Db 594 CGGCGCAAGGCCCAAGAAAGGGAAGTTCGCTCGGCCCTCAGGCGAGGCTCCGCGAC 653
Oy 361 CACCATCTGTCTCTCAAAATTAAGCCCTCTCTCTGCGCACTGCTGAAGCTGAAGAGATG 420
Db 654 CACCATCTGTCTCTCAAAATTAAGCCCTCTCTCTGCGCACTGCTGAAGCTGAAGAGATG 711
Oy 421 CCACCCCTCTCTGATGTTCTTCCAGCCGCTCGGCCCAACCCCGCCAGCTCCCTGAGTGA 480
Db 712 CCACCCCTCTCTGATGTTCTTCCAGCCGCTCGGCCCAACCCCGCCAGCTCCCTGAGTGA 771
Oy 481 GTTCTTCTGGGTGCTCTTTTATTTCTGGGTAGGAGCGGAGTCCGCTCTCTTTTGT 540
Db 772 GTTCTTCTGGGTGCTCTTTTATTTCTGGGTAGGAGCGGAGTCCGCTCTCTTTTGT 831
Oy 541 CCGTGAATTAATGAAGAAGCTCGGTAAGCAATTCGAATTAATTCAGCTGAGCTGAAT 600
Db 832 CCGTGAATTAATGAAGAAGCTCGGTAAGCAATTCGAATTAATTCAGCTGAGCTGAAT 891
Oy 601 TTTCAGTATGATGTAAGAGAGAGTGAAGTCAACCCCAATGCTCTGTGTAAAC 660
Db 892 TTTCAGTATGATGTAAGAGAGAGTGAAGTCAACCCCAATGCTCTGTGTAAAC 951
Oy 661 CGGAGTCAAGGCCAGGCTGCGAGAGTCAATCTTAGAAGTCACTGAGTGGGAGTATGCC 720
Db 952 CGGAGTCAAGGCCAGGCTGCGAGAGTCAATCTTAGAAGTCACTGAGTGGGAGTATGCC 1011
Oy 721 TTTTGAAGAGCTCCAGTGTCCATTCCTTCATCCGATGGGGGCAATTTTGAAGTCTCAGA 780
Db 1012 TTTTGAAGAGCTCCAGTGTCCATTCCTTCATCCGATGGGGGCAATTTTGAAGTCTCAGA 1071
Oy 781 GTGAGAGTACGTTTCTTAGGGCTGAGGGGCAATTCACACAGAGGCTCCCTGCTTG 840
  
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Db 1072 GTGAGAGTACGTTTCTTCTTGAAGGCTGAGGCGCAGTTCACATCAAGGCTCCCTGCTTG 1131
Oy 841 ACATTTCAAACTTCATGCTCTCTGAAAACCATTTCTTCGACAGAGATTTGGTTCGCGC 900
Db 1132 ACATTTCAAACTTCATGCTCTCTGAAAACCATTTCTTCGACAGAGATTTGGTTCGCGC 1191
Oy 901 CTGAGTGGGCTCTAGTACTCCAGATCAATCACTGAGCTTAACTGGGCTCGGCT 960
Db 1192 CTGAGTGGGCTCTAGTACTCCAGATCAATCACTGAGCTTAACTGGGCTCGGCT 1251
Oy 961 CGCTCTGAAAAGTCTTAAGAAAATCTTTCAGTTCGCTCTGAGAGGAGCTGGCCCGG 1019
Db 1252 CGCTCTGAAAAGTCTTAAGAAAATCTTTCAGTTCGCTCTGAGAGGAGCTGGCCCGG 1311
Oy 1020 GAGCGAAGAGCAAGCGGCGCTGCACAAACGAGCGCTGCTGGTGGTGAAGTCCGATG 1079
Db 1312 GAGCGAAGAGCAAGCGGCGCTGCACAAACGAGCGCTGCTGGTGGTGAAGTCCGATG 1371
Oy 1080 ACGCGAGGGGCTTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1139
Db 1372 ACGCGAGGGGCTTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1430
Oy 1140 CAGGAACCCCGCGCAAACTGTCGAGAGACACGTTGACAGAGAGGGGTTGATGACGA 1199
Db 1431 CAGGAACCCCGCGCAAACTGTCGAGAGACACGTTGACAGAGAGGGGTTGATGACGA 1490
Oy 1200 GCTGAGGTAGAAAACGCTCTCCGAGAAGGGAGAGATCATGTACGCCCGGAATGAGA 1259
Db 1491 GCTGAGGTAGAAAACGCTCTCCGAGAAGGGAGAGATCATGTACGCCCGGAATGAGA 1550
Oy 1260 CTTCTGTCAGATGCTGTGGGTTTGGCCGACGACATGATCCCTCCGAATGTGGTGGCAT 1319
Db 1551 CTTCTGTCAGATGCTGTGGGTTTGGCCGACGACATGATCCCTCCGAATGTGGTGGCAT 1610
Oy 1320 CCAAGATACGCCAATGTCAACAACATCAAGCCCTGGGCGACAGACGAGAGAGAGA 1379
Db 1611 CCAAGATACGCCAATGTCAACAACATCAAGCCCTGGGCGACAGACGAGAGAGAGA 1670
Oy 1380 CAGAGAAAAGAAAACACAGCATGAGACACAGTAAATTAATTAATTAATTAATTA 1439
Db 1671 CAGAGAAAAGAAAACACAGCATGAGACACAGTAAATTAATTAATTAATTAATTA 1730
Oy 1440 GCCCTCTGTCTGTCTTACTGCGCAGGAAATGGTACCAATTTTCTAGTGTGACCTTG 1499
Db 1731 GCCCTCTGTCTGTCTTACTGCGCAGGAAATGGTACCAATTTTCTAGTGTGACCTTG 1790
Oy 1500 ACAAGCTTTTTCGCAAGAAGAGAGATTTAAACACTGTTTCAAAACCCGGGAGTGG 1559
Db 1791 ACAAGCTTTTTCGCAAGAAGAGAGATTTAAACACTGTTTCAAAACCCGGGAGTGG 1850
Oy 1560 GCGTGTGTTAAAGAACCATTAATGCTTTAGACAGTGT 1599
Db 1851 GCGTGTGTTAAAGAACCATTAATGCTTTAGACAGTGT 1890
  
```

RESULT 13

ABT03280
 ID ABT03280 standard; CDNA; 625 BP.

XX ABT03280;

XX 05-SEP-2002 (first entry)

XX Human ovarian carcinoma associated coding sequence SEQ ID NO: 210.

XX Human; ovarian cancer; ovarian carcinoma; gene therapy; Immunotherapy;

XX cytostatic; gene; ss.

XX Homo sapiens.

XX W0200239885-A2.

XX 23-MAY-2002.

Db 1977 CATCAGCTGCTGCACACCCCTCTTTGTAAAGGGCCAAAGGCCCAAGAAAAGGGAAGTTC 1918
 Qy 331 TGGCTGGGGCCCTCAGGCGAGGGCTCCGCAACACACCTCGTTCCTCAATTAAGCCCTCTT 390
 Db 1917 TGGCTGGGGCCCTCAGGCGAGGGCTCCGCAACACACCTCGTTCCTCAATTAAGCCCTCTT 1858
 Qy 391 CTCGGCACACTGCTGAAGCTGAAGAGATGACACCCCTCCTGCAATTTGTTCTCCAGCCC 450
 Db 1857 CTCGGCACACTGCTGAAGCTGAAGAGATGCCACCCCTCCTGCAATTTGTTCTCCAGCCC 1798
 Qy 451 TGGCCCCCAACCCCACTCCCTGAGTGTCTTCTGGGTGTCTTATTCCTGGGT 510
 Db 1797 TGGCCCCCAACCCCACTCCCTGAGTGTCTTCTGGGTGTCTTATTCCTGGGT 1738
 Qy 511 AGGAGACGGGAGTCCGTCTCTTTCTTTCTGTCGCAATATATAAGAGCTCGTAA 570
 Db 1737 AGGAGACGGGAGTCCGTCTCTTTCTTTCTGTCGCAATATATAAGAGCTCGTAA 1678
 Qy 571 GCATTCTGAATTAATTCACCTGACTGAATTTTCAATATGATGTAAGAGAGAGTGG 630
 Db 1677 GCATTCTGAATTAATTCACCTGACTGAATTTTCAATATGATGTAAGAGAGAGTGG 1618
 Qy 631 AGTGAAGTTCAACCCCACTGCTGTGTAAACCGAGTCAAGGCCAGCTGGCAGTCACT 690
 Db 1617 AGTGAAGTTCAACCCCACTGCTGTGTAAACCGAGTCAAGGCCAGCTGGCAGTCACT 1558
 Qy 691 CCTTAGAGTCACTGAGTGGGCACTGCTTTGTAAAGCCCTCAAGTCCATTCACATC 750
 Db 1557 CCTTAGAGTCACTGAGTGGGCACTGCTTTGTAAAGCCCTCAAGTCCATTCACATC 1498
 Qy 751 CCTGATGGGGGATAGTTTGAAGTGCAGAGTGAAGTGTCTTTCTTAGGGCTGAGG 810
 Db 1497 CCTGATGGGGGATAGTTTGAAGTGCAGAGTGAAGTGTCTTTCTTAGGGCTGAGG 1438
 Qy 811 GCCAGTCCCACTCAAGGCTCCCTGCTTGAATTCAAACTTCAATGCTCTGAAAAACAT 870
 Db 1437 GCCAGTCCCACTCAAGGCTCCCTGCTTGAATTCAAACTTCAATGCTCTGAAAAACAT 1378
 Qy 871 TCTCTGCACAGAAATTTGCTGTTGCGGCTGAGTGGGCTCTGAGTCACTGAGACTCA 930
 Db 1377 TCTCTGCACAGAAATTTGCTGTTGCGGCTGAGTGGGCTCTGAGTCACTGAGACTCA 1318
 Qy 931 ATGACTGGGACTTTAGACTGCGGCTCGGCTGCTTGAAGTGTCTTGAAGAAATCTTCT 990
 Db 1317 ATGACTGGGACTTTAGACTGCGGCTCGGCTGCTTGAAGTGTCTTGAAGAAATCTTCT 1258
 Qy 991 CAGTCTCCTTGCAGAGGACTGGGCGCGGAGACGCAAGACAGGCGGCTGCAAAAGC 1050
 Db 1257 CAGTCTCCTTGCAGAGGACTGGGCGCGGAGACGCAAGACAGGCGGCTGCAAAAGC 1198
 Qy 1051 GGGCGCTCTCGGTTGGTGCAGTGCAGATGACGCGAGGCTTCTGTTGGTGGGCTGCT 1110
 Db 1197 GGGCGCTCTCGGTTGGTGCAGTGCAGATGACGCGAGGCTTCTGTTGGTGGGCTGCT 1138
 Qy 1111 GCAGCGACAGCGGCGAGCAGACACTTTCGACGAACACCCCGCAAACTGCTGCGAGAC 1170
 Db 1137 GCAGCGACAGCGGCGAGCAGACACTTTCGACGAACACCCCGCAAACTGCTGCGAGAC 1079
 Qy 1171 ACCGTTACAGAGGGGTTGATGACCGAGCTGAGAGTGAAGAAAGCTCCGAGAGAGG 1230
 Db 1078 ACCGTTACAGAGGGGTTGATGACCGAGCTGAGAGTGAAGAAAGCTCCGAGAGAGG 1019
 Qy 1231 AGGAGGATCATATGACGCCCGGAGAGTACCTCTGTCAGTGTCTTGGGTTGGCCCA 1290
 Db 1018 AGGAGGATCATATGACGCCCGGAGAGTACCTCTGTCAGTGTCTTGGGTTGGCCCA 959
 Qy 1291 GCCATGATCTTCGAATCTGTTGGGCAATCCAGCATACGCCCAATGTCACAACATCAGC 1350
 Db 958 GCCATGATCTTCGAATCTGTTGGGCAATCCAGCATACGCCCAATGTCACAACATCAGC 899
 Qy 1351 C 1351
 Db 898 C 898

RESULT 11
 AB054231
 ID AB054231 standard; cDNA: 1608 BP.
 XX
 AC AB054231;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HVCAG04 cDNA, SEQ ID NO:111.
 DE
 XX
 KW Human: ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive; chromosome 2q21-22;
 KW gene; ss.
 OS
 XX Homo sapiens.
 XX
 EN M0200200677-A1.
 XX
 PD 03-JAN-2002.
 XX
 PF 07-JUN-2001; 2001WO-US18569.
 XX
 PR 07-JUN-2000; 2000US-209467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX
 DR WP1: 2002-147878/19.
 XX P-PSDB: ABP41154.
 XX
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.
 PT ovarian cancer), immune disorders, cardiovascular disorders and
 PT neurological diseases -
 XX
 PS Claim 1; SEQ ID NO 111; 2922pp; English.
 CC
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovarian and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present

XX Homo sapiens.
 OS MO20061629-A1.
 PN 19-OCT-2000.
 PD 06-APR-2000; 2000WO-US09071.
 PF 09-APR-1999; 99US-0128694.
 PR 20-JAN-2000; 2000US-0176931.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 XX Ruben SM, Komatsoulis G;
 PI MPI: 2000-647420/62.
 DR P-PSDB; AAB63161.
 XX
 PT Isolated nucleic acid molecule encoding a human secreted protein is
 PT used in preventing, treating or ameliorating a medical condition -
 XX
 PS Claim 1: Page 440; 533pp; English.

CC AAF22373 to AAF22421 encode the human secreted proteins given in AAB63134
 CC to AAB63182. AAB63183 to AAB63231 represent more human secreted proteins
 CC and polypeptides homologous to them. Human secreted proteins have
 CC activities based on the tissues and cells the genes are expressed in.
 CC Examples of activities include: immunosuppressive; antitumor; anti-
 CC antihemetic; antiproliferative; cytostatic; cardiant; vasotropic;
 CC neuroprotective; neurotrophic; neuroprotective; antibacterial; virucide;
 CC fungicide; and ophthalmological. The polynucleotides and proteins can be
 CC used to prevent, treat or ameliorate a medical condition in e.g. humans,
 CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are
 CC also used in diagnosing a pathological condition or susceptibility to a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular
 CC disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral
 CC ischemia, angiodysplasia, nervous system disorders e.g. Alzheimer's
 CC disease, infections caused by bacteria, viruses and fungi and ocular
 CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis. The polypeptides can also be used as a food additive or
 CC preservative to increase or decrease storage capabilities. AAF22364 to
 CC AAF22372 and AAB63133 represent sequences used in the exemplification of
 CC the present invention.

SO Sequence 1953 BP; 428 A; 540 C; 524 G; 458 T; 3 other;

Query Match 74.48; Score 1205; DB 21; Length 1953;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1595; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 1 GGCAACTTTTGGGATGTTCTGCTTCAGGCTTGGCGTGAATTCAGTGTCTCA 60
 DB 1674 GGCAACTTTTGGGATGTTCTGCTTCAGGCTTGGCGTGAATTCAGTGTCTCA 1615
 QY 61 GTGTGAAGAATTCAGCTGAACAAGACTGCTCTCCCGAGTTCAATGTGAATTGAC 120
 DB 1614 GTGTGAAGAATTCAGCTGAACAAGACTGCTCTCCCGAGTTCAATGTGAATTGAC 1555
 QY 121 GGTGAAGCTTAAAGCATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180
 DB 1554 GGTGAAGCTTAAAGCATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 1495
 QY 181 CCGCAAGCTGTGTCATCATCAGCGGCTGTCTGATGCGCTTCCGGGATCAACAGTCTT 240
 DB 1494 CCGCAAGCTGTGTCATCATCAGCGGCTGTCTGATGCGCTTCCGGGATCAACAGTCTT 1435

QY 241 CTGTCCCGAGGAAAGTGAAGTCACTGTTGTCATGAGTGTGCAACACCCCTTTGTAA 300
 DB 1434 CTGTCCCGAGGAAAGTGAAGTCACTGTTGTCATGAGTGTGCAACACCCCTTTGTAA 1375
 QY 301 CGGCGCAAGGCCCAAGAAAGGGAAGTTCGCTCGGCTTCAGGCGCAGGCTCCGAC 360
 DB 1374 CGGCGCAAGGCCCAAGAAAGGGAAGTTCGCTCGGCTTCAGGCGCAGGCTCCGAC 1316
 QY 361 CAGCATCTGTTCCCAATTAAGCCCTCTCTGCGACACTGAGAAAGTGAAGATG 420
 DB 1315 CAGCATCTGTTCCCAATTAAGCCCTCTCTGCGACACTGAGAAAGTGAAGATG 1256
 QY 421 CCACCCCTCTCTGCAATTTGTTCTTCAGCCCTCGCCCAACCCCACTCTCTGATGA 480
 DB 1255 CCACCCCTCTCTGCAATTTGTTCTTCAGCCCTCGCCCAACCCCACTCTCTGATGA 1196
 QY 481 GTTCTTCTGGGTGCTCTTTATTTCTGGGTAGGAGCGGAGTCCGTTCTTTGTT 540
 DB 1195 GTTCTTCTGGGTGCTCTTTATTTCTGGGTAGGAGCGGAGTCCGTTCTTTGTT 1136
 QY 541 CTTGCAAAATATGAAGAGCTGTAAGCATTTCTGAATTAATTCAGCTGATGAT 600
 DB 1135 CTTGCAAAATATGAAGAGCTGTAAGCATTTCTGAATTAATTCAGCTGATGAT 1076
 QY 601 TTTCAATATGATTTGAAGAGAGGTGAGTGAAGTTCAACCCCTATCTGTGTAA 660
 DB 1075 TTTCAATATGATTTGAAGAGAGGTGAGTGAAGTTCAACCCCTATCTGTGTAA 1016
 QY 661 CGGAGTCAAGGCGAGGCGGAGAGTCACTGCTTGAAGTCACTGAGTGGGATGCTCC 720
 DB 1015 CGGAGTCAAGGCGAGGCGGAGAGTCACTGCTTGAAGTCACTGAGTGGGATGCTCC 956
 QY 721 TTTTGAAGCTCTCAAGTGTCCATTCATCCCTGATGGGGCATAGTTGAGACTGCA 780
 DB 955 TTTTGAAGCTCTCAAGTGTCCATTCATCCCTGATGGGGCATAGTTGAGACTGCA 896
 QY 781 GTGAGAGTACCTTTTCTTAGGCGTGAAGGCCAGTCTCCACTCAAGCTCCCTGCTG 840
 DB 895 GTGAGAGTACCTTTTCTTAGGCGTGAAGGCCAGTCTCCACTCAAGCTCCCTGCTG 836
 QY 841 ACATTCAACTTCATGCTCCGTAAGAAACATTCCTGACAGCAAGATGGCTGGTCCG 900
 DB 835 ACATTCAACTTCATGCTCCGTAAGAAACATTCCTGACAGCAAGATGGCTGGTCCG 776
 QY 901 CTGAGTTGGGCTCTGATGACTGAGACTCAATGACTGGGACTTAACATGAGGCTGCGCT 960
 DB 775 CTGAGTTGGGCTCTGATGACTGAGACTCAATGACTGGGACTTAACATGAGGCTGCGCT 716
 QY 961 CGCTCTGAAGAGTCTTAAAGAAATCTTCTCACTTCTCTGACAGAGACTGCGCCG 1020
 DB 715 CGCTCTGAAGAGTCTTAAAGAAATCTTCTCACTTCTCTGACAGAGACTGCGCCG 656
 QY 1021 ACGCGAAGCAAGGCGGCTGACAAAGCGGCGCTGCGGTGGTGGAGTGGCGCATGA 1080
 DB 655 ACGCGAAGCAAGGCGGCTGACAAAGCGGCGCTGCGGTGGTGGAGTGGCGCATGA 596
 QY 1081 CGGCGAGGCGCTTCTGTTGTTGCGTGTGCTGACAGGAGGCGGAGACACACCTTGC 1140
 DB 595 CGGCGAGGCGCTTCTGTTGTTGCGTGTGCTGACAGGAGGCGGAGACACACCTTGC 537
 QY 1141 ACGAACAACCGCGGAAGTCTGCGAGGACACCGTGTACAGAGGCGGTGATGACGAG 1200
 DB 536 ACGAACAACCGCGGAAGTCTGCGAGGACACCGTGTACAGAGGCGGTGATGACGAG 477
 QY 1201 CTGAGTTAGAAAAGTCTCCGAGAAAGGAGAGAGATCATGTACCGCGGAATGAGAC 1260
 DB 476 CTGAGTTAGAAAAGTCTCCGAGAAAGGAGAGAGATCATGTACCGCGGAATGAGAC 417
 QY 1261 CTGCTCACTGCTGCTTGGGTTGGCGGAGGAGCATGATCTCCGAATCTGTTGGCATC 1320
 DB 416 CTGCTCACTGCTGCTTGGGTTGGCGGAGGAGCATGATCTCCGAATCTGTTGGCATC 357
 QY 1321 CAGCATACGCGCCATATGTCAACAATACAGCTCTGGGAGACAGACAGAGAGAGAC 1380

PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -

PS Claim 2; Figure 15; 359pp; English.

XX The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for stimulating
 CC the release of tumour necrosis factor- α from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABR33536-ABR33657 represent human
 CC PRO protein coding sequences of the invention.
 CC
 CC
 CC

SO Sequence 1524 BP; 321 A; 433 C; 435 G; 335 T; 0 other;

Query Match 78.1%; Score 1264; DB 24; Length 1524;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGCACTTTTGGGATTTGTTGCTTCCAGGCTTTGGCTGCAAAATCCAGTGTACCA 60
 DB 141 GGCACTTTTGGGATTTGTTGCTTCCAGGCTTTGGCTGCAAAATCCAGTGTACCA 200
 QY 61 GTGGAAGAATTTCCAGGCAACAGACTGCTCTCCCGGAGTTCATTGTAATTCAC 120
 DB 201 GTGGAAGAATTTCCAGGCAACAGACTGCTCTCCCGGAGTTCATTGTAATTCAC 260
 QY 121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 180
 DB 261 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 320
 QY 181 CCGAAGCTTCCAGGCAACAGACTGCTCTCCCGGAGTTCATTGTAATTCAC 240
 DB 321 CCGAAGCTTCCAGGCAACAGACTGCTCTCCCGGAGTTCATTGTAATTCAC 380
 QY 241 CTGCTCCCAAGGCAACAGACTGCTCTCCCGGAGTTCATTGTAATTCAC 300
 DB 381 CTGCTCCCAAGGCAACAGACTGCTCTCCCGGAGTTCATTGTAATTCAC 440
 QY 301 CGGGCCAAAGGCAACAGACTGCTCTCCCGGAGTTCATTGTAATTCAC 360
 DB 441 CGGGCCAAAGGCAACAGACTGCTCTCCCGGAGTTCATTGTAATTCAC 500
 QY 361 CACCATCTGTCTCAAAATTAAGCCCTTCTGGGCAACATGCTGAAGCTGAAGAGATG 420
 DB 501 CACCATCTGTCTCAAAATTAAGCCCTTCTGGGCAACATGCTGAAGCTGAAGAGATG 560
 QY 421 CCAACCCCTCTGATGTTCTTCAAGCCCTCCGCCCAACCCCAACCCCTCTGATGTA 480
 DB 561 CCAACCCCTCTGATGTTCTTCAAGCCCTCCGCCCAACCCCAACCCCTCTGATGTA 620
 QY 481 GTTCTTCTGGGCTCTTATTTATTTGGGAGAGCGGAGTCCGTTCTTCTTGTGT 540
 DB 621 GTTCTTCTGGGCTCTTATTTATTTGGGAGAGCGGAGTCCGTTCTTCTTGTGT 680
 QY 541 CCGTGAAGTAATTAAGAGCTCGGTAAGCAATTTGTAATTAATTCAGCTGACTGAAT 600
 DB 681 CCGTGAAGTAATTAAGAGCTCGGTAAGCAATTTGTAATTAATTCAGCTGACTGAAT 740
 QY 601 TTTCAATGATCTTAAGAGAGAGGTGAGAGAAATTCACCCCATGCTGTGTAAAC 660
 DB 741 TTTCAATGATCTTAAGAGAGAGGTGAGAGAAATTCACCCCATGCTGTGTAAAC 800

QY 661 CGAGTCAAGCCCAAGGCTGCGCAAGTCACTCTTGAAGTCACTAGTGGCATTCGC 720
 DB 801 CGAGTCAAGCCCAAGGCTGCGCAAGTCACTCTTGAAGTCACTAGTGGCATTCGC 860
 QY 721 TTTTGAAGCTTCAAGGCTGCGCAAGTCACTCTTGAAGTCACTAGTGGCATTCGC 780
 DB 861 TTTTGAAGCTTCAAGGCTGCGCAAGTCACTCTTGAAGTCACTAGTGGCATTCGC 920
 QY 781 GTGAGATGACGTTTCTTAAGGCTGAGGCGCAGTTCCCACTCAAGGCTCCCTGCTTG 840
 DB 921 GTGAGATGACGTTTCTTAAGGCTGAGGCGCAGTTCCCACTCAAGGCTCCCTGCTTG 980
 QY 841 ACATTCAAATTAAGTCTGCTGAAGAAACATCTCTGACAGCAAAATTCAGTTCGCGCC 900
 DB 981 ACATTCAAATTAAGTCTGCTGAAGAAACATCTCTGACAGCAAAATTCAGTTCGCGCC 1040
 QY 901 CTGAGTTGGGCTCTAGTCACTGAGCAATGACTGAGGAGTCACTGAGGCTGGGCT 960
 DB 1041 CTGAGTTGGGCTCTAGTCACTGAGCAATGACTGAGGAGTCACTGAGGCTGGGCT 1100
 QY 961 CGCTTGAAAGTCTTGAAGAAATCTTCTCAATTCCTTCTGAGAGGAGTGGCGCGG 1020
 DB 1101 CGCTTGAAAGTCTTGAAGAAATCTTCTCAATTCCTTCTGAGAGGAGTGGCGCGG 1160
 QY 1021 ACGGGAAGCAACGGGCGCTGCAAAAGCGGCGCTGCGGTGAGTGCATGTA 1080
 DB 1161 ACGGGAAGCAACGGGCGCTGCAAAAGCGGCGCTGCGGTGAGTGCATGTA 1220
 QY 1081 CGGCAAGCGGCTTCTGCTGTTGGGCTGCTGAGAGCAGCAGGCGGAGCAGACACCTTGC 1140
 DB 1221 CGGCAAGCGGCTTCTGCTGTTGGGCTGCTGAGAGCAGCAGGCGGAGCAGACACCTTGC 1279
 QY 1141 ACGAACAACCGCGGAAAGTCTGCGAGACACCGTGTACAGAGCGGCTGTGACCGAG 1200
 DB 1280 ACGAACAACCGCGGAAAGTCTGCGAGACACCGTGTGTACAGAGCGGCTGTGACCGAG 1339
 QY 1201 CTGAGTGAAGAAAGCTTCCGGAAGGGGAGAGATCATGTAGCCCGGGAAGTGAAGAC 1260
 DB 1340 CTGAGTGAAGAAAGCTTCCGGAAGGGGAGAGATCATGTAGCCCGGGAAGTGAAGAC 1399
 QY 1261 CTGCTCAAGTCTGCTTGGGTTGGCGGAGGATGATCTCCGAATCTGTTGGGATC 1320
 DB 1400 CTGCTCAAGTCTGCTTGGGTTGGCGGAGGATGATCTCCGAATCTGTTGGGATC 1459
 QY 1321 CAGCATAGCGGCAATCTCAACAATCAAGCCCTGGGAGACAGAGAGGAGAGAC 1380
 DB 1460 CAGCATAGCGGCAATCTCAACAATCAAGCCCTGGGAGACAGAGAGGAGAGAC 1519
 QY 1381 AGAGA 1385
 DB 1520 AGAGA 1524

RESULT 8
 AAF22400/c
 ID AAF22400 standard; cDNA; 1953 BP.
 XX
 AC AAF22400;
 XX
 DT 26-MAR-2001 (first entry)
 XX
 DE Human secreted protein gene 28 sq ID NO:38.
 XX
 KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
 KW antirheumatic; antiproliferative; cyostatic; cardiant; vasotrophic;
 KW cerebroprotective; nootropic; neuroprotective; antibacterial; virocidic;
 KW fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;
 KW rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;
 KW cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;
 KW angiogenesis; nervous system disorder; Alzheimer's disease; infection;
 KW ocular disorder; corneal infection; wound healing; skin aging;
 KW food additive; preservative; ss.

QY 241 CTGCTCCCGAGGAACTGACACTGATTTGATCAGCTGCTGCAACACCCCTCTTTGTA 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 520 CTGCTCCCGAGGAACTGACACTGATTTGATCAGCTGCTGCAACACCCCTCTTTGTA 579
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 301 CGGCGCAAGGCGGCAAGGAGGAGTCTGCTGCGCCCTCAGGCCAGGGCTCCGCA 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 580 CGGCGCAAGGCGGCAAGGAGGAGTCTGCTGCGCCCTCAGGCCAGGGCTCCGCA 639
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 361 CACCATCTGTTCCCTCAAAATTAAGCCCTCTTCGCGCACACTGCTGAAGCTGAAGAGAT 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 640 CACCATCTGTTCCCTCAAAATTAAGCCCTCTTCGCGCACACTGCTGAAGCTGAAGAGAT 699
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 421 CCAACCCCTCTGATGATTTCTTCCAGCCCTGCCCCCAACCCCACTCCCTGAGTGA 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 700 CCAACCCCTCTGATGATTTCTTCCAGCCCTGCCCCCAACCCCACTCCCTGAGTGA 759
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 481 GTTCTCTTGGGCTGCTTTTATTCGGGTAGGAGCGGGAGTCCGTCTTCTTTGTT 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 760 GTTCTCTTGGGCTGCTTTTATTCGGGTAGGAGCGGGAGTCCGTCTTCTTTGTT 819
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 541 CTGTGCAATTAATGAAGAGCTCGGTAAAGCATTTCTGAATTAATCAGCCTGACTGAAT 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 820 CTGTGCAATTAATGAAGAGCTCGGTAAAGCATTTCTGAATTAATCAGCCTGACTGAAT 879
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 601 TTTCACTATGACTTGAAGAGAGAGGTGAGTGAAGATTCAACCCCATGCTGTGTAAC 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 880 TTTCACTATGACTTGAAGAGAGAGGTGAGTGAAGATTCAACCCCATGCTGTGTAAC 939
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 661 CGAGATCAAGGCGGAGCTGAGAGAGTCACTTGAAGTCACTGAGGAGGATCTGCGC 720
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 Db 940 CGAGATCAAGGCGGAGCTGAGAGAGTCACTTGAAGTCACTGAGGAGGATCTGCGC 999
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 Db 1000 TTTTGAAGGCTTCAGTGTCCATTCATCCCTGATGAGGAGGATTTGAGACTGACA 1059
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 QY 781 GTGAGAGTACGTTTCTTAAGGCTGAGGCGCAGTTCCCACTCAAGGCTCCCTGCTTG 840
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 Db 1060 GTGAGAGTACGTTTCTTAAGGCTGAGGCGCAGTTCCCACTCAAGGCTCCCTGCTTG 1119
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 QY 841 ACATTCAAATTCATGCTGCTGAAACCATTTCTGACAGAGAAATGGCTGGTTGGCG 900
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 Db 1120 ACATTCAAATTCATGCTGCTGAAACCATTTCTGACAGAGAAATGGCTGGTTGGCG 1179
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 901 CTGAGTTGGCTCTAGTACTGAGACTCAATGACTGGGACTGAGCTGCGGCT 960
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 Db 1180 CTGAGTTGGCTCTAGTACTGAGACTCAATGACTGGGACTGAGCTGCGGCT 1239
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 QY 961 CGCTCTGAAAAGTCTTAAGAAAATCTTCTCACTTCTCTGACAGAGACTGGCGCGG 1020
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 Db 1240 CGCTCTGAAAAGTCTTAAGAAAATCTTCTCACTTCTCTGACAGAGACTGGCGCGG 1299
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 Db 1300 ACAGGAAGACAAAGGCGGTGCAAAAGGCGGCTGTCGGGTGGGTGGATGGCATGTA 1359
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 QY 1141 ACAGAACCCCGCGAAATCTCTGAGAGACACCGTGTACAGAGGCGGTTGATACCGAG 1200
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 Db 1419 ACAGAACCCCGCGAAATCTCTGAGAGACACCGTGTACAGAGGCGGTTGATACCGAG 1478
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 QY 1201 CTGAGGTAGAAAAAGCTCTCGAGAAAGGAGAGAGATCATGACCGCGAGAGTGGAC 1260
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 Db 1479 CTGAGGTAGAAAAAGCTCTCGAGAAAGGAGAGAGATCATGACCGCGAGAGTGGAC 1538
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 Db 1539 CTGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1598
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 QY 1321 CAGCATACGGCAATGTACACAAATACGCCCTGGGACAGACAGAGAGAGAGAGAC 1380
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Db 1599 CAGCATACGGCAATGTACACAAATACGCCCTGGGACAGACAGAGAGAGAGAC 1658
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 Db 1659 AGAGAAAAAGAAAAACACAGCATGAGAAACACAGTAATGAATAAACCATTAATTTAG 1718
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 QY 1441 CCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
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 Db 1839 CTGCTTAAAGAAAGACCATTAATGCTTACAGAGTAAATTAATTAATTAATTAATTA 1897
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 RESULT 7
 ABR33543
 ID ABR33543 standard; cDNA: 1524 BP.
 XX
 AC ABR33543;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE cDNA encoding human PRO protein, Seq ID No 15.
 XX
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200208288-A2.
 XX
 PD 31-JAN-2002.
 XX
 PE 29-JUN-2001; 2001WO-US21066.
 XX
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US23325.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001WO-US17092.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI: 2002-172001/22.
 DR P-PSDB: AAB83599.
 XX

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Db 1000 TTTTGTAAAGCCCTCCAGTGTCCATTCATCCCTGATGGGGCATAGTTGAGACTGCAGA 1059
QY 781 GTGAGAGTACGTTTCTTAGGGCTGGAGGGGCACTTCCCACTCAAGCTCCCTCGCTTG 840
Db 1060 GTGAGAGTACGTTTCTTAGGGCTGGAGGGGCACTTCCCACTCAAGCTCCCTCGCTTG 1119
QY 841 ACATTCAAACTTCATGCTCTGAAAAACCATTCCTCTGACAGCAAAATTTGGCTTTCGGGC 900
Db 1120 ACATTCAAACTTCATGCTCTGAAAAACCATTCCTCTGACAGCAAAATTTGGCTTTCGGGC 1179
QY 901 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTTGAAGCTGGGCTCGGCT 960
Db 1180 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTTGAAGCTGGGCTCGGCT 1239
QY 961 CCGCTCTGAAAAGTGTCTTAAAGAAAATCTTCTAGTCTCTTGGACAGAGACTGGGCGGG 1020
Db 1240 CCGCTCTGAAAAGTGTCTTAAAGAAAATCTTCTAGTCTCTTGGACAGAGACTGGGCGGG 1299
QY 1021 ACGCGAAGAGCAAGCGGGGCTGACACAAAGCGGGGCTGCTGGTGGTGGAGTGGCCATGTA 1080
Db 1300 ACGCGAAGAGCAAGCGGGGCTGACACAAAGCGGGGCTGCTGGTGGTGGAGTGGCCATGTA 1359
QY 1081 CCGCGAGGCGCTCTCTGCTGCTGGGCTCTGACAGCAGCGGCGGACAGACACTTTC 1140
Db 1360 CCGCGAGGCGCTCTCTGCTGCTGGGCTCTGACAGCAGCGGCGGACAGACACTTTC 1418
QY 1141 ACGAACCACCGCGGCACTGCTGCGAGGACACCGGTATACAGAGCGGGTGTATACCGGAG 1200
Db 1419 ACGAACCACCGCGGCACTGCTGCGAGGACACCGGTATACAGAGCGGGTGTATACCGGAG 1478
QY 1201 CTGAGGTAGAAAACGCTCTCGAGAGAGGGGAGAGGATCATGTACGCCCGGAGTAGGAC 1260
Db 1479 CTGAGGTAGAAAACGCTCTCGAGAGAGGGGAGAGGATCATGTACGCCCGGAGTAGGAC 1538
QY 1261 CTCGTCAGAGTGTGTGGTGGTGGGCTGGCCGACCATGATCTCCCAATCTGTTGGCATC 1320
Db 1539 CTCGTCAGAGTGTGTGGTGGTGGGCTGGCCGACCATGATCTCCCAATCTGTTGGCATC 1598
QY 1321 CAGCATAGGCGCAATGTCTACAAACATAGCCCTGGGCGAGACAGAGGAGGAGGAGAC 1380
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Db 1659 AGAGAAAAGAAAACACAGCATGAGAACACAGTAATGAATGAATGAATGAATGAATGA 1718
QY 1441 CCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Db 1719 CCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1778
QY 1501 CAGCTTCTTTTGGCACAAGAGAGAGATTAACACTGTTTCAACCCGGGAGGATTTGG 1560
Db 1779 CAGCTTCTTTTGGCACAAGAGAGAGATTAACACTGTTTCAACCCGGGAGGATTTGG 1838
QY 1561 CTGCTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAATTTTAAAAA 1619
Db 1839 CTGCTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAATTTTAAAAA 1897

```

RESULT 6
ABLA0352 standard; cDNA; 1897 BP.

ABLA0352;
28-JUN-2002 (first entry)
Ovarian carcinoma O1034C/0591S consensus nucleotide sequence.
Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
Homo sapiens.

```

XX Key Location/Qualifiers
FH CDS 260..685
FT /tag- a
FT /product= "Ovarian carcinoma protein O1034C/0591S"
XX
XX US200204491-A1.
XX
XX 10-JAN-2002.
XX
XX 03-APR-2001; 2001US-0825294.
XX
XX 10-SEP-1999; 99US-0394374.
XX 01-MAY-2000; 2000US-0561778.
XX 15-AUG-2000; 2000US-0640173.
XX 07-SEP-2000; 2000US-0656668.
XX 14-NOV-2000; 2000US-0713550.
XX
XX (XUJ/) XU J.
XX (STOL/) STOLK J A.
XX (ALGA/) ALGATE P A.
XX (FLIN/) FLING S P.
XX
XX Xu J, Stolk JA, Algate PA, Fling SP;
XX
XX WPI: 2002-171027/22.
XX P-PSDB: ABB09417.
XX
XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX prevention and/or treatment of cancer, especially ovarian cancer -
XX
XX Claim 1a: Page 127-128; 131pp; English.
XX
XX The invention relates to ovarian tumour polynucleotides and polypeptides
XX that may be utilised in cancer therapy, for example in a vaccine or
XX gene therapy. Polypeptides and polynucleotides of the invention are
XX useful for detecting a cancer in a patient, for stimulating and/or
XX expanding T-cells specific for a tumour protein, and for inhibiting the
XX development of a cancer in a patient. They are also useful for
XX stimulating an immune response in a patient, and for treating a cancer in
XX a patient and for determining the presence of a cancer in a patient.
XX The isolated polynucleotides of the invention are useful for their
XX ability to selectively form duplex molecules with complementary stretches
XX of the entire desired gene or gene fragments, with designing and
XX preparing ribozyme molecules for inhibiting expression of tumour
XX polypeptides in tumour cells. Polypeptides and polynucleotides of the
XX invention are also useful in recombinant DNA molecules to direct
XX expression of a polypeptide in appropriate host cells. The current
XX sequence represents the ovarian carcinoma O1034C/0591S consensus
XX nucleotide sequence.
XX
XX SO Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other:
XX
XX Query Match 86.2%; Score 1396; DB 24; Length 1897;
XX Best local similarity 99.8%; Pred. No. 0;
XX Matches 1616; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
XX
XX QY 1 GCGAAGTCTTTGGGATGTTGTTCTGCTTCCAGGCTTTGGCGTCAATTCAGTGTACCA 60
XX DB 280 GCGAAGTCTTTGGGATGTTGTTCTGCTTCCAGGCTTTGGCGTCAATTCAGTGTACCA 339
XX
XX QY 61 GTGTGAAGATTCACCTCAACAGACAGTGTCTGCTTCCAGGCTTTGGCGTCAATTCAGTGTACCA 120
XX DB 340 GTGTGAAGATTCACCTCAACAGACAGTGTCTGCTTCCAGGCTTTGGCGTCAATTCAGTGTACCA 399
XX
XX QY 121 GGTGAAGCTTCAAGACATGTGTGAGAAAGAGTGAAGCAAGTGGCGGATCATGTA 180
XX DB 400 GGTGAAGCTTCAAGACATGTGTGAGAAAGAGTGAAGCAAGTGGCGGATCATGTA 459
XX
XX QY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTGTATGCTTGGCGGATCATGCTT 240
XX DB 460 CCGCAAGTCTGTGATCATCAGCGGCTGTGTATGCTTGGCGGATCATGCTT 519

```

Db	901	CTGAGTTGGGCTCTAGTGAAGTCTGACAGACTGAAAGTACGTGGGACCTTTAAGACTGTGGGCTCGGCT	960
Qy	961	CGCTCTGAAAAGTGTCTTAAAGAAAATCTTCTCACTTCTCTTGCAGAGACTGTGGCGCGG	1020
Db	961	CGCTCTGAAAAGTCTTAAAGAAAATCTTCTCACTTCTCTTGCAGAGACTGTGGCGCGG	1020
Qy	1021	ACGGGAAGAGCAACGGGCGCTGTGCACAAAGCGGGCGCTGTGCGGTGGTGGAGTCCGATGA	1080
Db	1021	ACGGGAAGAGCAACGGGCGCTGTGCACAAAGCGGGCGCTGTGCGGTGGTGGAGTCCGATGA	1080
Qy	1081	CGGCGACGGCGCTTCTCGTGGTTGGCGTGTCTGACGACAGCGCGGACGACAGACTTTGC	1140
Db	1081	CGGCGACGGCGCTTCTCGTGGTTGGCGTGTCTGACGACAGCGCGGACGACAGACTTTGC	1140
Qy	1141	ACGGAACCCCGCGGAACCTCTCGAGAGACACCTGTGTACAGAGCGGGTGTGATGCACAG	1200
Db	1141	ACGGAACCCCGCGGAACCTCTCGAGAGACACCTGTGTACAGAGCGGGTGTGATGCACAG	1200
Qy	1201	CTGAGGTAGAAAAAGTCTCTCGAAGAGGGGAGGAGTATGATAGCCCGGAAGTAGAGAC	1260
Db	1201	CTGAGGTAGAAAAAGTCTCTCGAAGAGGGGAGGAGTATGATAGCCCGGAAGTAGAGAC	1260
Qy	1261	CTCTGTCAGTGTGTCTTGGGTTTGGCGGACGCTATCTCTCCGANTCTGGTTGGGCATC	1320
Db	1261	CTCTGTCAGTGTGTCTTGGGTTTGGCGGACGCTATCTCTCCGANTCTGGTTGGGCATC	1320
Qy	1321	CAGCATACGGCCAAATGTCAACAACATAGCCCTGGGCGACACAGACAGAGGAGAGAC	1380
Db	1321	CAGCATACGGCCAAATGTCAACAACATAGCCCTGGGCGACACAGACAGAGGAGAGAC	1380
Qy	1381	AGAGAAAAGAAAAACACAGCATGAGAAACACAGTAAATGAATAAACCATAAATATTTAG	1440
Db	1381	AGAGAAAAGAAAAACACAGCATGAGAAACACAGTAAATGAATAAACCATAAATATTTAG	1440
Qy	1441	CCCCCTGTTTCTGTGTACTGTGACGAGGAATGTGTCAATTTTTCAGTGTGGACTGA	1500
Db	1441	CCCCCTGTTTCTGTGTACTGTGACGAGGAATGTGTCAATTTTTCAGTGTGGACTGA	1500
Qy	1501	CAGCTTCTTTTGGCCACAGGACAGAGAAATTTTAACTGTTCCTTCAACCCCGGGGAGTTGG	1560
Db	1501	CAGCTTCTTTTGGCCACAGGACAGAGAAATTTTAACTGTTCCTTCAACCCCGGGGAGTTGG	1560
Qy	1561	CTGTGCTTAAAGAACACCATTAATAGCTTTAGACAGTGTAAAAAAGAAAAAAGAAAAA	1619
Db	1561	CTGTGCTTAAAGAACACCATTAATAGCTTTAGACAGTGTAAAAAAGAAAAAAGAAAAA	1619
RESULT 5			
ABT03284			
ID	ABT03284	standard; cDNA; 1897 BP.	
XX	ABT03284;		
AC			
XX	05-SEP-2002 (first entry)		
DT			
DE	Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.		
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XX	Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;:		
KM	cytostatic; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200239885-A2.		
XX			
PD	23-MAY-2002.		
XX			
PF	13-NOV-2001; 2001WO-US45395.		
XX			
PR	14-NOV-2000; 2000US-0713550.		
PR	03-APR-2001; 2001US-0825294.		
PR	02-OCT-2001; 2001US-0970966.		
PA	(CORI-) CORIXA CORP.		

XX Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
PI
XX
XX WPI: 2002-500186/53.
DR
XX
XX Novel ovarian cancer polypeptide and polynucleotide, useful for
PT detecting the presence of ovarian cancer in a patient, and in
PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
PT
XX
XX
PS Claim 2: Page 196; 197pp; English.
XX
XX The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention.
XX
XX Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other;
50

Query Match	Best Local Similarity	Score	ID	Length
86.2%	99.8%	1396	DB 24	1897
Matches 1616; Conservative 0; Mismatches 2; Indels 1; Gaps 1				
QY	1	GGCAACTTTTGGGGATTTGTTCTTGGCTTCACAGCTTTGCGCTGCAAAATTCAGTGTCCACCA	60	
DB	280	GGCAACTTTTGGGGATTTGTTCTTGGCTTCACAGCTTTGCGCTGCAAAATTCAGTGTCCACCA	339	
QY	61	GTTGGAAGAAATTCAGCTGACACAGCAGCTGCTCCGCCGAGTTTCATTTGAAATTGAC	120	
DB	340	GTTGGAAGAAATTCAGCTGACACAGCAGCTGCTCCGCCGAGTTTCATTTGAAATTGAC	399	
QY	121	GGTAAAGCTTCAAGACATGTGTTCAGAAANAATGATGAGCAAAAGTCCCGGAGATCATGTA	180	
DB	400	GGTAAAGCTTCAAGACATGTGTTCAGAAANAATGATGAGCAAAAGTCCCGGAGATCATGTA	459	
QY	181	CCGGAATCTCTGTGATCATCAGCGGCGTGTCTCATTCGCTCTCGCGGATACAGTCTT	240	
DB	460	CCGGAATCTCTGTGATCATCAGCGGCGTGTCTCATTCGCTCTCGCGGATACAGTCTT	519	
QY	241	CTMGTCCTCCACAGGGAACCTGAATCTCAATTTGCATCAGCTGTGCAACAACCCCTCTTTGAA	300	
DB	520	CTMGTCCTCCACAGGGAACCTGAATCTCAATTTGCATCAGCTGTGCAACAACCCCTCTTTGAA	579	
QY	301	CGGGCCCAAGGCCCAAGAAAGGGGAAGTTCTGCTCGGCGCTCAGGCCAGGGCTCGGCAC	360	
DB	580	CGGGCCCAAGGCCCAAGAAAGGGGAAGTTCTGCTCGGCGCTCAGGCCAGGGCTCGGCAC	639	
QY	361	CACATCTCTGTCTCAAAATTAACCCCTCTTTCGGGCACACAGCTGAAGCTGAAGCAATG	420	
DB	640	CACATCTCTGTCTCAAAATTAACCCCTCTTTCGGGCACACAGCTGAAGCTGAAGCAATG	699	
QY	421	CCACCCCTCTGATGATTTCTTCCAGGCCCTGCGCCCAACCCCCACCTCCCTGATGTA	480	
DB	700	CCACCCCTCTGATGATTTCTTCCAGGCCCTGCGCCCAACCCCCACCTCCCTGATGTA	759	
QY	481	GTTTCTCTGGGTGCTCTTATTTCTGGGTAGGGAAGCGGAGTCCGTCTCTTTTGT	540	
DB	760	GTTTCTCTGGGTGCTCTTATTTCTGGGTAGGGAAGCGGAGTCCGTCTCTTTTGT	819	
QY	541	CCGTGCAAAATTAATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGACTAAT	600	
DB	820	CCGTGCAAAATTAATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGACTAAT	879	
QY	601	TTTTCAGTATGACTTGAAGGAAGAGGTGAGTGAAGATCACCCCAATGTCTGTGAAC	660	
DB	880	TTTTCAGTATGACTTGAAGGAAGAGGTGAGTGAAGATCACCCCAATGTCTGTGAAC	939	
QY	661	CGGAGTCAAGGCCAGGCTGCGCAGAGTCAGTCTCTTGAAGTCACTGAGTGGGCACTTCC	720	
DB	940	CGGAGTCAAGGCCAGGCTGCGCAGAGTCAGTCTCTTGAAGTCACTGAGTGGGCACTTCC	999	
QY	721	TTTTGTAAAGCTTCAGTGTCAATTCATCCCTGATGGGGGATAGTTTGAGACTGACA	780	

DE Ovarian carcinoma sequence isolate 57887 extended cDNA.
XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
KM ss.
XX Homo sapiens.
OS
XX US2002004491-A1.
PN
XX 10-JAN-2002.
PD
XX
XX 03-APR-2001; 2001US-0825294.
PF
XX 10-SEP-1999; 9905-0394374.
PR 01-MAY-2000; 2000US-0561778.
PR 15-AUG-2000; 2000US-0640173.
PR 07-SEP-2000; 2000US-0656668.
PR 14-NOV-2000; 2000US-0713550.
XX
XX (XUJ/) XU J.
PA (STOL/) STOLK J A.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PI XU J, Stolk JA, Algate PA, Fling SP;
XX WPI; 2002-171027/22.
XX
XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
PT prevention and/or treatment of cancer, especially ovarian cancer -
XX
XX Claim 1a; Page 119-120; 131pp; English.
XX
XX The invention relates to ovarian tumour polynucleotides and polypeptides
CC that may be utilised in cancer therapy, for example in a vaccine or
CC gene therapy. Polypeptides and polynucleotides of the invention are
CC useful for detecting a cancer in a patient, for stimulating and/or
CC expanding T-cells specific for a tumour protein, and for inhibiting the
CC development of a cancer in a patient. They are also useful for
CC stimulating an immune response in a patient, and for treating a cancer in
CC a patient and for determining the presence of a cancer in a patient.
CC The isolated polynucleotides of the invention are useful for their
CC ability to selectively form duplex molecules with complementary stretches
CC of the entire desired gene or gene fragments, and for designing and
CC preparing ribozyme molecules for inhibiting expression of tumour
CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
CC invention are also useful in recombinant DNA molecules to direct
CC expression of a polypeptide in appropriate host cells. The current
CC sequence represents the extended cDNA sequence of ovarian carcinoma
CC isolate 57887 given in record ABL48956.
XX
XX
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Query Match 100.0%; Score 1619; DB 24; Length 1619;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GGCACATTTTGGGAGATGTTCTTCTCCAGAGCTTGGCGTGAACATCAGTGTACCA 60
QY 61 GTGTGAAGATTCACAGTGAACAGACATGCTCTCCCGGAGTTTCATTTGTAATTCAC 120
DB 61 GTGTGAAGATTCACAGTGAACAGACATGCTCTCCCGGAGTTTCATTTGTAATTCAC 120
QY 121 GTGTGAAGATTCATGTGTGAGAAAGATGATGAGCAAGTCCGGGATCATGTA 180
DB 121 GTGTGAAGATTCATGTGTGAGAAAGATGATGAGCAAGTCCGGGATCATGTA 180
QY 181 CCGCAAGTCTGTGATCATCAAGCGGCTGTCTCATCGCTCTGCGGGTACCAAGTCTT 240
DB 181 CCGCAAGTCTGTGATCATCAAGCGGCTGTCTCATCGCTCTGCGGGTACCAAGTCTT 240

QY 241 CTGCTCCCGAGGAAAGTCACTAGTTTGCATCAGCTGCTGCAACACCCCTTTGTAA 300
DB 241 CTGCTCCCGAGGAAAGTCACTAGTTTGCATCAGCTGCTGCAACACCCCTTTGTAA 300
QY 301 CGGGCCAAAGGCGCCAAAGAAAGGGAAGTTCCTGCGGCTCAGGCGAGGCTCCGCAC 360
DB 301 CGGGCCAAAGGCGCCAAAGAAAGGGAAGTTCCTGCGGCTCAGGCGAGGCTCCGCAC 360
QY 361 CACCATCTGTTCTCAATATGAGCTCTTCTGCGCACACGCTGGAAGTGAAGAGATG 420
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QY 421 CCACCCCTCTCGATTTGTTCTCCAGCCCTCCGCCCAACCCCACTCCCTGATGA 480
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QY 481 GTTCTTCTGCGGTGCTCTTTATTTCTGGGTAGGAGGCGGAGTCCGTTCTTTGTT 540
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QY 1261 CTGCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
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XX 14-NOV-2000; 2000US-0713550.
PR 03-APR-2001; 2001US-0825294.
PR 02-OCT-2001; 2001US-0970966.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX WPI: 2002-500186/53.
XX
XX Novel ovarian cancer polypeptide and polynucleotide, useful for
XX detecting the presence of ovarian cancer in a patient, and in
XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
XX
XX
XX Claim 2: Page 195; 197pp: English.
XX
XX The present invention provides human ovarian cancer associated proteins
XX and coding sequences. The sequences can be used in the diagnosis and
XX treatment of ovarian cancers. The present sequence is a coding sequence
XX of the invention.
SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other:
Query Match 100.0%; Score 1619; DB 24; Length 1619;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GGCACATTTTGGCGATTTCTTCTGCTCCAGGCTTGGCGTCAATTCAGTCTACCA 60
QY 61 GTGTGAAGAAATTCACGCTGACACAGACGCTGCTCCCGGCTCAATTCAGTCTAC 120
DB 61 GTGTGAAGAAATTCACGCTGACACAGACGCTGCTCCCGGCTCAATTCAGTCTAC 120
QY 121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAATGCGGAGTATGTA 180
DB 121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAATGCGGAGTATGTA 180
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QY 1021 ACAGGAGAGGCAAGGCGGCTGCAAAAGGCGGCTGCTGCTGCTGCTGCTGCTGCT 1080
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QY 1081 CGCGAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
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QY 1201 CTGAGTGAAGAAAGCTCTCGAGAAAGGAGAGATGATGATGATGATGATGATGAT 1260
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RESULT 3
ABL40345
ID ABL40345 standard; cDNA; 1619 BP.
XX ABL40345;
XX
XX 28-JUN-2002 (first entry)
XX

PT detecting the presence of ovarian cancer in a patient, and in
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
 PT
 XX
 PS Claim 2: Page 189-190; 197PP; English.

XX The present invention provides human ovarian cancer associated proteins
 CC and coding sequences. The sequences can be used in the diagnosis and
 CC treatment of ovarian cancers. The present sequence is a coding sequence
 CC of the invention.

XX Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 100.0%; Score 1619; DB 24; Length 1619;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGGATGTTGCTTCTGCTCAGGCTTGGCTGCAAAATCAGTGTACCA 60
 DB 1 GGCACCTTTTGGGATGTTGCTTCTGCTCAGGCTTGGCTGCAAAATCAGTGTACCA 60
 QY 61 GTGTGAAGATTCAGGCTGAACAGACGCTGCTCCGCCAGTTGATTTGATTTGAC 120
 DB 61 GTGTGAAGATTCAGGCTGAACAGACGCTGCTCCGCCAGTTGATTTGATTTGAC 120
 QY 121 GGTGAACCTTCAAGACATGTCAGAAAGAGATGATGAGCAAAAGTCCGGATCATGTA 180
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 DB 301 CCGGCGCAAGGCGCCCAAGAAAGGGAAGTTCTGCTGCGGCTCAGGCGGCTCCGAC 360
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 DB 841 ACATTCAAACTTCATGCTCCTGAAGAACCATTTCTGCGAGAGAAATGGCTGTTGCGCC 900
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 DB 1561 CTGCTTGAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAATTAATTAATTAATTAAT 1619

RESULT 2

ABT03281
 ID ABT03281 standard; cDNA; 1619 BP.

XX AC ABT03281;

XX DT 05-SEP-2002 (first entry)

XX Human ovarian carcinoma associated coding sequence SEQ ID NO: 211.

XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

XX cytosolic; gene; ss.

XX Homo sapiens.

XX MO200239885-A2.

XX PD 23-MAY-2002.

XX PF 13-NOV-2001; 2001WO-US45395.

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 15:03:08 ; Search time 318.774 Seconds
(without alignments)
11437.514 Million cell updates/sec

Title: US-09-970-966-211

Perfect score: 1619

Sequence: 1 ggcacatttcgcgattgt.....aaaaaaaaaaaaaaaaaaaa 1619

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 10

Total number of hits satisfying chosen parameters: 1309984

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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7	1264	78.1	1524	24	ABK33543
8	1205	74.4	1953	21	AAF22400
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C	10	1149	71.0	2528	22	AAD18690	Human G protein co
C	11	1030	63.6	1608	24	ABQ54231	Human ovarian anti
C	12	1014	62.6	1890	22	ABQ38445	Human CDNA encodin
C	13	486	30.0	625	24	ABT03280	Human ovarian carc
C	14	486	30.0	625	24	ABT03280	Human ovarian carc
C	15	486	30.0	625	24	ABT03280	Human ovarian carc
C	16	386	23.8	1362	24	ABT03279	Human ovarian carc
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C	18	366	22.6	587	22	ABT03279	Human ovarian carc
C	19	364	22.5	444	22	AAH50766	Primer specific fo
C	20	315	19.5	369	22	AAH50766	Human tumour assoc
C	21	315	19.5	369	22	AAH50766	Human ovarian carc
C	22	315	19.5	369	22	AAH50766	Human ovarian carc
C	23	315	19.5	369	22	AAH50766	Human ovarian carc
C	24	310	19.1	396	22	ABT03085	Human ovarian carc
C	25	310	19.1	396	22	ABT03085	Human ovarian carc
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C	31	250	15.4	591	22	AAH50766	Primer specific fo
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C	36	125	7.7	381	24	ABT03283	Human ovarian carc
C	37	120	7.4	430	24	ABT03283	Human ovarian carc
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ALIGNMENTS

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AC	ABT03277	
DT	05-SEP-2002	(first entry)
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KW		Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
KW		cytostatic; gene; ss.
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OS		Homo sapiens.
XX		
PN	WO200239885-A2.	
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PD	23-MAY-2002.	
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PF	13-NOV-2001; 2001WO-US45395.	
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PR	14-NOV-2000; 2000US-0713550.	
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XX	02-OCT-2001; 2001US-0970966.	
PA	(CORI-) CORIXA CORP.	
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PI	Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;	
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DR	WPI; 2002-500186/53.	
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PT	Novel ovarian cancer polypeptide and polynucleotide; useful for	

264

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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Job time : 6567.22 secs

RESULT 45
AC005250/c 94336 bp DNA linear PRI 01-MAR-2002
LOCUS Homo sapiens BAC clone CTA-318M5 from 7q22, complete sequence.
DEFINITION AC005250
AC005250.1 GI:3287719
VERSION HTG.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 94336)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 94336)
AUTHORS Courtney, L., Nelson, J., Mohlmann, P., Bauer, C. and Morris, M.
TITLE The sequence of Homo sapiens BAC clone CTA-318M5
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 94336)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-JUL-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 4 (bases 1 to 94336)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 5 (bases 1 to 94336)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: saplens@wustl.wustl.edu
----- Summary Statistics -----
Center project name: H_RG318M05

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/CTB/CHR7>, send mailto:egreen@nhgri.nih.gov, or see <http://genome.wustl.edu/gsc>
SOURCE INFORMATION:
Clone CTA-318M5 is from a release of the human BAC library CTTB-HS-A. The library contains cloned DNA from human sperm. See:

FEATURES

SOURCE

Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (<http://www.resgen.com>).
VECTOR: pBelOBAC11
Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:

Actual start of this clone is at base position 1 of CTA-318M5; actual end is at base position 94336 of CTA-318M5.

Location/Qualifiers

1..94336
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
/map="7q22"
/clone="CTA-318M5"
/clone_id="CTTB-HS-A"
5..251
/rpl_family="L1"
395..531
/rpl_family="L1"
547..1005
/rpl_family="ERV1"
742..1162
/note="match to EST BE160466 (NID:g8623187)"
1171..1313
/note="match to EST BG167998 (NID:g12674701)"
1176
/note="match to EST BE160466 (NID:g8623187)"
1650..1772
/rpl_family="MIR"
1773..2057
/rpl_family="Alu"
2058..2157
/rpl_family="MIR"
2067..2438
/note="match to EST A1590771 (NID:g4599819) tw25c03.x1"
2369..2499
/rpl_family="GA-rich"
2702..2810
/rpl_family="(TA)n"
2901..2940
/rpl_family="MIR"
2941..3043
/rpl_family="U6"
3044..3331
/rpl_family="L1"
3215..3253
/rpl_family="(TG)n"
3572..3720
/rpl_family="CRL"
3686..3851
/note="match to EST BF811896 (NID:g12141104)"
3940..3963
/rpl_family="(T)n"
5812..5897
/rpl_family="L2"
5898..6176
/rpl_family="Alu"
6177..6298
/rpl_family="L2"
6241..6783
/note="match to EST A1860282 (NID:g5513898) w101b11.x1"
6443..6717
/rpl_family="MIR"
6784..6804
/rpl_family="AT-rich"
6795..6846
/rpl_family="Alu"
6847..7842
/rpl_family="ERVK"
7843..8080
/rpl_family="Alu"

AUTHORS
TITLE
JOURNAL

Strausberg, R.
Direct Submission
Submitted (11-Jul-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
Contact: amadan@systemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

FEATURES

source

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAC Plate: 34 Row: 0 Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.

Location/Qualifiers

CDS

1..3889
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:26926 IMAGE:4838423"
/tissue_type="Testis"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Vector: pBluescript"
384..1532
/codon_start=-1
/product="Similar to RIKEN CDNA 0610013117 gene"
/protein_id="AAH34500.1"
/db_xref="GI:21759791"
/translation="MEWTFKEMFLERFLPTIKMSDLSDHDLGVFKSHLVVTP
YAFILIRVREKRVASPLAKSGIKETVKKYVPPNYLVEFPHSTROPLOTITGL
AKKNLTROYERFRSRNRDERSLKFOEDACWGRFAFLITAGIAFLDKRWLTD
LMEWANGIPKQPLPSQIWTYILMSFVWSLLFRLGDKRDLAHIHHLAISLM
SEWCANIRSGTLVMIADVADIMLESKAFMSYAGWTCNTLFEFFSTFFISRI
VPEWILCTLILPMYHLEPFYSIFLNLQIMLOVLIWGYIILKMLNCIPMKSI
ODVRSDDDYEEEEEETKEMDCLKNGIGAERHLIPNGOHG"

BASE COUNT
ORIGIN

1072 a 860 c 859 g 1098 t

Query Match 1.6%; Score 26; DB 9; Length 3889;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1594 CAGCTGTAATAAAAAAAAAAAAAA 1619
Db 3844 CAGTGTAAAAAATAAAAAAAAAA 3869

RESULT 44
AF044209 7940 bp mRNA linear PRI 01-SEP-1998
LOCUS Homo sapiens nuclear receptor co-repressor N-COR mRNA, complete
DEFINITION cds.
AF044209
VERSION AF044209.1 GI:3510602
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
Mang, J., Hoshino, T., Redner, R.L., Kajiyaya, S. and Liu, J.M.
ETC, fusion partner in t(8;21) acute myeloid leukemia, represses

REFERENCE
AUTHORS
TITLEJOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

complex
Proc. Natl. Acad. Sci. U.S.A. 95 (18), 10860-10865 (1998)
98393736
9724795
2 (bases 1 to 7940)
REFERENCE
Mang, J. and Liu, J.M.
Direct Submission
Submitted (22-JAN-1998) Hematology Branch, National Heart, Lung and
Blood Institute, Bldg. 10, Rm. 7C103, 9000 Rockville Pike,
Bethesda, MD 20892, USA

FEATURES

source

CDS

1..7940
/organism="Homo sapiens"
/db_xref="taxon:9606"
241..7563
/codon_start=-1
/product="nuclear receptor co-repressor N-COR"
/protein_id="AAC33550.1"
/db_xref="GI:3510603"

BASE COUNT
ORIGIN

2437 a 1942 c 1894 g 1667 t

Query Match 1.6%; Score 26; DB 9; Length 7940;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1594 CAGCTGTAATAAAAAAAAAAAAAA 1619
Db 7909 CAGTGTAAAAAATAAAAAAAAAA 7934

```

REFERENCE 1 (bases 1 to 1409)
AUTHORS Eshei, D., Prusky, D. and Dimoor, A.
TITLE Exoglucanase of Alternaria alternata
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1409)
AUTHORS Eshei, D., Prusky, D. and Dimoor, A.
TITLE Direct Submission
JOURNAL Submitted (09-AUG-1999) Postharvest Sciences, Volcani Center, POB 6, Bet-Dagan 50250, Israel

FEATURES
source
1. 1409
/organism="Alternaria alternata"
/db_xref="taxon:5599"
1. 1409
/gene="C1"
4. 1275
/gene="C1"
/codon_start=1
/product="exoglucanase"
/protein_id="AA05699.1"
/db_xref="GI:6179889"
/translation="MTWQSTKAGSCNKNKIVIDANWRLHKKEGYDNCYTNEMD
ATACPDNKAACANCAVDGADYSGYGTAGSNLSLKPTKGSYSTNGSRITLMKRD
TTEWKEFTGNOEFTPDVDVSNLPCGFCGALFYVSMADGLKRYSTNKAAGKCTGY
CDACCPRLKRTKINGENYEGKRPSSNDANAGVGHSCCAEMDIWENASTATPES
CSTTEQSKDSDGCGGTISADRTAGVCDPCDGNSTRMGVKDFYGGKTVDSKRTF
VTFQFTGDMETIKRFYVQNGKTIADPASPAPVEGNSITTKCDQOKAVFGPTTF
KDKGAMMAKALANGVLMVSLMDHYSNNLMDSTYPTDKNPDITDLGTRGECETS
SGVPADVPSQHADATVYVSNIKFGLPNTFC"

BASE COUNT 393 a 325 c 382 g 309 t

Query Match 1.6%; Score 26; DB 8; Length 1409;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1594 CAGGTGTAATAAAAAAAAAAAAAA 1619
DB 1383 CAGGTGTAATAAAAAAAAAAAAAA 1408

RESULT 41
LOCUS AX056994 2481 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 11 from Patent WO0075340.
ACCESSION AX056994
VERSION AX056994.1 GI:12309857
KEYWORDS
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 2481)
REFERENCE Butler, K.H., Farnodu, O.O., Gutteridge, S. and Maxwell, C.A.
AUTHORS Magnesium chelate
TITLE Patent: WO 0075340-A 11 14-DEC-2000;
JOURNAL E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES
source
1. 2481
/organism="Glycine max"
/db_xref="taxon:3847"

BASE COUNT 783 a 489 c 589 g 620 t

Query Match 1.6%; Score 26; DB 6; Length 2481;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1594 CAGGTGTAATAAAAAAAAAAAAAA 1619
DB 2424 CAGGTGTAATAAAAAAAAAAAAAA 2449

```

```

RESULT 42
LOCUS AF514845
DEFINITION Rana catesbeiana epithelial sodium channel ENac beta subunit mRNA, complete cds.
ACCESSION AF514845
VERSION AF514845
KEYWORDS AF514845.1 GI:21435743
SOURCE bullfrog.
ORGANISM Rana catesbeiana
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;
Agarana.
REFERENCE 1 (bases 1 to 2745)
AUTHORS Jensik, P.J., Holbird, D. and Cox, T.
TITLE Cloning and partial characterization of an amiloride-sensitive sodium channel (fEnac) from adult bullfrog skin
JOURNAL J. Comp. Physiol. B, Biochem. Syst. Environ. Physiol. (2002) In press
2 (bases 1 to 2745)
REFERENCE Jensik, P.J., Holbird, D. and Cox, T.
AUTHORS Direct Submission
TITLE Submitted (22-MAY-2002) Physiology, Southern Illinois University, 1135 Lincoln Drive, Carbondale, IL 62901, USA
JOURNAL location/Qualifiers
1. 2745
/organism="Rana catesbeiana"
/db_xref="taxon:8400"
/tissue_type="skin epithelium"
168. 2135
/codon_start=1
/product="epithelial sodium channel ENac beta subunit"
/protein_id="AA053958.1"
/db_xref="GI:21435744"
/translation="MTTISNISHSEVMKRTKRLFTTRALHMQKPGYTYELLWVF
CMMNTNTHGPKRIYSEGPKRKRYVMFILLTFLAALVFWQMGVVIOTLYSGVSYLSIGF
NEMWFPAYVCVNVNPPKRYKVKHLHLDLQVDTALDRIOFSSQSGIPANNINON
VTLDPSLMNMPFLVVIDEHPNNTIYVNFSDSTDSOINNTKGNQFAPARYVAI
ELCTNNRTOCSYENFTSGAVALKDWLYLQFNISFSTISPEEVKNGXQAEMLTLCMF
GGPCSYRNPTTHFHODYNGNCYTFNMGQSGQELBSANAGAFGLKAVLDITQKEIIP
FLOSTAAARITLHQRSFFPLADQGLIYAMPGETSIJAVLEDOTOHLKAVYSSCTVDGS
DIPVANAYISKFNSSYSIOCLRSCFQELMKCAVYLFPLNHAHYCNQEDPDWV
PCYVIMIDTVSHREOCINMCQPCNDNSNKTISMADMP5AAAEIMIFVLSEYDTS
LDITVRNDGIMRLNIYEEFENYRSISEPTNIVMLSLNMGQFGPMGSGVLCITTEF
GELLIDCMTITLIKLAWTRDRQKRRQYNDPPYVAELVAISNSGQFHDSDNOV
STRIPCTPPPNDSLRKQIDAIDVYSSDE"

BASE COUNT 853 a 381 c 545 g 766 t

Query Match 1.6%; Score 26; DB 5; Length 2745;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1594 CAGGTGTAATAAAAAAAAAAAAAA 1619
DB 2719 CAGGTGTAATAAAAAAAAAAAAAA 2744

RESULT 43
LOCUS BC034500
DEFINITION Homo sapiens, similar to RIKEN CDNA 0610013117 gene, clone
ACCESSION BC034500
VERSION BC034500.1 GI:21759790
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3889)

```

repeat_region	23117..23351	/note="L1M1 repeat: matches 1882..2493 of consensus"
misc_feature	join(23433..23587,23905..24080)	
repeat_region	/note="match: GSS: Em:A0745958"	
repeat_region	23646..24715	/note="L1MC repeat: matches 1115..2227 of consensus"
repeat_region	24716..25027	/note="AluX repeat: matches 1..312 of consensus"
repeat_region	25028..25409	/note="L1MC repeat: matches 743..1115 of consensus"
repeat_region	27260..27378	/note="L1M2 repeat: matches 5391..5471 of consensus"
repeat_region	27379..27683	/note="Aluub repeat: matches 2..312 of consensus"
repeat_region	27684..27829	/note="L1M2 repeat: matches 5471..5630 of consensus"
repeat_region	27830..27938	/note="L1M2 repeat: matches 6063..6166 of consensus"
misc_feature	complement(27908..28191)	
misc_feature	/note="match: GSS: Em:A0235270"	
gene	complement(27918..28199)	
gene	/note="match: GSS: Em:B74240"	
gene	join(27994..28372,28928..29009)	
CDS	join(27994..28372,28928..29009)	
	/note="DA446H13.2 (RPL23A (60S ribosomal protein 23A) pseudogene)	
	match: proteins: Sw:P29316 Sw:O07761 Tr:Q9TNR9 Tr:O48553 Sw:Q20647 Tr:O81229 Sw:O22644 Sw:P48162 Tr:O97118"	
	/pseudo	
	/codon_start=1	
misc_feature	/evidence=not_experimental	
misc_feature	complement(28093..28377)	
misc_feature	/note="match: GSS: Em:A0568541"	
misc_feature	complement(28133..28377)	
misc_feature	/note="match: GSS: Em:B6785"	
misc_feature	complement(28181..28377)	
misc_feature	/note="match: GSS: Em:A027573"	
misc_feature	28192..28375	
misc_feature	/gene="DA446H13.2"	
misc_feature	/note="match: GSS: Em:B16501"	
misc_feature	28192..28308	
misc_feature	/gene="DA446H13.2"	
misc_feature	/note="match: GSS: Em:A0178192"	
misc_feature	28200..28375	
misc_feature	/gene="DA446H13.2"	
misc_feature	/note="match: GSS: Em:A0164257"	
misc_feature	28202..28375	
misc_feature	/gene="DA446H13.2"	
misc_feature	/note="match: GSS: Em:A0036657"	
misc_feature	28221..28323	
misc_feature	/gene="DA446H13.2"	
misc_feature	/note="match: GSS: Em:A0145980"	
misc_feature	28264..28375	
misc_feature	/gene="DA446H13.2"	
misc_feature	/note="match: GSS: Em:A003673"	
misc_feature	join(28324..28371,28947..29064)	
misc_feature	/note="match: GSS: Em:A0178192"	
repeat_region	28376..28925	
repeat_region	/note="M17B repeat: matches 1..448 of consensus"	
repeat_region	29053..29152	
repeat_region	/note="25 copies 4 mer aag 76% conserved"	
repeat_region	29660..29707	
repeat_region	/note="8 copies 6 mer caccaca 87% conserved"	
repeat_region	29662..29705	
repeat_region	/note="11 copies 4 mer caca 90% conserved"	
repeat_region	30354..30466	
repeat_region	/note="L2 repeat: matches 2634..2746 of consensus"	
repeat_region	30874..30954	
repeat_region	/note="MIR repeat: matches 160..250 of consensus"	
repeat_region	31806..31957	
repeat_region	/note="MIR repeat: matches 52..207 of consensus"	

Query Match	Best Local Similarity	Score 26;	DB 8;	Length 1275;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY 1594 CAGTGTAAAAA	1619			
DB 1196 CAGTGTAAAAA	1221			
RESULT 40				
AF176571				
LOCUS	AF176571	1409 bp	mRNA	linear
DEFINITION	Alternaria alternata exoglucanase (cl1) mRNA, complete cds.			
ACCESSION	AF176571			
VERSION	AF176571.1			
KEYWORDS	Alternaria alternata			
SOURCE	Alternaria alternata			
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria; Alternaria alternata group.			

misc_feature 99368..110419 /note="assembly-fragment"
 misc_feature 110520..124151 /note="assembly-fragment"
 misc_feature 124252..141079 /note="assembly-fragment"
 misc_feature 141180..160980 /note="assembly-fragment"
 misc_feature 161081..185614 /note="assembly-fragment"
 misc_feature 185715..214411 /note="assembly-fragment"
 BASE COUNT 59577 a 46639 c 46482 g 59706 t 2007 others
 ORIGIN
 Query Match 1.7% Score 27; DB 2; Length 214411;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1593 ACAGTGTAAAAAAAAAAAAAAAAAAAA 1619
 Db 80773 ACAGTGTAAAAAAAAAAAAAAAAAAAA 80799
 RESULT 38
 AL133395/C
 LOCUS
 DEFINITION AL133395 217929 bp DNA linear PRI 22-DEC-2000
 Contains the 3' end of the gene for a novel protein similar to KIA1059 (ortholog of mouse VPS10 domain receptor protein SORCS), an RPL23A (60S ribosomal protein 23A) pseudogene, ESTs, STS and GSSs, complete sequence.
 AL133395
 VERSION AL133395.21 GI:10045255
 KEYWORDS HTG; KIAA1059; RPL23A; SORCS; VPS10 domain.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 217929)
 Bird.C.
 Direct Submission
 Submitted (11-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequests@sanger.ac.uk
 On Sep 9, 2000 this sequence version replaced gi:9943953.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
 Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at
 http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone compigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr10
 This sequence is the entire insert of clone RP11-446H13. The true left end of clone RP11-699H2 is at 128287 in this sequence. The true right end of clone RP11-41D21 is at 75932 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. RP11-446H13 is from the library RPLC1-11.2 constructed by the group of Pieter de Jong. For further details see
 http://www.chori.org/bacpac/home.htm
 VECTOR: pBACE3.6.

FEATURES
 source
 Location/Qualifiers
 1..217929
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="10"
 /clone="RP11-446H13"
 /clone_lib="RPLC1-11.2"
 1157..1438
 /note="Alusq repeat: matches 5..286 of consensus"
 1652..1703
 /note="Charlie3 repeat: matches 802..850 of consensus"
 1889..2188
 /note="AluY repeat: matches 9..308 of consensus"
 2471..2531
 /note="L1BP1 repeat: matches 5922..5979 of consensus"
 2532..2624
 /note="L1BP1 repeat: matches 6039..6151 of consensus"
 2628..2689
 /note="31 copies 2 mer aa 69% conserved"
 3591..4071
 /note="match: GSS: Em:AQ215368"
 3764..3816
 /note="L2 repeat: matches 2656..2708 of consensus"
 complement(4214..4593)
 /note="match: GSS: Em:AQ516952"
 4344..4687
 /note="MSRD repeat: matches 1..394 of consensus"
 4634..6643
 /note="MSRD-internal repeat: matches 7..1651 of consensus"
 6582..6771
 /note="MSRD repeat: matches 204..394 of consensus"
 8471..8598
 /note="2 copies 64 mer 85% conserved"
 9137..9438
 /note="AluY repeat: matches 1..302 of consensus"
 11951..12152
 /note="MIR repeat: matches 16..205 of consensus"
 12027..12332
 /note="match: GSS: Em:AQ461290"
 13042..13203
 /note="MIR repeat: matches 93..260 of consensus"
 13204..13680
 /note="LRR22 repeat: matches 5..509 of consensus"
 13681..13741
 /note="MIR repeat: matches 34..93 of consensus"
 16416..16730
 /note="AlusX repeat: matches 5..310 of consensus"
 17322..17384
 /note="Alus repeat: matches 15..77 of consensus"
 17855..17931
 /note="MIR repeat: matches 47..113 of consensus"
 17932..18227
 /note="AluY repeat: matches 5..309 of consensus"
 18228..18321
 /note="MIR repeat: matches 113..239 of consensus"
 18961..19248
 /note="AlusX repeat: matches 5..292 of consensus"
 complement(19592..20040)
 /note="match: GSS: Em:AQ359125"
 20092..20223
 /note="FLM-C repeat: matches 1..131 of consensus"
 20286..20341
 /note="28 copies 2 mer ac 85% conserved"
 20300..20343
 /note="11 copies 4 mer acac 95% conserved"
 21326..21831
 /note="match: GSS: Em:AQ560506"
 21616..22005
 /note="match: GSS: Em:AQ191866"
 22069..22376
 /note="AluY repeat: matches 1..307 of consensus"
 22747..23126
 /note="L1 repeat: matches 4745..5127 of consensus"

```

misc_feature      47492..59604
                  /note="assembly_fragment"
misc_feature      59705..74258
                  /note="assembly_fragment"
misc_feature      74359..93680
                  /note="assembly_fragment"

Query Match      1.7%: Score 27: DB 2: Length 212690;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1593 ACAGCTGTAACAAAAA 1619
    |||
Db 42174 ACAGCTGTAACAAAAA 42200

RESULT 37
AC069297      214411 bp DNA linear HTG 25-MAY-2000
LOCUS         Mus musculus chromosome 12 clone RP23-2N7 strain C57BL6/J, WORKING
DEFINITION   DRAFT SEQUENCE, 19 unordered pieces.
ACCESSION    AC069297.1 GI:8072378
VERSION      AC069297
KEYWORDS     HTG; PHASE1; HTG; DRAFT.
SOURCE       Mus musculus.
ORGANISM     Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 214411)
AUTHORS      Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,
              Bouffard,G.G., Dietrich,N.L., Eagle,W.O., Gupta,D., Ho,S.-L.,
              Huang,M.C., Idol,J., Lee-Lin,S.-O., Maduro,Q.L., Maduro,V.B.,
              Mastrian,S.D., McCloskey,J.C., Morse,E., Ojodu,M.A., Pearson,R.,
              Stantitop,S., Summers,T.J., Thomas,J.W., Thomas,P.J.,
              Tionsgon,E.E., Touchman,J.W., Tran,J.T., Vogt,J.L., Walker,M.A.,
              Wechterdy,K.D. and Green,E.D.
              NISC Mouse Sequencing Initiative
              Unpublished
              2 (bases 1 to 214411)
              Green,E.D.
              Direct Submission
              Submitted (25-MAY-2000) NIH Intramural Sequencing Center, 8717
              Grovemont Circle, Gaithersburg, MD 20877, USA
              ----- Genome Center
              Center: NIH Intramural Sequencing Center
              Center code: NISC
              Web site: http://www.nisc.nih.gov
              Contact: nisc.mouse@nhgri.nih.gov
              ----- Project Information
              Center Project name: us
              Center Clone name: 002N07
              ----- Summary Statistics
              Sequencing vector: plasmid; n/a; 100% of reads
              Chemistry: Dye-terminator Big Dye; 100% of reads
              Assembly program: Phrap; version 0.990319
              Consensus quality: 204922 bases at least Q40
              Consensus quality: 207590 bases at least Q30
              Consensus quality: 209017 bases at least Q20
              Insert size: 205000; agarose-fp
              Insert size: 248000; pulse-field-gel
              Insert size: 212611; sum-of-ctrls
              Quality coverage: 5.40x in Q20 bases; agarose-fp
              Quality coverage: 4.46x in Q20 bases; pulse-field-gel
              Quality coverage: 5.20x in Q20 bases; sum-of-ctrls
              -----
              * NOTE: This is a 'working draft' sequence. It currently
              * consists of 19 contigs. The true order of the pieces
              * is not known and their order in this sequence record is
              * arbitrary. Gaps between the contigs are represented as
              * runs of N, but the exact sizes of the gaps are unknown.
              * This record will be updated with the finished sequence
              * as soon as it is available and the accession number will
              * be preserved.

```

FEATURES

source

```

* 1
* 2372 2371: contig of 2371 bp in length
* 2472 2471: gap of unknown length
* 7037 7036: contig of 4566 bp in length
* 7137 7136: gap of unknown length
* 11837 11837: contig of 4701 bp in length
* 11938 11937: gap of unknown length
* 11938 16456: contig of 4519 bp in length
* 16457 16556: gap of unknown length
* 16557 24064: contig of 7508 bp in length
* 24065 24165: gap of unknown length
* 24165 30373: contig of 6208 bp in length
* 30373 30472: gap of unknown length
* 30472 38478: contig of 8006 bp in length
* 38478 38579: gap of unknown length
* 38579 47748: contig of 9170 bp in length
* 47749 47848: gap of unknown length
* 47849 56374: contig of 8526 bp in length
* 56375 56474: gap of unknown length
* 56475 68247: contig of 11773 bp in length
* 68248 68347: gap of unknown length
* 68348 78809: contig of 10462 bp in length
* 78810 78909: gap of unknown length
* 78910 89212: contig of 10303 bp in length
* 89213 89312: gap of unknown length
* 89313 99267: contig of 9955 bp in length
* 99268 99367: gap of unknown length
* 99368 110419: contig of 11052 bp in length
* 110420 110519: gap of unknown length
* 110520 124151: contig of 13632 bp in length
* 124152 124251: gap of unknown length
* 124252 141079: contig of 16828 bp in length
* 141080 141179: gap of unknown length
* 141180 160980: contig of 19801 bp in length
* 160981 161080: gap of unknown length
* 161081 185614: contig of 24534 bp in length
* 185615 214411: contig of 28697 bp in length.
*
* Location/Qualifiers
*   1..214411
*     /organism="Mus musculus"
*     /strain="C57BL6/J"
*     /db_xref="taxon:10090"
*     /chromosome="12"
*     /clone="RP23-2N7"
*   /clone_1fb="RPCT mouse BAC library 23"
*   1..2371
*     /note="assembly_fragment"
*   2472..7036
*     /note="assembly_fragment"
*   7137..11837
*     /note="assembly_fragment"
*   11938..16456
*     /note="assembly_fragment"
*   16557..24064
*     /note="assembly_fragment"
*   24165..30372
*     /note="assembly_fragment"
*   vector_end:17
*     vector_side:left"
*   30473..38478
*     /note="assembly_fragment"
*   38579..47748
*     /note="assembly_fragment"
*   47849..56374
*     /note="assembly_fragment"
*   56475..68247
*     /note="assembly_fragment"
*   68348..78809
*     /note="assembly_fragment"
*   78910..89212
*     /note="assembly_fragment"
*   89313..99267
*     /note="assembly_fragment"

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TITLE	Direct Submission
JOURNAL	Submitted (15-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	On May 15, 2002 this sequence version replaced g1:20531892.

```

* 4202 4301: gap of 100 bp
* 4302 4985: contig of 684 bp in length
* 4986 5085: gap of 100 bp
* 5086 5675: contig of 594 bp in length
* 5680 5779: gap of 100 bp
* 5780 6465: contig of 687 bp in length
* 6467 6566: gap of 100 bp
* 6567 7975: contig of 1409 bp in length
* 7976 8075: gap of 100 bp
* 8076 9524: contig of 1445 bp in length
* 9525 9624: gap of 100 bp
* 9625 11091: contig of 1467 bp in length
* 11092 11191: gap of 100 bp
* 11192 12839: contig of 1648 bp in length
* 12840 12939: gap of 100 bp
* 12940 16045: contig of 3110 bp in length
* 16050 16149: gap of 100 bp
* 16150 19066: contig of 2917 bp in length
* 19067 19166: gap of 100 bp
* 19167 26753: contig of 7587 bp in length
* 26754 26853: gap of 100 bp
* 26854 35082: contig of 8223 bp in length
* 35083 35182: gap of 100 bp
* 35183 79627: contig of 44445 bp in length
* 79628 79727: gap of 100 bp
* 79728 97908: contig of 18181 bp in length
* 97909 98008: gap of 100 bp
* 98009 119320: contig of 21312 bp in length
* 119321 119420: gap of 100 bp
* 119421 142295: contig of 22875 bp in length
* 142296 142395: gap of 100 bp
* 142396 166670: contig of 24275 bp in length
* 166671 166770: gap of 100 bp
* 166771 197264: contig of 30494 bp in length
* 197265 197364: gap of 100 bp
* 197365 209572: contig of 12208 bp in length.

```

FEATURES

source

```

Location/Qualifiers
1. .209572
/db_xref="taxon:10090"
/clone="RP23-41263"
/clone_id="RP23-41263"
1. .4201
/note="assembly-fragment
clone_end:SP6
vector_side:left"
misc_feature
4302. .4985
/note="assembly-fragment"
misc_feature
5086. .5679
/note="assembly-fragment"
misc_feature
5780. .6466
/note="assembly-fragment"
misc_feature
6567. .7975
/note="assembly-fragment"
misc_feature
8076. .9524
/note="assembly-fragment"
misc_feature
9625. .11091
/note="assembly-fragment"
misc_feature
11192. .12839
/note="assembly-fragment"
misc_feature
12940. .16049
/note="assembly-fragment"
misc_feature
16150. .19066
/note="assembly-fragment"
misc_feature
19167. .26753
/note="assembly-fragment"
misc_feature
26854. .35082
/note="assembly-fragment"
misc_feature
35183. .79627
/note="assembly-fragment"
misc_feature
79728. .97908
/note="assembly-fragment"
misc_feature
98009. .119320

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/note="assembly-fragment"
119421. .142295
/note="assembly-fragment"
142396. .166670
/note="assembly-fragment"
166771. .197264
/note="assembly-fragment"
197365. .209572
/note="assembly-fragment
clone_end:SP6
vector_side:right"

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BASE COUNT 63310 a 40377 c 40347 g 63732 t 1806 others

Query Match 1.7% Score 27; DB 2; Length 209572;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1593 ACAGTGTAAAAA 1619
DB 204291 ACAGTGTAAAAA 204317

```

RESULT 36
AC110232
LOCUS
DEFINITION
Mus musculus clone RP23-67H24, WORKING DRAFT SEQUENCE, 26 ordered
pieces.
AC110232.4 GI:20800203
VERSION
HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS
Mus musculus.
SOURCE
Mus musculus.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 212690)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-67H24
Unpublished
2 (bases 1 to 212690)
Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N.,
Anderson,S., Barina,N., Bastien,V., Boguslavsky,L., Boukhalter,B.,
Brown,A., Camarata,J., Campolano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Galdyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kelle,C., LaRoque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Liu,G., Maclean,C.,
Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Meldrum,J., Menus,L., Milnova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Roselli,M., Roy,A., Santos,R., Schauer,S., Schupbach,R., Seaman,S.,
Severy,P., Spencer,B., Strange,Thomam,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 212690)

```

TITLE
JOURNAL
REFERENCE
AUTHORS

Anderson,S., Barina,N., Bastien,V., Bloom,E., All,A., Allen,N.,
Boukhalter,B., Brown,A., Camarata,J., Campolano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Galdyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,

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misc-feature      /rpt_family="L2"
6625. .6628
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(NID:910797985)"
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6652. .6934
6651. .7090
repeat_region    /rpt_family="L2"
7091. .7404
repeat_region    /rpt_family="Alu"
7375. .7426
repeat_region    /rpt_family="(A)n"
7503. .7784
repeat_region    /rpt_family="Alu"
7650. .7671
repeat_region    /rpt_family="AT-rich"
7816. .8125
repeat_region    /rpt_family="Alu"
8100. .8151
repeat_region    /rpt_family="(TAA)n"
8144. .8534
repeat_region    /rpt_family="ERV1"
8535. .8804
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misc-feature      /Note="similar to Homo sapiens EST BG940653
(NID:914340025)"
8874. .9366
/Note="similar to Homo sapiens EST AL545950
(NID:912878612)"
8877. .9753
misc-feature      /Note="similar to Homo sapiens EST AL539591
(NID:912868947)"
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(NID:915998167)"
8877. .9366
/Note="similar to Homo sapiens EST B1222665
(NID:914676109)"
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8877. .9133
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(NID:914340025)"
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8962. .9144
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(NID:917177822)"
8976. .9411
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8982. .9519
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xv20d05.x1"

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Query Match      1.7%; Score 27; DB 9; Length 195782;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1593 ACAGTGTAAAAA 1619
DB 55644 ACAGTGTAAAAA 55670
RESULT 35

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AC099615
LOCUS             209572 bp      DNA      linear   HTG 16-NOV-2001
DEFINITION       Mus musculus clone RP23-41263, WORKING DRAFT SEQUENCE, 19 unordered
ACCESSION        AC099615
VERSION          AC099615.1 GI:16946996
KEYWORDS         HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE           Mus musculus
ORGANISM         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
REFERENCE        Birren, B., Linton, L., Nusbaum, C. and Lander, E.
AUTHORS          1 (bases 1 to 209572)
TITLE            Mus musculus, clone RP23-41263
JOURNAL          Unpublished
REFERENCE        2 (bases 1 to 209572)
AUTHORS          Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE            Mus musculus, clone RP23-41263
JOURNAL          Unpublished
REFERENCE        2 (bases 1 to 209572)
AUTHORS          Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE            Mus musculus, clone RP23-41263
JOURNAL          Unpublished

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TITLE            JOURNAL
COMMENT          Submitted (16-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WTHR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L17310
Center clone name: 412.G.3
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 204261 bases at least Q40
Consensus quality: 206670 bases at least Q30
Consensus quality: 207399 bases at least Q20
Insert size: 200000; agarose-efp
Insert size: 207772; sum-of-ctrls
Quality coverage: 8.2 in Q20 bases; agarose-efp
Quality coverage: 7.9 in Q20 bases; sum-of-ctrls
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 4201: contig of 4201 bp in length

```

OY 1593 ACAGTGTAAAAA 1619
 Db 166939 ACAGTGTAAAAA 166965

RESULT 34
 AC074389 195782 bp DNA linear PRI 10-JAN-2002
 LOCUS Homo sapiens BAC clone RP11-510K8 from 7, complete sequence.
 DEFINITION AC074389
 VERSION AC074389.8 GI:18042461
 KEYWORDS HTG.
 SOURCE
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Sulston, J.E. and Waterston, R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 99053792
 PUBMED 9847074

REFERENCE
 AUTHORS Cordes, M., Doeber, A., Hawkins, M. and Kozlowski, A.
 TITLE The sequence of Homo sapiens BAC clone RP11-510K8
 JOURNAL Unpublished (2002)
 REFERENCE 3 (bases 1 to 195782)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (30-JUL-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA

REFERENCE
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (03-JAN-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 REFERENCE 5 (bases 1 to 195782)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (10-JAN-2002) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Jan 3, 2002 this sequence version replaced gl:14209801.

REFERENCE
 AUTHORS Center: Washington University Genome Sequencing Center
 TITLE Web site: <http://genome.wustl.edu/gsc>
 JOURNAL Contact: saplens@wustl.edu
 COMMENT Summary Statistics
 Center project name: H_NH0510K08

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information

about the map position of this sequence, see
<http://www.nhgri.nih.gov/DIR/CTB/CHR7>, send
<mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
 The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Rateno, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://Dacpac.med.buffalo.edu>)
 VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is RP11-16P10, 2000 bp overlap. Actual start of this clone is at base position 112086 of RP11-510K8. RP11-16P10; actual end is at base position 195782 of RP11-510K8.

Data from AC093734 was used to finish this clone, AC074389. There is single M13 clone coverage from 64639 to 64773.

FEATURES

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 1. 195782
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 /db_xref="taxon:9606"
 /chromosome="7"
 /map="7"
 /clone="RP11-510K8"
 /clone_id="RPCI-11"
 3. 269
 /rpt_family="L1"
 304. 372
 /rpt_family="MIR"
 558. 736
 /rpt_family="Alu"
 807. 844
 /rpt_family="(TTCA)n"
 946. 1126
 /rpt_family="C-rich"
 1099. 1278
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 1417. 1585
 /rpt_family="CT-rich"
 1621. 1647
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 2190. 2265
 /rpt_family="(GGCTG)n"
 2261. 2383
 /rpt_family="MIR"
 2804. 3125
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 3175. 3277
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 3599. 3761
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 3762. 4059
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 4030. 4073
 /rpt_family="A-rich"
 4060. 4157
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 4173. 4432
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 5572. 5740
 /rpt_family="MIR"
 5736. 6058
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 6036. 6588
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 6222. 6225
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 6506. 6560
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ACCESSION AC074245
 VERSION AC074245.3 GI:9887809
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 179364)
 AUTHORS Waterston, R.H.
 TITLE The sequence of Homo sapiens clone
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 179364)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (22-JUL-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 COMMENT On Aug 24, 2000 this sequence version replaced gi:9665207.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 ----- Project Information -----
 Center project name: H_NH0341F08
 ----- Summary Statistics -----
 Sequencing vector: MJ3; 100%
 Sequencing chemistry: Dye-terminator Big Dye; 0% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 167601 bases at least Q40
 Consensus quality: 170488 bases at least Q30
 Consensus quality: 171954 bases at least Q20
 Insert size: 179000; agarose-fp
 Insert size: 177364; sum-of-contigs
 Quality coverage: 4.14 in Q20 bases; agarose-fp
 Quality coverage: 4.29 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 21 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 *
 * 1 1477: contig of 1477 bp in length
 * 1478 1577: gap of unknown length
 * 1578 3789: contig of 2222 bp in length
 * 3800 3889: gap of unknown length
 * 3900 6403: contig of 2504 bp in length
 * 6404 6503: gap of unknown length
 * 6504 10328: contig of 3825 bp in length
 * 10329 10428: gap of unknown length
 * 10429 13400: contig of 2972 bp in length
 * 13401 13500: gap of unknown length
 * 13501 18872: contig of 5372 bp in length
 * 18873 18972: gap of unknown length
 * 18973 25292: contig of 6320 bp in length
 * 25293 25392: gap of unknown length
 * 25393 30836: contig of 5444 bp in length
 * 30837 30936: gap of unknown length
 * 30937 36567: contig of 5611 bp in length
 * 36568 36667: gap of unknown length
 * 36668 45390: contig of 8623 bp in length
 * 45391 45490: gap of unknown length
 * 45491 55146: contig of 9756 bp in length
 * 55147 55246: gap of unknown length
 * 55247 66342: contig of 11096 bp in length
 * 66343 66442: gap of unknown length
 * 66443 76462: contig of 10020 bp in length
 * 76463 76562: gap of unknown length

FEATURES
 source
 1..179364
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="2"
 /clone="RP11-341F8"
 1..1477
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 clone_end:17
 vector_side:left"
 1578..3789
 /note="assembly_name:Contig11"
 3900..6403
 /note="assembly_name:Contig12"
 6504..10328
 /note="assembly_name:Contig13"
 10429..13400
 /note="assembly_name:Contig14"
 13501..18872
 /note="assembly_name:Contig15"
 18973..25292
 /note="assembly_name:Contig16"
 25393..30836
 /note="assembly_name:Contig17"
 30937..36567
 /note="assembly_name:Contig18"
 36668..45290
 /note="assembly_name:Contig19"
 45391..55146
 /note="assembly_name:Contig20"
 55247..66342
 /note="assembly_name:Contig21"
 66443..76462
 /note="assembly_name:Contig22"
 76563..89099
 /note="assembly_name:Contig23"
 89200..102001
 /note="assembly_name:Contig24"
 102102..119488
 /note="assembly_name:Contig25"
 119589..135844
 /note="assembly_name:Contig26
 clone_end:SP6
 vector_side:left"
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 153742..175739
 /note="assembly_name:Contig28"
 175840..177387
 /note="assembly_name:Contig29"
 177488..179364
 /note="assembly_name:Contig29"
 misc_feature
 56993 a 32967 c 33013 g 54383 t 2008 others
 BASE COUNT
 ORIGIN
 Query Match 1.7%: Score 27; DB 2; Length 179364;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 27: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1593 ACAGTGTAAAAA 1619
 DB 31571 ACAGTGTAAAAA 31545

RESULT 31
 AC126321/c 151602 bp DNA linear HTG 05-JUL-2002
 LOCUS Polypterinus bichir clone -22F22, *** SEQUENCING IN PROGRESS ***; 1
 DEFINITION ordered piece.

AC126321 151602 bp DNA linear HTG 05-JUL-2002
 AC126321.1 GI:21699164
 HTG: HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.

AC126321.1 GI:21699164
 HTG: HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
 KEYWORDS Polypterinus bichir.
 SOURCE Polypterinus bichir.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Polypteriformes; Polypteridae; Polypterus.

REFERENCE 1 (bases 1 to 151602)
 Birren, B., Nusbaum, C. and Lander, E.
 TITLE Polypterinus bichir, clone -22F22
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 151602)
 Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
 Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B.,
 Camarata, J., Chang, J., Chararo, B., Choepel, Y., Collymore, A.,
 Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
 Fardo, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
 Gardys, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
 Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
 Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
 Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
 McCarthy, M., Melgrim, J., Meneus, L., Milhova, T., Mieng, V.,
 Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Noddu, C., Nozman, C. H.,
 O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
 Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
 Roman, J., Roy, A., Schauer, S., Schnupbach, R., Seaman, S., Severy, P.,
 Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
 Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
 Zembek, L., Zimmer, A. and Zody, M.

TITLE Direct Submission
 JOURNAL Submitted (05-JUL-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: MIBR

Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu

Project Information
 Center project name: L20497
 Center clone name: 22_F_22

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 1 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submittor.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 151602: contig of 151602 bp in length.
 Location/Qualifiers

FEATURES
 source
 1. 151602
 /organism="Polypterinus bichir"
 /db_xref="taxon:31136"
 /clone="22F22"
 /clone_1lb="Bichir"

BASE COUNT 48679 a 27446 c 26903 g 48574 t
 ORIGIN

Query Match 1.7%; Score 27; DB 2; Length 151602;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1591 AGACGTGTAAAAA 1617
 DB 80517 AGACGTGTAAAAA 80491

RESULT 32

AC027118 170255 bp DNA linear PRI 23-APR-2002
 LOCUS Homo sapiens chromosome 10 clone RP11-573111, complete sequence.
 AC027118.9 GI:19774390

AC027118.9 GI:19774390
 HTG.
 HOMO SAPIENS.
 Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 170255)
 Smith, D.R.
 TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
 Sequence Data

REFERENCE 2 (bases 1 to 170255)
 Smith, D.R.
 TITLE Direct Submission
 JOURNAL Submitted (27-MAR-2000) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA

REFERENCE 3 (bases 1 to 170255)
 Smith, D.R.
 TITLE Direct Submission
 JOURNAL Submitted (28-MAR-2002) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA

REFERENCE 4 (bases 1 to 170255)
 Smith, D.R.
 TITLE Direct Submission
 JOURNAL Submitted (23-JAN-2002) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA

REFERENCE 5 (bases 1 to 170255)
 Smith, D.R.
 TITLE Direct Submission
 JOURNAL Submitted (23-APR-2002) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA

COMMENT On Mar 28, 2002 this sequence version replaced g1:18266621.
 Location/Qualifiers

FEATURES
 source
 1. 170255
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="10"
 /clone="RP11-573111"
 /clone_1lb="RP11-573111"
 /clone_1lb="RP11-573111"
 /clone_1lb="RP11-573111"

BASE COUNT 53463 a 30250 c 31205 g 55337 t
 ORIGIN

Query Match 1.7%; Score 27; DB 9; Length 170255;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1593 ACAGTGTAAAAA 1619
 DB 136987 ACAGTGTAAAAA 137013
 RESULT 33
 AC074245 179364 bp DNA linear HTG 24-AUG-2000
 LOCUS Homo sapiens chromosome 2 clone RP11-341F8, WORKING DRAFT SEQUENCE,
 21 unordered pieces.

```

FEATURES
  * 82417 84866: contig of 2450 bp in length
  * 84867 84966: gap of unknown length
  * 84967 87959: contig of 2993 bp in length
  * 87960 88059: gap of unknown length
  * 88060 92874: contig of 4815 bp in length.
    Location/Qualifiers
      1..92874
        /organism="Rattus norvegicus"
        /db_xref="taxon:10116"
        /clone="CH230-286021"
BASE COUNT 23927 a 19653 c 20425 g 23828 t 5041 others
ORIGIN
Query Match 1.7%; Score 27; DB 2; Length 92874;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1222 GAGAGGAGGAGGATCATGTACGCC 1248
      |||
Db 75643 GAGAGGAGGAGGATCATGTACGCC 75669

RESULT 29
AL807806/c 127524 bp DNA linear HTG 17-AUG-2002
LOCUS Mus musculus chromosome X clone RP23-67K19, *** SEQUENCING IN
DEFINITION PROGRESS ***, 2 unordered pieces.
ACCESSION AL807806
VERSION AL807806.4 GI:22416117
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVERFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 127524)
  Whitehead, S.
  Direct Submission
  Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
  Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
  humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
  On Aug 21, 2002 this sequence version replaced gi:21694507.
  ----- Genome Center
  Center: Wellcome Trust Sanger Institute
  Center code: SC
  Web site: http://www.sanger.ac.uk
  Contact: humquerry@sanger.ac.uk
  ----- Project Information
  Center project name: bm67K19
  ----- Summary Statistics
  Assembly program: XGAP4; version 4.5
  Chemistry: Dye-terminator; 100% of reads
  Consensus quality: 127311 bases at least Q40
  Consensus quality: 127389 bases at least Q30
  Consensus quality: 127413 bases at least Q20
  Insert size: 127424; sum-of-contigs
  Insert size: 142249; 4.2% error; agarose-fp
  Quality coverage: 8.11x in Q20 bases; sum-of-contigs Quality
  coverage: 7.35x in Q20 bases; agarose-fp
  -----
  * NOTE: This is a 'working draft' sequence. It currently
  * consists of 2 contigs. The true order of the pieces
  * is not known and their order in this sequence record is
  * arbitrary. Gaps between the contigs are represented as
  * runs of N, but the exact sizes of the gaps are unknown.
  * This record will be updated with the finished sequence
  * as soon as it is available and the accession number will
  * be preserved.
  * 1 24018: contig of 24018 bp in length
  * 24019 24118: gap of 100 bp
  * 24119 127524: contig of 103406 bp in length.
    Location/Qualifiers
      1..127524
        /organism="Mus musculus"
FEATURES
  source

```

```

      /db_xref="taxon:10090"
      /chromosome="X"
      /clone="RP23-67K19"
      /clone_11b="RPCI-23"
      1..24018
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        /note="assembly-fragment:00777.0"
BASE COUNT 37921 a 23572 c 23357 g 42574 t 100 others
ORIGIN
Query Match 1.7%; Score 27; DB 2; Length 127524;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1593 ACAGGTAAAAA 1619
      |||
Db 87560 ACAGGTAAAAA 87534

RESULT 30
AL645938/c 138851 bp DNA linear ROD 11-APR-2002
LOCUS Mouse DNA sequence from clone RP23-15E24 on chromosome 1, complete
DEFINITION sequence.
ACCESSION AL645938
VERSION AL645938.9 GI:20145949
KEYWORDS HTG.
SOURCE house mouse.
ORGANISM Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1
  Corby, N.
  Direct Submission
  Submitted (11-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
  Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
  humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
  On Apr 12, 2002 this sequence version replaced gi:20135756.
  During sequence assembly data is compared from overlapping clones.
  Where differences are found these are annotated as variations
  together with a note of the overlapping clone name. Note that the
  variation annotation may not be found in the sequence submission
  corresponding to the overlapping clone, as we submit sequences with
  only a small overlap as described above.
  This sequence was finished as follows unless otherwise noted: all
  regions were either double-stranded or sequenced with an alternate
  chemistry or covered by high quality data (i.e., phred quality >=
  30); an attempt was made to resolve all sequencing problems, such
  as compressions and repeats; all regions were covered by at least
  one plasmid subclone or more than one M13 subclone; and the
  assembly was confirmed by restriction digest. The following
  abbreviations are used to associate primary accession numbers given
  in the feature table with their source databases: Em: EMBL; Sw:
  SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP
  database can be found at
  http://www.sanger.ac.uk/Projects/C_elegans/wormpep
  from the RPCI-23 Mouse PAC library
  constructed by the group of Pieter de Jong.
  For further details see http://www.choil.org/bacpac/home.htm
  VECTOR: pBac3.6.
    Location/Qualifiers
      1..138851
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        /db_xref="taxon:10090"
        /chromosome="1"
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        /clone_11b="RPCI-23"
BASE COUNT 40695 a 25907 c 27333 g 44916 t
ORIGIN
Query Match 1.7%; Score 27; DB 10; Length 138851;
Best Local Similarity 100.0%; Pred. No. 0.001;

```

Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
 Rivers, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savary, G.,
 Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I.,
 Sodergren, E., Soneike, T., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
 Tansey, J., Taylor, C., Taylor, T., Telirod, B., Thomas, N., Thomas, S.,
 Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S.,
 Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorilla, S., Nelson, D.,
 Weinstein, G. and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 92874)
 Worley, K.C.
 Direct Submission
 Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 92874)
 Worley, K.C.
 Direct Submission
 Submitted (17-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 13, 2002 this sequence version replaced gi:20303189.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GRJD
 Center clone name: CH230-286021
 ----- Summary Statistics
 Sequencing vector: Plasmid
 Chemistry: Dye-terminator Big Dye: 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 32512 bases at least Q40
 Consensus quality: 34515 bases at least Q30
 Consensus quality: 35930 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 50 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1
 * 1057: contig of 1057 bp in length
 * 1058 1157: gap of unknown length
 * 1158 2410: contig of 1253 bp in length
 * 2411 2510: gap of unknown length
 * 2511 3571: contig of 1061 bp in length
 * 3572 3671: gap of unknown length
 * 3672 5259: contig of 1588 bp in length
 * 5260 5359: gap of unknown length
 * 5360 6436: contig of 1077 bp in length
 * 6437 6536: gap of unknown length
 * 6537 7705: contig of 1169 bp in length
 * 7706 7805: gap of unknown length
 * 7806 8911: contig of 1106 bp in length
 * 8912 9011: gap of unknown length
 * 9012 10370: contig of 1359 bp in length
 * 10371 10470: gap of unknown length
 * 10471 11914: contig of 1444 bp in length
 * 11915 12014: gap of unknown length
 * 12015 13145: contig of 1131 bp in length
 * 13146 13245: gap of unknown length
 * 13246 14584: contig of 1339 bp in length
 * 14585 14684: gap of unknown length
 * 14685 16404: contig of 1720 bp in length
 * 16405 16505: gap of unknown length
 * 16506 17655: contig of 1151 bp in length
 * 17656 17755: gap of unknown length
 * 17756 19240: contig of 1485 bp in length
 * 19241 19341: gap of unknown length
 * 19342 20648: contig of 1307 bp in length
 * 20649 20748: gap of unknown length
 * 20749 22171: contig of 1424 bp in length
 * 22172 22271: gap of unknown length
 * 22272 23762: contig of 1491 bp in length
 * 23763 23862: gap of unknown length
 * 23863 25556: contig of 1694 bp in length
 * 25557 25657: gap of unknown length
 * 25658 26711: contig of 1055 bp in length
 * 26712 26811: gap of unknown length
 * 26812 28747: contig of 1936 bp in length
 * 28748 28847: gap of unknown length
 * 28848 30564: contig of 1717 bp in length
 * 30565 30664: gap of unknown length
 * 30665 32045: contig of 1382 bp in length
 * 32046 32146: gap of unknown length
 * 32147 33729: contig of 1583 bp in length
 * 33730 33829: gap of unknown length
 * 33830 35524: contig of 1695 bp in length
 * 35525 35624: gap of unknown length
 * 35625 37292: contig of 1668 bp in length
 * 37293 37392: gap of unknown length
 * 37393 38486: contig of 1094 bp in length
 * 38487 38586: gap of unknown length
 * 38587 40145: contig of 1559 bp in length
 * 40146 40245: gap of unknown length
 * 40246 41925: contig of 1680 bp in length
 * 41926 42025: gap of unknown length
 * 42026 43669: contig of 1644 bp in length
 * 43670 43770: gap of unknown length
 * 43771 45714: contig of 1944 bp in length
 * 45715 45813: gap of unknown length
 * 45814 47315: contig of 1502 bp in length
 * 47316 47415: gap of unknown length
 * 47416 48852: contig of 1437 bp in length
 * 48853 48953: gap of unknown length
 * 48954 50511: contig of 1559 bp in length
 * 50512 50611: gap of unknown length
 * 50612 52672: contig of 2061 bp in length
 * 52673 52772: gap of unknown length
 * 52773 54274: contig of 1502 bp in length
 * 54275 54374: gap of unknown length
 * 54375 56993: contig of 2619 bp in length
 * 56994 57093: gap of unknown length
 * 57094 59515: contig of 2422 bp in length
 * 59516 59615: gap of unknown length
 * 59616 61878: contig of 2263 bp in length
 * 61879 61978: gap of unknown length
 * 61979 64520: contig of 2542 bp in length
 * 64521 64621: gap of unknown length
 * 64622 67430: contig of 2810 bp in length
 * 67431 67530: gap of unknown length
 * 67531 68852: contig of 1322 bp in length
 * 68853 68953: gap of unknown length
 * 68954 70700: contig of 1748 bp in length
 * 70701 72350: gap of unknown length
 * 72351 72450: gap of unknown length
 * 72451 74728: contig of 2178 bp in length
 * 74729 74829: gap of unknown length
 * 74830 76922: contig of 2194 bp in length
 * 76923 77022: gap of unknown length
 * 77023 79345: contig of 2323 bp in length
 * 79346 79446: gap of unknown length
 * 79447 82316: contig of 2871 bp in length
 * 82317 82416: gap of unknown length

CDS

```

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/translation="MNNKKNRSGVQGVKMGISODELPVKNLEHKNVYFYOKCIYGP
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PHNKVYDDEVAIDPSLEVEHPRYDVAIDGAIYRCIYLEGSKISAEILKRAN
KLKSTACPMFYSRIRYKVRKSTRLPLEHLEPDEGNAPRTSRSLVAHESKRS
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VANGDIHTPTPKSKPELSAATEOTPTSRKSLIKSATSRLEAGCPRSIHLNIV
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GITTAATPMTSPQMKIRAGELSPMQORTDLPANDSSKSELQAREQLHVSVPK
SLPCREPERENIVAFLEGGIDODCGCMYVSGVGTCTATVGTITLQRMKONEL
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VDELIDICNRRODVVNLDMPTSAKIVVITANMDLPERLMGKVSRLGTPRL
TFQPSYKHOLOEITARLGSEETPKGAVALVARKVANAAGDARALDICRAREID
TAAKCYTMLHVOQALABMTASAKVQAIRNCSREQIFLQIAAEVTRIVGEETEG
VYQOEVITAAFMGVTFPPPGRALRCLSKLGAERLLISEHSRNDLFQKILLNSADLIH
YALRVEEMVN"
BASE COUNT      847 a      864 c      821 g      623 t
ORIGIN

```

```

Query Match      1.7%  Score 27; DB 3; Length 3155;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1593 ACAGTGTAAAAA 1619
|||||
Db 3127 ACAGTGTAAAAA 3153

```

```

RESULT 27      48206 bp  DNA  linear  ROD 19-JUL-2002
LOCUS      AL645986
DEFINITION  Mouse DNA sequence from clone DN-35368 on chromosome 1, complete
sequence.
ACCESSION      AL645986
VERSION      AL645986.6  GI:18855238
KEYWORDS      HTG.
SOURCE      Mus musculus.
ORGANISM      Mus musculus.
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE      1 (bases 1 to 48206)
JOURNAL      Direct Submission
COMMENT      Submitted (18-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humqueres@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Feb 21, 2002 this sequence version replaced gi:11529535.
During sequence assembly data is compared from overlapping clones.
Where differences are found they are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; Sw,
SWISSPROT; Tr, TrEMBL; Wp, WormPeP; Information on the WormPeP

```

database can be found at
<http://www.sanger.ac.uk/Projects/C.elegans/wormpep> -----
 Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humqueres@sanger.ac.uk

DN-35368 is from a DIL (Diabetes and Inflammation Laboratory) NOD
 Mouse BAC library
 VECTOC: PBAC3.6.

FEATURES
 source
 Location/Qualifiers
 1..48206
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /chromosome="1"
 /clone="DN-35368"
 /clone_lib="NOD mouse library"

```

BASE COUNT      14007 a      8876 c      9129 g      16194 t
ORIGIN

```

```

Query Match      1.7%  Score 27; DB 10; Length 48206;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1593 ACAGTGTAAAAA 1619
|||||
Db 33779 ACAGTGTAAAAA 33753

```

```

RESULT 28      92874 bp  DNA  linear  HTG 17-JUL-2002
LOCUS      AC112072
DEFINITION  Rattus norvegicus clone CH230-286021, *** SEQUENCING IN PROGRESS
sequence.
ACCESSION      AC112072
VERSION      AC112072.3  GI:21744373
KEYWORDS      HTG; HTGS_PHASE1.
SOURCE      Norway rat.
ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 92874)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barberia,J., Benton,J., Bimuge,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Butrell,K.L., Byrd,N.C.,
Carton,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dethorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,T., Dinh,H.H.,
Douthwaite,K.J., Drepper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escoto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.,
Homs,I.F., Howard,S., Huber,J., Huiyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsone,E., Kelly,S., Khan,U., Kling,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lien,C., Liu,J., Liu,W., Louiseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,B.,
Massey,E., Mawliny,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nkokenko,S., Ogun,H., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,

```

TITLE
JOURNAL

Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:cdna@hgc.ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)

COMMENT

NEO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; CDNA full insert
sequencing: Research Association for Biotechnology; CDNA library
construction, 5'- & 3'-end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).

FEATURES
source

Location/Qualifiers
1. 1614
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="KATO2340"
/cell_line="KATO III"
/cell_type="signal-ring cell carcinoma"
/clone_lib="KAT"
/note="cloning vector pME18SFL3"

misc-feature

1. 1614
/note="highly similar to HUMTSLC Homo sapiens
transcription factor SL1 mRNA"

BASE COUNT

557 a 296 c 337 g 424 t

ORIGIN

Query Match 1.7%; Score 27; DB 9; Length 1614;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1593 ACAGTGTAACAAAAA 1619

DB 1581 ACAGTGTAACAAAAA 1607

RESULT 25

LOCUS

BC028978 2625 bp mRNA linear PRI 16-MAY-2002

DEFINITION

Homo sapiens, clone IMAGE:3919084, mRNA.

ACCESSION

BC028978.1 GI:20810049

VERSION

BC028978.1 GI:20810049

KEYWORDS

Homo sapiens.

SOURCE

Homo sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 2625)

AUTHORS

Strausberg, R.

TITLE

Direct Submission

JOURNAL

Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov

COMMENT

Tissue Procurement: ATCC/DCMT/DMP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amgdbcm.tmc.edu
Guanarone, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 42 Row: b Column: 17.

FEATURES
source

Location/Qualifiers
1. 2625
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3919084"
/tissue_type="Skin, melanotic melanoma."
/clone_lib="NIH_MGC_72"
/lab_host="DH10B"
/note="Vector: PCMV-SPOrt6"

BASE COUNT

860 a 538 c 502 g 725 t

ORIGIN

Query Match 1.7%; Score 27; DB 9; Length 2625;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1593 ACAGTGTAACAAAAA 1619

DB 2567 ACAGTGTAACAAAAA 2593

RESULT 26

LOCUS

AY094780 3155 bp mRNA linear INV 15-APR-2002

DEFINITION

Drosophila melanogaster LD11626 full insert cDNA.

ACCESSION

AY094780

VERSION

AY094780.1 GI:20151546

KEYWORDS

FLI-CDNA.

SOURCE

Drosophila melanogaster.

ORGANISM

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Iphydroidea; Drosophilidae; Drosophila.

REFERENCE

1 (bases 1 to 3155)

AUTHORS

Stapleton, M., Broksstein, P., Hong, L., Agdayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Krommiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Munoz, J., Paclob, J., Paragas, V., Park, S.,
Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
and Ceolnik, S.

TITLE

Direct Submission

JOURNAL

Submitted (03-APR-2002) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA

COMMENT

Sequence submitted by:

ORGANISM

Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory

SOURCE

Berkeley, CA 94720

This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our web site
(<http://fruitfly.berkeley.edu>) or send email to
cdna@fruitfly.berkeley.edu.

FEATURES

source

Location/Qualifiers
1. 3155
/organism="Drosophila melanogaster"

gene

gene

/strain="Y; cn bw sp"
/db_xref="taxon:7227"
/map="43D3-43D3"

gene

1. 3155
/gene="Orcl1"

/note="alignment with genomic scaffold AE003840 and gene
has no introns and polyA tail is encoded in the genomic"

MDQANDSLASYVAGQNNRRLSNKDKGLQNTSLPLTVKGLTAEDTRILAYOSGANG
IIGPNHGAQRLDYVPPNNKGEYVKAAGVPEVLADGVRPGRGNVTKALALASGTF
IGRRVYSLPAEGAGVRAKVLQMLRDEFELTMALSCRSRLKETTSHITVADMDTPRVN
PRAIPRL"

BASE COUNT 332 a 199 c 249 g 306 t

Query Match 1.7%; Score 27; DB 8; Length 1086;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1593 ACAGGTGTAATAAAAAAAAAAAAAAAAAA 1619
Db 1053 ACAGGTGTAATAAAAAAAAAAAAAAAAAA 1079

RESULT 22
AY118558 1114 bp mRNA linear INV 15-JUN-2002
LOCUS Drosophila melanogaster LD37258 full insert cDNA.
ACCESSION AY118558 GI:21428533
VERSION AY118558.1
KEYWORDS FLI_CDNA.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1114)
Stapleton, M., Brockslein, P., Hong, L., Agbayan, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, Y., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Kionmiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C. J., Nuno, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Rubin, G. M.,
and Celislier, S.
Direct Submission
Submitted (07-JUN-2002) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription errors of unspliced precursor RNAs, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our web site
(http://fruitfly.berkeley.edu) or send email to
cdna@fruitfly.berkeley.edu

FEATURES
source location/Qualifiers
1..1114
/organism="Drosophila melanogaster"
/strain="y: cn bw sp"
/db_xref="taxon:7227"
1..1114
/gene="CG13601"
/db_xref="FLYBASE:FBgn0039126"
48..815
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/note="Longest ORF"
/codon_start=1
/product="LD37258p"
/protein_id="AAM49927.1"
/db_xref="GI:21428534"

gene
CDS

1..1114
/organism="Drosophila melanogaster"
/strain="y: cn bw sp"
/db_xref="taxon:7227"
1..1114
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/db_xref="FLYBASE:FBgn0039126"
48..815
/gene="CG13601"
/note="Longest ORF"
/codon_start=1
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/db_xref="GI:21428534"

/db_xref="FLYBASE:FBgn0039126"
/translation="WVGVPAAKIGILAIKOVSPRIANVIRSNKSSPFPKTYICMP
PAQFVNVVETKRMALNNGRVNPPINEMARILGANLICEFTIPISGALLIFEX
SROTLEKKNELAOSKEMELNMLENFRERDDAOIRETRVLADLDSNTRFW
KEPIOEYVDFDDTPDOSASANPKRFBSDLIDPOGMAFRALHFLDIOIFVDGRNRKA
KEALQHLDEVAQVLEQSLGEAVNVASSLPKADL"

BASE COUNT 334 a 259 c 278 g 243 t

Query Match 1.7%; Score 27; DB 3; Length 1114;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1593 ACAGGTGTAATAAAAAAAAAAAAAAAAAA 1619
Db 1066 ACAGGTGTAATAAAAAAAAAAAAAAAAAA 1092

RESULT 23
AX285020 1368 bp DNA linear PAT 20-NOV-2001
LOCUS AX285020
DEFINITION Sequence 825 from Patent WO0179556.
ACCESSION AX285020
VERSION AX285020.1 GI:17045708
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Lillie, J., Brown, J. L., Bolt, A. and van Hufel, C.
Novel genes, compositions and methods for the identification,
assessment, prevention, and therapy of human cancers
Patent: WO 0179556-A 825 25-OCT-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
1..1368
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 517 a 312 c 321 g 213 t 5 others

Query Match 1.7%; Score 27; DB 6; Length 1368;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1593 ACAGGTGTAATAAAAAAAAAAAAAAAAAA 1619
Db 459 ACAGGTGTAATAAAAAAAAAAAAAAAAAA 485

RESULT 24
AK026521 1614 bp mRNA linear PRI 29-SEP-2000
LOCUS AK026521
DEFINITION Homo sapiens cDNA: FLJ22868 fis, clone KAT02340, highly similar to
HDMTFSLC Homo sapiens transcription factor SL1 mRNA.
ACCESSION AK026521
VERSION AK026521.1 GI:10439398
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens
Homo sapiens stager-ring cell carcinoma cell_line:KATO III cDNA to
mRNA, clone_11b:KAT clone:KAT02340.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Matsunabe, K., Kumagai, A., Itakura, S., Yamazaki, M., Tashiro, H.,
Ota, T., Suzuki, Y., Odayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,
Nakamura, Y., Isogai, T., and Sugano, S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1614)
Sugano, S., Suzuki, Y., Ota, T., Odayashi, M., Nishi, T., Isogai, T.,
Shibahara, T., Tanaka, T. and Nakamura, T.

1..1614
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1..1614
/gene="SL1"
/db_xref="FLYBASE:FBgn0039126"
48..815
/gene="SL1"
/note="Longest ORF"
/codon_start=1
/product="SL1"
/protein_id="AAM49927.1"
/db_xref="GI:21428534"

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* 43021 43120: gap of unknown length
* 43121 44790: contig of 1670 bp in length
* 44791 44890: gap of unknown length
* 44891 46626: contig of 1736 bp in length
* 46627 46726: gap of unknown length
* 46727 47819: contig of 1093 bp in length
* 47820 47919: gap of unknown length
* 47920 49621: contig of 1702 bp in length
* 49622 49721: gap of unknown length
* 49722 51446: contig of 1725 bp in length
* 51447 53382: gap of unknown length
* 53383 53483: gap of unknown length
* 53483 55863: contig of 2381 bp in length
* 55864 55963: gap of unknown length
* 55964 58398: contig of 2435 bp in length
* 58399 58498: gap of unknown length
* 58499 61923: contig of 3425 bp in length
* 61924 62023: gap of unknown length
* 62024 65252: contig of 3229 bp in length
* 65253 65352: gap of unknown length
* 65353 67262: contig of 1910 bp in length
* 67263 67362: gap of unknown length
* 67363 69710: contig of 2348 bp in length
* 69711 69810: gap of unknown length
* 69810 73439: contig of 3629 bp in length
* 73440 73539: gap of unknown length
* 73540 76475: contig of 2936 bp in length
* 76476 76575: gap of unknown length
* 76576 80568: contig of 3993 bp in length
* 80569 80668: gap of unknown length
* 80669 84177: gap of unknown length
* 84178 84277: gap of unknown length
* 84278 89159: contig of 4882 bp in length
* 89160 89259: gap of unknown length
* 89260 92924: contig of 3665 bp in length
* 92925 93024: gap of unknown length
* 93025 96972: contig of 3948 bp in length
* 96973 97072: gap of unknown length
* 97073 100972: contig of 3900 bp in length
* 100973 101072: gap of unknown length
* 101073 107076: contig of 6004 bp in length
* 107077 107176: gap of unknown length
* 107177 113525: contig of 6349 bp in length
* 113526 113625: gap of unknown length
* 113626 119430: contig of 5805 bp in length
* 119431 125703: gap of unknown length
* 119531 125703: contig of 6173 bp in length.

```

```

FEATURES
  source
    1..125703
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      /db_xref="taxon:10116"

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Query Match      1.9%: Score 30; DB 2; Length 125703;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1590 TAGACAGTGTAAAAA 1619
    |||||||
DB 37842 TAGACAGTGTAAAAA 37813

```

```

RESULT 20
AF150733 487 bp mRNA linear PRI 04-MAY-2000
LOCUS Homo sapiens AD-014 protein mRNA, complete cds.
DEFINITION AF150733
ACCESSION AF150733
VERSION AF150733.1 GI:7688664
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE 1 (bases 1 to 487)
AUTHORS Fu,S., Gu,Y., Li,Y., Peng,Y., Gu,J., Zhang,L., Jiang,C., Yu,Y.,
Fu,G., Wang,Y., Chen,Z., and Han,Z.
TITLE A novel gene expressed in human adrenal gland
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 487)
AUTHORS Fu,S., Gu,Y., Li,Y., Peng,Y., Gu,J., Zhang,L., Jiang,C., Yu,Y.,
Fu,G., Wang,Y., Chen,Z., and Han,Z.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-1999) Chinese National Human Genome Center at
Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
Shanghai 201203, P. R. China
LOCATION/Qualifiers

```

```

FEATURES
  source
    1..487
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /tissue-type="adrenal gland"
      /note="protein x 0007"
      /codon_start=1
      /product="AD-014 protein"
      /protein_id="AAP67473.1"
      /db_xref="GI:7688665"
      /translation="MVKLSKAKQRLQQLFKGSOFAIRWGFPLVITLGSFKRADPDM
PEPVLSLIMG"

```

```

BASE COUNT 135 a 101 c 128 g 122 t 1 others
ORIGIN

```

```

Query Match      1.7%: Score 27; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1593 ACAGTGTAAAAA 1619
    |||||||
DB 452 ACAGTGTAAAAA 478

```

```

RESULT 21
AF082874 1086 bp mRNA linear PLN 20-AUG-1998
LOCUS Medicago sativa glycolate oxidase mRNA, partial cds.
DEFINITION AF082874
ACCESSION AF082874
VERSION AF082874.1 GI:3435305
KEYWORDS Medicago sativa.
SOURCE Medicago sativa.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

```

```

REFERENCE 1 (bases 1 to 1086)
AUTHORS Stout,J.M. and McKersie,B.D.
TITLE Gene expression in alfalfa
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1086)
AUTHORS Stout,J.M. and McKersie,B.D.
TITLE Direct Submission
JOURNAL Submitted (07-AUG-1998) Plant Biotechnology Division, Dept of Plant
Agriculture, University of Guelph, Crop Science Building, Guelph,
Ont N1G 2W1, Canada
LOCATION/Qualifiers

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FEATURES
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    1..1086
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        /db_xref="GI:3435306"
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ACCESSION AC123338
 VERSION AC123338.2 GI:21671554
 HTG: HTGS_PHASE1.
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 125703)

REFERENCE 1 (bases 1 to 125703)
 AUTHORS Muzny D.M., Adams C., Adio-Oduola B., Al-Osman F.R., Allen C., Alsbrooks S.L., Amaralunge H.C., Are J.R., Ayale M., Banks T., Barabara V., Benton J., Blmage K., Blankenburg K., Bonin D., Bouck J., Bowls S., Brileva M., Brown E., Brown M., Bryant N.P., Bulay C., Burch P., Burkett C., Burrell K.L., Byrd N.C., Carron T.F., Carter M., Cavazos S.R., Chacko J., Chavez D., Chen G., Chen R., Chen Z., Chowdhry I., Christopoulos C., Cleveland C.D., Cox C., Coyle M.D., Dathorne S.R., David R., Davila M.L., Davis C., Davy Carroll L., Dederich D.A., Delaney K.R., Delgado O., Denn A.L., Ding Y., Dinh H.H., Douthwaite K.J., Draper H., Dugan-Rocha S., Durbin K.J., Earhart C., Edgar D., Edwards C.C., Elhaj C., Escoto M., Falls T., Ferraguto D., Flagg N., Ford J., Foster P., Frantz P., Gabisi A., Gao J., Garcia A., Garner T., Garza N., Gill R., Gorrell J.H., Guevara W., Gunaratne P., Hale S., Hamilton K., Harris C., Harris K., Hart M., Havlak P., Hawes A., Hernandez J., Hernandez O., Hodgson A., Hognes M., Holloway C., Hollins B., Homsi F., Howard S., Huber J., Hulik S., Hume J., Jackson L.E., Jacobson B., Jia Y., Johnson R., Jolivet S., Joudh S., Karlsson E., Kelly S., Khan U., King L., Korvah J., Kovar C., Kratoch J., Kuresh A., Landy N., Leal B., Lewis L.C., Lewis L., Li J., Li Z., Lichtarge O., Lieu C., Liu J., Liu W., Louised H., Lozado R.J., Lu X., Lucier A., Lucier R., Luna R., Ma J., Maheshwari M., Mapua P., Martin R., Marindale A., Martinez E., Massey E., Mawhney E., McLeod M.P., Meador M., Mel G., Metzker M., Miner G., Miner Z., Mitchell T., Mohabat K., Morgan M., Morris S., Moser N., Neal D., Newton J., Newton N., Nguyen A., Nguyen N., Nguyen N., Nickerson E., Nwokenwo S., Ogun M., Okunolu G., Oregunye N., Oviedo R., Pace A., Payton B., Peery J., Perez L., Peters L., Pickens R., Primus E., Pu L., Quides M., Ren Y., Rives M., Rojas A., Rojibokan I., Rolfe M., Ruiz S., Savary G., Scherer S., Scott G., Shen H., Shoostari N., Sisson I., Sodergren E., Sotolake T., Sparks A., Stanley H., Stone H., Sutton A., Svatik A., Tabor P., Tameris A., Tameris K., Tang H., Tansley J., Taylor C., Taylor T., Teitord B., Thomas N., Thomas S., Umanil K., Vasquez M., Vera V., Villalob D., Vinson R., Wang Q., Wang S., Ward-Moore S., Warren R., Washington C., Watlington S., Williams G., Williamson A., Wlarczyk R., Wooden S., Worley K., Wu C., Wu Y., Wu Y.F., Zhou J., Zorilla S., Nelson D., Weinstock G. and Gibbs R.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Unpublished
 2 (bases 1 to 125703)
 Direct Submission
 Submitted (29-MAY-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 125703)
 Direct Submission
 Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 2, 2002 this sequence version replaced gi:21240186.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc.help@bcm.tmc.edu
 ----- Project Information
 Center project name: GUSC
 Center clone name: CH230-71J19

----- Summary Statistics

Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; Version 0.990329
 Consensus quality: 82161 bases at least Q40
 Consensus quality: 88014 bases at least Q30
 Consensus quality: 92229 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 NOTE: This is a "working draft" sequence. It currently
 consists of 52 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1	1165:	contig of 1165 bp in length
*	1166:	gap of unknown length
*	1266:	contig of 1381 bp in length
*	2647:	gap of unknown length
*	2747:	contig of 1559 bp in length
*	4306:	gap of unknown length
*	4405:	gap of unknown length
*	5848:	contig of 1442 bp in length
*	5947:	gap of unknown length
*	7595:	contig of 1648 bp in length
*	7696:	gap of unknown length
*	8847:	contig of 1151 bp in length
*	8946:	gap of unknown length
*	10063:	contig of 1117 bp in length
*	10647:	gap of unknown length
*	10664:	gap of unknown length
*	10664:	gap of unknown length
*	11482:	contig of 1318 bp in length
*	11481:	gap of unknown length
*	11581:	gap of unknown length
*	11582:	contig of 1071 bp in length
*	12652:	gap of unknown length
*	12752:	gap of unknown length
*	13756:	contig of 1004 bp in length
*	13856:	gap of unknown length
*	14899:	contig of 1043 bp in length
*	14900:	gap of unknown length
*	15000:	gap of unknown length
*	15000:	gap of unknown length
*	16179:	contig of 1179 bp in length
*	16278:	gap of unknown length
*	16279:	contig of 1436 bp in length
*	17714:	gap of unknown length
*	17815:	contig of 1691 bp in length
*	19505:	gap of unknown length
*	19606:	gap of unknown length
*	21884:	contig of 2279 bp in length
*	21885:	gap of unknown length
*	21985:	gap of unknown length
*	23369:	contig of 1585 bp in length
*	23670:	gap of unknown length
*	23670:	gap of unknown length
*	25429:	contig of 1760 bp in length
*	25529:	gap of unknown length
*	25530:	gap of unknown length
*	26823:	contig of 1294 bp in length
*	26923:	gap of unknown length
*	26924:	gap of unknown length
*	28501:	contig of 1578 bp in length
*	28502:	gap of unknown length
*	29631:	contig of 1030 bp in length
*	29731:	gap of unknown length
*	29732:	contig of 1082 bp in length
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*	30913:	gap of unknown length
*	32629:	contig of 1716 bp in length
*	32729:	gap of unknown length
*	32730:	contig of 1173 bp in length
*	33902:	contig of 1173 bp in length
*	34002:	gap of unknown length
*	34003:	gap of unknown length
*	34003:	gap of unknown length
*	35366:	contig of 1364 bp in length
*	35466:	gap of unknown length
*	35467:	gap of unknown length
*	37117:	contig of 1651 bp in length
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*	38825:	contig of 1608 bp in length
*	38926:	gap of unknown length
*	41573:	contig of 2648 bp in length
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*	43020:	contig of 1347 bp in length


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1525..1552
repeat_region     /rpt_family="(TTTA)n"
1526..1814
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6131..6178
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8776..8838
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9743..9895
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15183..15321
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15183..15321
misc_feature      /note="match to EST BG755617 (NID:g14064270)"
15183..15321
misc_feature      /note="match to EST H06756 (NID:g870288) y183b07.r1"
15184..15321
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15184..15321
misc_feature      /note="match to EST BG184021 (NID:g13705708)"
15184..15320
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15184..15320
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15767..15789
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15864..18081
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misc_feature      18931..19337
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y175b04.s1"
misc_feature      18938..19409
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af46b10.s1"
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repeat_region     19406..19426
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misc_feature      19407..19710
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misc_feature      19498..19795
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misc_feature      19873..20090
/note="match to EST BG200485 (NID:g13722172)"
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(NID:g11767217)"

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QY 30 CAGGCTTTCGCGTCAATTCACAGTCTACAGTGAAGAAATTCAGTGAACAACGACT 89
DB 15324 CAGGCTTTCGCGTCAATTCACAGTCTACAGTGAAGAAATTCAGTGAACAACGACT 15265

QY 90 GCTCCTCCCGCAGCTTCAATTCGAAATTCACAGTGAAGAAATTCAGTGAACAACGACT 149
DB 15264 GCTCCTCCCGCAGCTTCAATTCGAAATTCACAGTGAAGAAATTCAGTGAACAACGACT 15205

QY 150 AAGTGATGAGCAAGTCCCG 171
DB 15204 AAGTGATGAGCAAGTCCCG 15183

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RESULT 17
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LOCUS      Mus musculus chromosome UNK clone RP23-462P13, WORKING DRAFT
DEFINITION
SEQUENCE, 5 unordered pieces.
ACCESSION
AC124493
VERSION
AC124493.2 GI:21699722
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE
house mouse.
ORGANISM
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 209885)
AUTHORS
McPherson,J.D. and Waterston,R.H.
TITLE
The sequence of Mus musculus clone
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 209885)
AUTHORS
McPherson,J.D. and Waterston,R.H.
TITLE
Direct Submission
JOURNAL
Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE
3 (bases 1 to 209885)
AUTHORS
McPherson,J.D. and Waterston,R.H.
TITLE
Direct Submission

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AXI36556      AXI36556      591 bp      DNA      linear      PAT 30-MAY-2001
LOCUS
DEFINITION   Sequence 478 from Patent EP1067182.
ACCESSION   AXI36556
VERSION     AXI36556.1 GI:14727960
KEYWORDS
SOURCE      human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 591)
AUTHORS     Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and
            Hayashil, K.
TITLE       Secretory protein or membrane protein
JOURNAL     Patent: EP 1067182-A 478 10-JAN-2001;
            Helix Research Institute (JP)
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source      1..591
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            /db_xref="taxon:9606"
BASE COUNT   108 a 198 c 173 g 109 t 3 others
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Best Local Similarity 100.0%; Pred. No. 1,6e-135;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGCACCTTTTGGCGGATTTCTTCTTCCAGGCTTTGCGTGCAATTCAGTGTACCA 60
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DB 294 GGCACCTTTTGGCGGATTTCTTCTTCCAGGCTTTGCGTGCAATTCAGTGTACCA 353
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OY 61 GTTGAGAGATTCAGTGTGAGCAAGAGTGTCTCTCCCGGAGTTCATTGATTCAC 120
    |||||||
DB 354 GTTGAGAGATTCAGTGTGAGCAAGAGTGTCTCTCCCGGAGTTCATTGATTCAC 413
    |||||||

OY 121 GGTGAACCTTCAGATGTGTCTGTCAGAAAGATGATGAGCAAGTCCGGGATCATGTA 180
    |||||||
DB 414 GGTGAACCTTCAGATGTGTCTGTCAGAAAGATGATGAGCAAGTCCGGGATCATGTA 473
    |||||||

OY 181 CCGCAAGTCTGTGATCATGAGCGGCTGTCTCATGCTCTCCCGGATGACAGTCTT 240
    |||||||
DB 474 CCGCAAGTCTGTGATCATGAGCGGCTGTCTCATGCTCTCCCGGATGACAGTCTT 533
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OY 241 CTGCTCCCA 250
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DB 534 CTGCTCCCA 543
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RESULT 16
AC010974/c      147131 bp      DNA      linear      PRI 01-MAR-2002
LOCUS
DEFINITION   Homo sapiens BAC clone RP11-159N20 from 2, complete sequence.
ACCESSION   AC010974
VERSION     AC010974.9 GI:19033964
KEYWORDS
SOURCE      Homo sapiens.
ORGANISM     Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 147131)
AUTHORS     Sulston, J.E. and Waterston, R.
TITLE       Toward a complete human genome sequence
JOURNAL     Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE     99063792
PUBMED     9847074
REFERENCE   2 (bases 1 to 147131)
AUTHORS     Vanbrunt, A. and Stromatt, C.
TITLE       The sequence of Homo sapiens BAC clone RP11-159N20
JOURNAL     Unpublished (2001)
REFERENCE   3 (bases 1 to 147131)
AUTHORS     Waterston, R.H.
TITLE       Direct Submission
JOURNAL     Submitted (28-SEP-1999) Genome Sequencing Center, Washington

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REFERENCE
AUTHORS     MO 63108, USA
TITLE       4 (bases 1 to 147131)
JOURNAL     Direct Submission
            Submitted (23-MAR-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5 (bases 1 to 147131)
AUTHORS     Waterston, R.
TITLE       Direct Submission
JOURNAL     Submitted (01-MAR-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
            On Mar 1, 2002 this sequence version replaced gi:13435273.
            ----- Genome Center
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site: http://genome.wustl.edu/gsc
            Contact: sapiens@wustl.wustl.edu
            ----- Summary Statistics
            Center project name: H_NH0159N20
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NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E.,
Tateno, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at http://www.choil.org
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP11-458A7, 200 bp overlap; the
clone sequenced to the right is RP11-258B17. Actual start of this
clone is at base position 1 of RP11-159N20; actual end is at base
position 147131 of RP11-159N20.

There are polymorphic base differences in the overlap between the
clone RP11-159N20 and RP11-258B17.

FEATURES
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            . 118..1013
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            984..1176
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Best Local Similarity 99.8%; Pred. No. 6.9e-203;
Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1196 CCGAGTGAAGTGAAGAAAGCTCCGAGAGAGGAGAGATCATGATGACCGGGAAGT 1255
DB 431 CCGAGCTGAGTGAAGAAAGCTCCGAGAGAGGAGAGATCATGATGACCGGGAAGT 372
QY 1256 AGGACCTGCTCCAGTGTCTGTTGGTGGCCGAGCCATGATCCTCCGAATCTGTTGG 1315
DB 371 AGGACCTGCTCCAGTGTCTGTTGGTGGCCGAGCCATGATCCTCCGAATCTGTTGG 312
QY 1316 GCATCCAGCATAGCGGCAATGTACACAAATCAGCCCTGGGAGAGAGAGAGGGA 1375
DB 311 GCATCCAGCATAGCGGCAATGTACACAAATCAGCCCTGGGAGAGAGAGAGGGA 252
QY 1376 GAGACAGAGAAAGAAACACAGCATGAGAAACAGTAATGAATAAACCATAAATA 1435
DB 251 GAGACAGAGAAAGAAACACAGCATGAGAAACAGTAATGAATAAACCATAAATA 192
QY 1436 TTTAGCCCCCTGCTGCTGCTTACTGCGGAGAAATGTTTCAACCCGGGGGA 1555
DB 191 TTTAGCCCCCTGCTGCTGCTTACTGCGGAGAAATGTTTCAACCCGGGGGA 132
QY 1496 CTTCACACCTCTTTTGGCCACAGAGAGAAATTAACATGTTTCAACCCGGGGGA 1555
DB 131 CTTCACACCTCTTTTGGCCACAGAGAGAAATTAACATGTTTCAACCCGGGGGA 72
QY 1556 GTTGCTGTGTTAAAGAAAGCACTAAATGCTTTACAGCTTAAACCAAAAAA 1610
DB 71 GTTGCTGTGTTAAAGAAAGCACTAAATGCTTTACAGCTTAAACCAAAAAA 17

RESULT 13
AX093381 369 bp DNA linear PAT 30-MAR-2001
LOCUS
DEFINITION Sequence 199 from Patent WO0118046.
ACCESSION AX093381
VERSION AX093381.1 GI:13509829
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 369).
AUTHORS Xu,J. and Stolk,J.A.
TITLE Ovarian tumor sequences and methods of use therefor
JOURNAL Patent: WO 0118046-A 199 15-MAR-2001;
CORIXA CORPORATION (US)
FEATURES
source
1. 369
Location/Qualifiers
misc_feature 1..369
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BASE COUNT 82 a 109 c 90 g 86 t 2 others
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Best Local Similarity 100.0%; Pred. No. 6.3e-174;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 30 CAGGCTTTCGCTGCAAAATCCAGTGTACAGTGAAGATTCACCTGAACAAGACT 89
QY 90 GCTCCTCCCGGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 149
DB 90 GCTCCTCCCGGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 149

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QY 150 AAGTATGAGCAAGATGCGGGGATCATATGATACCGAATGCTGTGATCATACAGGCT 209
DB 150 AAGTATGAGCAAGATGCGGGGATCATATGATACCGAATGCTGTGATCATACAGGCT 209
QY 210 GTCTCATGCTCTTGGCGGGGTACAGTCCCTGCTCCCGAGGAAAGTAACTGATGTT 269
DB 210 GTCTCATGCTCTTGGCGGGGTACAGTCCCTGCTCCCGAGGAAAGTAACTGATGTT 269
QY 270 GCATGAGTGTGCAACACCCCTTTTGAACGGGCAAGGCCCAAGAAAGGGAAGTT 329
DB 270 GCATGAGTGTGCAACACCCCTTTTGAACGGGCAAGGCCCAAGAAAGGGAAGTT 329
QY 330 CTGCTCGGCGCTCA 344
DB 330 CTGCTCGGCGCTCA 344

RESULT 14
AX093191 396 bp DNA linear PAT 30-MAR-2001
LOCUS
DEFINITION Sequence 9 from Patent WO0118046.
ACCESSION AX093191
VERSION AX093191.1 GI:13509640
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 396).
AUTHORS Xu,J. and Stolk,J.A.
TITLE Ovarian tumor sequences and methods of use therefor
JOURNAL Patent: WO 0118046-A 9 15-MAR-2001;
CORIXA CORPORATION (US)
FEATURES
source
1. 396
Location/Qualifiers
misc_feature 1..396
/db_xref="taxon:9606"
BASE COUNT 90 a 117 c 95 g 92 t 2 others
ORIGIN
Query Match 19.1%; Score 310; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 5.6e-171;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGCGGATGTTCTTCTCCAGGCTTGGCGTGAATCCAGTGTACCA 60
DB 11 GGCACCTTTTGGCGGATGTTCTTCTCCAGGCTTGGCGTGAATCCAGTGTACCA 70
QY 61 GTGTGAAGAAATTCACGCTGACAGACAGTCTCTCCCGAGTTCAATGTAATGCAC 120
DB 71 GTGTGAAGAAATTCACGCTGACAGACAGTCTCTCCCGAGTTCAATGTAATGCAC 130
QY 121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGTATGAGCAAAAGTGGCGGATCATGTA 180
DB 131 GGTGAAGCTTCAAGACATGTGTCAAGAAAGTATGAGCAAAAGTGGCGGATCATGTA 190
QY 181 CCGCAGTCTCTGATCATATGAGCGGCTGTCTCATGCTCTCCGAGTACAGTCTT 240
DB 191 CCGCAGTCTCTGATCATATGAGCGGCTGTCTCATGCTCTCCGAGTACAGTCTT 250
QY 241 CTGCTCCCGAGGAAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 251 CTGCTCCCGAGGAAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 310
QY 301 CCGGCGCAAG 310
DB 311 CCGGCGCAAG 320

RESULT 15

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1. .1362
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2q21-22"
/tissue_type="brain"
/dev_stage="fetal"
1. .1362
/gene="GPR39"
1. .1362
/cds
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/product="GPR39"
/protein_id="AAC26082.1"
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/translating="MSPSLPGSDSCSIIIDSHVPEFVATNKKITLIVLIIIVMG
LGNSTATRVQVLOKGYLOKEVTDHWSLACSDLVILGMEFYITINPLTTS
SYLTKHTEFLFACSYATLHLTLSEFERYIAICHPEYKAVSGPCQVKLIGFW
VTSALVALPILFAMTEYPLVNPVSHRGLTNSRSTHNEOPTSNMSISCTNLSMT
VFGSISGAPVYVYLVSVAFMCMWVYLMKSGSLAGTRPQLKSESEERT
ARQITIFLRLVITLAVCMKPNRIRIMAAKPKHDWTSYRAYMILPSEETFEY
LSSVINPLLYVSSQDFRVFVVOYLCCRLSLQANHEKRLRVASHSTTSARVORPL
LFASRRSSARREKIFLSTFQSAEPQSKSLSLESLPNSGAPNANSAALNGQE
HEV"
BASE COUNT      263 a      435 c      362 g      302 t
ORIGIN
Query Match      23.8%; Score 386; DB 9; Length 1362;
Best Local Similarity 99.8%; Pred. No. 6.9e-216; Indels 1; Gaps 1;
Matches 506; Conservative 0; Mismatches 0;
QY 845 TCAAACTGCTGCTCGTGAACCATCTCTGACAGAGATTTGGCTGTTCCGCCCTGA 904
D 1362 TCAAACCTTCATGCTCTCGTGAACCATCTCTGACAGAGATTTGGCTGTTCCGCCCTGA 1303
QY 905 GTTGGGCTCTAGTACTCGAGACTCAATGACCTGAGCTTGGGGCTGGCCCTGCT 964
D 1302 GTTGGGCTCTAGTACTCGAGACTCAATGACCTGAGCTTGGGGCTGGCCCTGCT 1243
QY 965 CTGAAGGTGCTTAAAGAAATCTTCTCAGTTCTCTTGCAGAGAGACTGGCGCGGAGCG 1024
D 1242 CTGAAGGTGCTTAAAGAAATCTTCTCAGTTCTCTTGCAGAGAGACTGGCGCGGAGCG 1183
QY 1025 GAAGAGCAAGCGGCGCTGCAACAAAGCGGCGCTGCTGGTGGTGGATGGGCAATGACGG 1084
D 1182 GAAGAGCAAGCGGCGCTGCAACAAAGCGGCGCTGCTGGTGGTGGATGGGCAATGACGG 1123
QY 1085 CAGCGGCTCTGCTGGTGGGCTGCTGACGACGAGCGGCGACAGCAGCAGCCTTGCACGA 1144
D 1122 CAGCGGCTCTGCTGGTGGGCTGCTGACGACGAGCGGCGACAGCAGCAGCAGCAGC -TGCACGA 1064
QY 1145 ACACCCCGCGAAGCTGCTGCGAGGAGACACCGTGTACAGAGCGGCTGTATGACCGAGACTGA 1204
D 1063 ACACCCCGCGAAGCTGCTGCGAGGAGACACCGTGTACAGAGCGGCTGTATGACCGAGACTGA 1004
QY 1205 GGTAGAAAAGCTGCTCGAAGAAAGGAGGAGGATCATGTACGCCCGGAAGTAGAGACTCG 1264
D 1003 GGTAGAAAAGCTGCTCGAAGAAAGGAGGAGGATCATGTACGCCCGGAAGTAGAGACTCG 944
QY 1265 TCCAGTCGCTGCTGGCTTGGCCCGAGCCAGCATGATCTCCGAATCTGTTGGGCACTCCAGC 1324
D 943 TCCAGTCGCTGCTGGCTTGGCCCGAGCCAGCATGATCTCCGAATCTGTTGGGCACTCCAGC 884
QY 1325 ATACGCCCAATGTACAAACATCAGCC 1351
D 883 ATACGCCCAATGTACAAACATCAGCC 857

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RESULT 11
AX136698/C      587 bp      DNA      linear      PAT 30-MAY-2001
LOCUS      AX136698

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DEFINITION      Sequence 620 from Patent EP1067182.
ACCESSION      AX136698
VERSION      AX136698.1
KEYWORDS      GI:14273102
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 587)
AUTHORS      Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and
Hayashii, K.
TITLE      Secretory protein or membrane protein
JOURNAL      Patent: EP 1067182-A 620 10-JAN-2001;
Helix Research Institute (Jp)
FEATURES
source
1. .587
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT      117 a      162 c      140 g      162 t      6 others
ORIGIN
Query Match      22.6%; Score 366; DB 6; Length 587;
Best Local Similarity 99.8%; Pred. No. 4.5e-204; Indels 0; Gaps 0;
Matches 416; Conservative 0; Mismatches 1;
QY 1183 AGCGGTTGATGACCGAGCTGAGTAGAAAAAGCTCTCCGAAAGGAGAGAGATCATG 1242
D 417 AGCGGTTGATGACCGAGCTGAGTAGAAAAAGCTCTCCGAAAGGAGAGAGATCATG 358
QY 1243 TACGCCCGGAAGTAGACCTCGTCGAGTCGCTGGGTTGGCCGAGCATGATCCTC 1302
D 357 TACGCCCGGAAGTAGACCTCGTCGAGTCGCTGGGTTGGCCGAGCATGATCCTC 298
QY 1303 CGAATCTGTTGGGCAATCCAGCATACGGCCAAATGTACACAAATGACCCCTGGCAGCA 1362
D 297 CGAATCTGTTGGGCAATCCAGCATACGGCCAAATGTACACAAATGACCCCTGGCAGCA 238
QY 1363 CGAGCAGAGAGGAGAGACAGAGAAAAAGAAACACAGCATGGAACACAGTAAATGATA 1422
D 237 CGAGCAGAGAGGAGAGACAGAGAAAAAGAAACACAGCATGGAACACAGTAAATGATA 178
QY 1423 AAACCATTAATTTTAAAGCCCTCTGTTGCTTACTGCGCCAGAAATGGTACCAAT 1482
D 177 AAACCATTAATTTTAAAGCCCTCTGTTGCTTACTGCGCCAGAAATGGTACCAAT 118
QY 1483 TTTCAGTGTGGACTGTACAGCTCTTTTCCCAAGCAGAGAGAGATTTAAGTACTGTT 1542
D 117 TTTCAGTGTGGACTGTACAGCTCTTTTCCCAAGCAGAGAGAGATTTAAGTACTGTT 58
QY 1543 CAACCCGCGGAGTGTGCTGTAAAGAAAGCAATTAATGCTTTAGACAGTGT 1599
D 57 CAACCCGCGGAGTGTGCTGTAAAGAAAGCAATTAATGCTTTAGACAGTGT 1

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RESULT 12
AX150120/C      444 bp      DNA      linear      PAT 08-JUN-2001
LOCUS      AX150120
DEFINITION      Sequence 95 from Patent WO0136685.
ACCESSION      AX150120
VERSION      AX150120.1
KEYWORDS      GI:14348148
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 444)
AUTHORS      Kroes, R.A., Moskal, J.R. and Yamamoto, H.
TITLE      Differential gene expression in cancer
JOURNAL      Patent: WO 0136685-A 95 25-MAY-2001;
Nyxis Neurotherapies, Inc. (US)
FEATURES
source
1. .444
/organism="Homo sapiens"

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Db 225 AGACGACGGGCGCTGCCAACAAGCGGGCGCTGCTGGTGAGTGCGCATGTACGGCA 284
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Db 285 GGGCCTTCTCGTGGTGGCCCTGCTGACGCGACGAGCGGACACAGACCTTGCAGGAC 343
QY 1147 ACCCGCGGAACCTCTGCGAGGACACCGTGTACAGAGCGGGTTGATGACCGAGCTGAG 1206
Db 344 ACCCGCGGAACCTCTGCGAGGACACCGTGTACAGAGCGGGTTGATGACCGAGCTGAG 403
QY 1207 TAGAAAAACGTCCTCGAAGGAGGAGAGATCATGTACCGCCCGGAGTAGTAGAGCTGTC 1266
Db 404 TAGAAAAACGTCCTCGAAGGAGGAGAGATCATGTACCGCCCGGAGTAGTAGAGCTGTC 463
QY 1267 CAGTCGTCTGGTGGTGGCCGACGCCATGATCTCCGAACTGTGTTGGGATTCACGAT 1326
Db 464 CAGTCGTCTGGTGGTGGCCGACGCCATGATCTCCGAACTGTGTTGGGATTCACGAT 523
QY 1327 ACGGCGAATGTACAAATACAGCCCTGGGACAGACAGAGAGGAGAGAGAGAGAA 1386
Db 524 ACGGCGAATGTACAAATACAGCCCTGGGACAGACAGAGAGAGAGAGAGAGAA 583
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Db 584 AAAAAAACAAGCATGAGAACACAGTAATGAATAAATTAATTAATTTAGCCCTC 643
QY 1447 TGTTCCTGCTACTGCGCCAGGAATGTACCAATTTTTCAGTGTGGACTGACAGCTT 1506
Db 644 TGTTCCTGCTACTGCGCCAGGAATGTACCAATTTTTCAGTGTGGACTGACAGCTT 703
QY 1507 CTTTTCGACAGACAGAGAAATTAATTAACCTGTTCAACCCGGGGAGATTGGCTGTG 1566
Db 704 CTTTTCGACAGACAGAGAAATTAATTAACCTGTTCAACCCGGGGAGATTGGCTGTG 763
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RESULT 9
AX319942/c 1362 bp DNA linear PAT 14-DEC-2001
LOCUS AX319942
DEFINITION Sequence 1 from Patent WO0181634.
ACCESSION AX319942
VERSION AX319942.1 GI:17901489
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Galvin, K.A. and Rudolph-Owen, L.A.
TITLE Methods and compositions for the diagnosis and treatment of
JOURNAL cardiovascular and tumorigenic disease using 4941
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source location/Qualifiers
1..1362
/organism="Homo sapiens"
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/codon_start=1
/protein_id="CAD19381.1"
/db_xref="GI:17901490"
/translation="WASPSLPQSDSQIIDSHVPEFVATWIKITLLVLIIFVMG
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VTSALVALPLEFAMGTEPLVNVPSHRELTNRSTRHHEPNSNNSICTNLSKRT
VQSSIFGAFVYLVYLLSVAFKMNQVLYMSKSGSLAGTRPPOLRKSSEEST
ARROITIFRLIVYTLVACGMNQIRIKMAAKPKHDKTRVFAFYMTLLPFSTFEY
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BASE COUNT 263 a 435 c 362 g 302 t
ORIGIN
HEV"
Query Match 23.8%; Score 386; DB 6; Length 1362;
Best Local Similarity 99.8%; Pred. No. 6; 9e-216;
Matches 506; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 845 TCACACTTATGCTCTCTGAACACATTTCTCTGACAGCAATTTGCTGTTGCGCCCTGA 904
Db 1362 TCACACTTATGCTCTCTGAACACATTTCTCTGACAGCAATTTGCTGTTGCGCCCTGA 1303
QY 905 GTGGGCTCTAGAGACTCAGACTCAATATGCTGGAGCTTAGAGTGGCTGCGCTCCT 964
Db 1302 GTGGGCTCTAGAGACTCAGACTCAATATGCTGGAGCTTAGAGTGGCTGCGCTCCT 1243
QY 965 CTGAAAAGTCTTAAAGAAATCTTCACTTCTCTTGCAGAGACTGCGCGGAGCG 1024
Db 1242 CTGAAAAGTCTTAAAGAAATCTTCACTTCTCTTGCAGAGACTGCGCGGAGCG 1183
QY 1025 GAAGAGCAACGGGCGCTGCACAAAGCGGGCGCTGTCGTTGAGTGCATGTACCG 1084
Db 1182 GAAGAGCAACGGGCGCTGCACAAAGCGGGCGCTGTCGTTGAGTGCATGTACCG 1123
QY 1085 CAGGCGCTTCTGCTGTTGGCTGCTGCTGACAGACAGCGGCGACACACTTGCACGA 1144
Db 1122 CAGGCGCTTCTGCTGTTGGCTGCTGCTGACAGACAGCGGCGACACACTTGCACGA 1064
QY 1145 ACACCCCGCGAAACGTCGCGAGACACCGCTGTACAGAGCGGGTGTATGACCGAGCTGA 1204
Db 1063 ACACCCCGCGAAACGTCGCGAGACACCGCTGTACAGAGCGGGTGTATGACCGAGCTGA 1004
QY 1205 GGTAGAAAACGCTCTCCGAGAGAGGAGATATATAGCCCGGAGATAGACCTCG 1264
Db 1003 GGTAGAAAACGCTCTCCGAGAGAGGAGATATATAGCCCGGAGATAGACCTCG 944
QY 1265 TCCAGTCTGCTTGGCTTGGCCGACGACATGATCTCCGATGCTGTTGGGATCCAGC 1324
Db 943 TCCAGTCTGCTTGGCTTGGCCGACGACATGATCTCCGATGCTGTTGGGATCCAGC 884
QY 1325 ATAGGCGCAATGTCAACATCAGCC 1351
Db 883 ATAGGCGCAATGTCAACATCAGCC 857

RESULT 10
AF034633/c 1362 bp mRNA linear PRI 13-JUL-1998
LOCUS AF034633
DEFINITION Homo sapiens orphan G protein-coupled receptor (GPR39) mRNA,
ACCESSION AF034633
VERSION AF034633.1 GI:2654160
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS McKee, K.K., Tan, C.P., Palyha, O.C., Liu, J., Feighner, S.D.,
Hreniuk, D.L., Smith, R.G., Howard, A.D., and Van Der Ploeg, L.H.
TITLE Cloning and characterization of two human G protein-coupled
JOURNAL receptor genes (GPR38 and GPR39) related to the growth hormone
MEDLINE secretagogue and neurotensin receptors
98110578
9441746
2 (bases 1 to 1362)
McKee, K.K., Tan, C.P., Palyha, O.C., Liu, J., Feighner, S.D.,
Hreniuk, D.L., Smith, R.G., Van Der Ploeg, L.H.T., and Howard, A.D.
Direct Submission
Submitted (17-NOV-1997) Biochemistry and Physiology, Merck and Co.,
Inc., PO Box 2000, Rahway, NJ 07065, USA
location/Qualifiers

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contact: nisc_mgc@nhl.nih.gov
 Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
 Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Snyder, B., Stantrick, S., Thomas, P.J.,
 Tjongson, E.E., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A.,
 Zhang, L.H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 39 Row: b Column: 19

This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis. Similarity but not identity to protein.

FEATURES

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1. 946

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/db_xref="taxon:9606"

/clone="MGC:29643 IMAGE:3641660"

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/lab_host="DH10B-R"

/note="Vector: pOTB7"

261. 686

/codon_start=1

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/protein_id="AAH17318.1"

/db_xref="GI:16878240"

/translation="MNVLGIAAFPCGLFLPFAIDIQCYCEPFLNDSSPERIV
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CDS

BASE COUNT 197 a 292 c 261 g 196 t

Query Match 40.0%; Score 648; DB 9; Length 946;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 281 GGCACCTTTTGGCGATGTTCTTGCCTCCAGGCTTTGCGCTGCAATCCAGTCTTCCA 340
 61 GTGTGAAGAATTCACGCTGACACGAGTCTCTCCCGGAGTTCATTTGAAATTCGAC 120
 341 GTGTGAAGAATTCACGCTGACACGAGTCTCTCCCGGAGTTCATTTGAAATTCGAC 400
 121 GGTGACGTTCAAGCATGTGTGACAGAAAGATGAGCAAAAGTCCCGGAGTTCATGTA 180
 401 GGTGACGTTCAAGCATGTGTGACAGAAAGATGAGCAAAAGTCCCGGAGTTCATGTA 460
 181 CCGCAAGTCTGTGATGATGAGGCGCTGTCTCTGCTCTGCGGAGTTCAGTCTT 240
 461 CCGCAAGTCTGTGATGATGAGGCGCTGTCTCTGCTCTGCGGAGTTCAGTCTT 520
 241 CTGCTCTCCAGGAAATGCACTGATTGATGATGATGATGATGATGATGATGATGAT 300
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 581 CCGGCGCAAGGCGCAAGAAAGGGAATTTCTGCTCTGCGGAGTTCAGTCTT 640
 361 CACGATCCGCTCTCAATTTAGCCCTCTGCGGAGTTCAGTCTT 420
 641 CACGATCCGCTCTCAATTTAGCCCTCTGCGGAGTTCAGTCTT 700
 421 CCACCCCTCTCTGATTTGTTTCCAGGCTTCGCCCCCAACCCCTCTCTGATGTA 480
 701 CCACCCCTCTCTGATTTGTTTCCAGGCTTCGCCCCCAACCCCTCTCTGATGTA 760
 481 GTTCTCTCTGATTTGTTTCCAGGCTTCGCCCCCAACCCCTCTCTGATGTA 540

Db 761 GTTCTCTCTGATTTGTTTCCAGGCTTCGCCCCCAACCCCTCTCTGATGTA 820
 QY 541 CCTGTGCAATATGAAAGCTCGCTTAAGCATCTGAATTAATTCAGCTGATGAT 600
 Db 821 CCTGTGCAATATGAAAGCTCGCTTAAGCATCTGAATTAATTCAGCTGATGAT 880
 QY 601 TTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 648
 Db 881 TTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 928

RESULT 8

BC011449

LOCUS

BC011449

DEFINITION

BC011449

ACCESSION

BC011449.1

VERSION

GI:15277472

KEYWORDS

SOURCE

ORGANISM

Homo sapiens.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 826)

Strausberg, R.

Direct Submission

Submitted (25-JUN-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

Contact: MGC help desk

Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC/DC/DP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

Contact: amadan@systemsbiology.org

Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia

Greene, Mark Kettelman and Anuradha Madan

REMARK

COMMENT

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 25 Row: n Column: 18This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis.

Location/Qualifiers

1. 826

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4026092"

/tissue_type="Skin, melanotic melanoma."

/clone_lib="NIH_MGC_20"

/lab_host="DH10B-R"

/note="Vector: pOTB7"

FEATURES

source

1. 826

/organism="Homo sapiens"

/db_xref="taxon:9606"

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 Best Local Similarity 99.7%; Pred. No. 1; 7e-307;
 Matches 711; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

907 TGGGCTCTAGTACTGAGACTGAGACTGAGACTGAGACTGAGACTGAGACTGAGACT 966
 105 TGGGCTCTAGTACTGAGACTGAGACTGAGACTGAGACTGAGACTGAGACTGAGACT 164
 QY 967 GAAAGTCTTAAAGAAATCTTCTCACTTCTCTTCTGAGAGAGAGAGAGAGAGAG 1026
 Db 165 GAAAGTCTTAAAGAAATCTTCTCACTTCTCTTCTGAGAGAGAGAGAGAGAGAG 224
 QY 1027 AGAGCAAGGCGCTGCAAGAGGCGGCTGCGGAGTGAAGTGAAGTGAAGTGAAG 1086

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 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1594; Conservative 0; Mismatches 2; Indels 4; Gaps 4;

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 353 GGCACATTTTGGCGATGTTCTTGTCTCCAGGCTTTGGCGTGAATTCACAGTCTTCCA
 61 GTTGGAAGAAATTCAGCTGGAACAACGAGCTGCTCTCCCGAGTTTCATTTGAATTCAC
 354 GTTGGAAGAAATTCAGCTGGAACAACGAGCTGCTCTCCCGAGTTTCATTTGAATTCAC
 413 GTTGGAAGAAATTCAGCTGGAACAACGAGCTGCTCTCCCGAGTTTCATTTGAATTCAC
 121 GGTGAAGTTTCAACATGCTGCTGGAAGAAGATGATGAGCAAGTCCGGGATCATGTA
 414 GGTGAAGTTTCAACATGCTGCTGGAAGAAGATGATGAGCAAGTCCGGGATCATGTA
 473 GGTGAAGTTTCAACATGCTGCTGGAAGAAGATGATGAGCAAGTCCGGGATCATGTA
 181 CCGCAAGTCTGTGATCATCAGGCGCTGTCTCATGCGCTTGGCGGGATACAGTCTT
 474 CCGCAAGTCTGTGATCATCAGGCGCTGTCTCATGCGCTTGGCGGGATACAGTCTT
 533 CCGCAAGTCTGTGATCATCAGGCGCTGTCTCATGCGCTTGGCGGGATACAGTCTT
 241 CTGCTCCCCAGGGAAGTGAATCAGTTTGCATCAGCTGCTGCAACACCCCTTTGTA
 534 CTGCTCCCCAGGGAAGTGAATCAGTTTGCATCAGCTGCTGCAACACCCCTTTGTA
 593 CTGCTCCCCAGGGAAGTGAATCAGTTTGCATCAGCTGCTGCAACACCCCTTTGTA
 301 CCGGCGCAAGGCGCCAGAAAGGGAAGTGTGCTGCGCCCTGAGCGCAAGGCTCCGCA
 594 CCGGCGCAAGGCGCCAGAAAGGGAAGTGTGCTGCGCCCTGAGCGCAAGGCTCCGCA
 653 CCGGCGCAAGGCGCCAGAAAGGGAAGTGTGCTGCGCCCTGAGCGCAAGGCTCCGCA
 361 CACCATCTCTTCTCTCAATTAATTAAGCCCTCTCTGCGACACTGCTGAAGTGAAGATG
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RESULT 7
 BC017318 946 bp mRNA linear PRI 09-NOV-2001
 LOCUS
 DEFINITION Homo sapiens, clone MGC:29643 IMAGE:3641660, mRNA, complete cds.
 VERSION BC017318.1 GI:16878239
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homini; Homo.
 1 (bases 1 to 946)
 AUTHORS
 TITLE
 JOURNAL
 DIRECT SUBMISSION
 Submitted (05-NOV-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 CONTACT: MGC help desk
 Email: gcaps-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>

REMARK
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CDS

Location/Qualifiers
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HEV"

BASE COUNT 516 a 766 c 677 g 567 t 2 others
ORIGIN

Query Match 71.0%; Score 1149; DB 6; Length 2528;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1319; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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2157 CTCCTCCCGAGTGTCAATGTGTAATGACAGGTGAAGTTCAGACATGTGTGAGAAAGA 2098
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RESULT 6
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LOCUS
DEFINITION
SEQUENCE
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX136281 1890 bp. DNA linear PAT 30-MAY-2001
Sequence 203 from Patent EP1067182.
AX136281
AX136281.1 GI:14272687

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1890)
Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
Secretory protein or membrane protein
Patent: EP 1067182-A 203 10-JAN-2001;
Helix Research Institute (JP)

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RESULT 9
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DEFINITION Homo sapiens, clone MGC:29643 IMAGE:364160, mRNA, complete cds.
ACCESSION BC017318
VERSION BC017318.1 GI:16878239
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 946)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
COMMENT
NTH-MGC Project URL: http://mgc.ncl.nih.gov
Contact: MGC help desk
Email: g9apbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Sequencing Center: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland.
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov

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FEATURES

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/INL at: <http://image.lnl.gov>
 Series: IRAL Plate: 39 Row: b Column: 19
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
 Location/Qualifiers

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BASE COUNT      197 a      292 c      261 g      196 t
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Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 CCACCCCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
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RESULT 10
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LOCUS      Mus musculus chromosome UNK clone RP23-462P13, WORKING DRAFT
DEFINITION      SEQUENCE, 5 unordered pieces.

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ACCESSION      AC124493
VERSION        AC124493.2
KEYWORDS       HTGS, HTGS_PHASE1, HTGS_DRAFT, HTGS_FULLTOP,
SOURCE         house mouse.
ORGANISM       Mus musculus
REFERENCE      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS       1 (bases 1 to 209885)
TITLE         McPherson, J.D. and Waterston, R.H.
JOURNAL       The sequence of Mus musculus clone
REFERENCE      2 (bases 1 to 209885)
AUTHORS       McPherson, J.D. and Waterston, R.H.
TITLE         Unpublished
JOURNAL       McPherson, J.D. and Waterston, R.H.
REFERENCE      3 (bases 1 to 209885)
AUTHORS       McPherson, J.D. and Waterston, R.H.
TITLE         Submitted (05-JUL-2002) Genome Sequencing Center, 4444 Forest Park
JOURNAL       Submitted (05-JUL-2002) Genome Sequencing Center, 4444 Forest Park
COMMENT        Submitted (05-JUL-2002) Genome Sequencing Center, 4444 Forest Park
               On Jul 5, 2002 this sequence version replaced g1:21426614.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.wustl.edu
Center project name: M_BA0462P13

----- Summary Statistics -----
Sequencing vector: M13, 0%
Sequencing vector: plasmid, 100%
Chemistry: Dye-terminator Big Dye, 100% of reads
Assembly program: Phrap, version 0.990319
Consensus quality: 208484 bases at least Q40
Consensus quality: 209285 bases at least Q20
Insert size: 206000; agarose-fp
Insert size: 212112; sum-of-ctrls
Quality coverage: 0.00 in Q20 bases; agarose-fp
Quality coverage: 11.62 in Q20 bases; sum-of-ctrls

----- NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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11332 11431: gap of unknown length
11432 28617: contig of 17186 bp in length
28618 28717: gap of unknown length
28718 48454: contig of 20737 bp in length
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Best Local Similarity 70.96; Pred. No. 1.2e-161;
Matches 1041; Conservative 0; Mismatches 373; Indels 54; Gaps 13;

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RESULT 11
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LOCUS      AX319942
DEFINITION      Sequence 1 from Patent WO0181634.
ACCESSION      AX319942
VERSION      AX319942.1 GI:17901489
KEYWORDS
SOURCE
ORGANISM      human.
                Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1      Galvin,K.A. and Rudolph-Owen,L.A.
    Methods and compositions for the diagnosis and treatment of
    cardiovascular and tumorigenic disease using 4941
    Patent: WO 0181634-A 1 01-NOV-2001;
    Millennium Pharmaceuticals, Inc. (US)
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LOCUS AC112072 92874 bp DNA linear HTG 17-JUL-2002
 DEFINITION Rattus norvegicus clone CH230-286021. *** SEQUENCING IN PROGRESS
 *** 50 unordered pieces.
 AC112072.3 GI:21744373
 HTG: HTGS_PHAHEL.
 KEYWORDS Norway rat.
 SOURCE Rattus norvegicus
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 92874)
 Muzny,D.M., Adams,C., Adio-Oduola,B., Alt-osman,F.R., Allen,C.,
 Alstbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayala,M., Banks,T.,
 Barbieri,J., Benton,J., Blomage,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
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 Weinstein,G. and Gibbs,R.
 TITLE Unpublished
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
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 AUTHORS
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 JOURNAL
 COMMENT
 Direct Submission
 Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 92874)
 Worley,K.C.
 Direct Submission
 Submitted (17-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 13, 2002 this sequence version replaced gi:20303189.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information

Center project name: GRJD
 Center clone name: CH230-286021
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 32512 bases at least Q40
 Consensus quality: 34515 bases at least Q30
 Consensus quality: 35930 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 50 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 5360 6436: contig of 1077 bp in length
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BASE COUNT      23927 a 19653 c 20425 g 23828 t 5041 others
ORIGIN

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Db 75519 CTGCTTGGCATCTCTGAGAGTCAAGCGGCGGAGCAGAGAAC-TGCCAGAAATCTTCCGA 75577

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Db 75578 ACTGCTGAGAGAGAGAGTGTGTAGAGAGAGGTTGACCAAGAGCTGAGTGAAGAAAGG 75637

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OY 1277 TGGCTTGGCCGAGCAGATGATCTCTGGAATCTGCTTGGGATCCAGCATTAAGGCCAATG 1336
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Db 75698 TGGCTTGGCTGAGGAGATGATCTCTGGAATCTGCTTGGGATCCAGCATTAAGGCCAATG 75757

OY 1337 TCACAAATCAGCCCTGGGAGACAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1396
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 75758 TCACAAATCAGCTCTGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 75816

OY 1397 CAGCATGAGAACACATGAATGAATAAA--CCATTAATATTTAGCCCTCTGCTTCTG 1453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 75817 CAGCATGAGAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 75876

OY 1454 -TGCTTCTGCGGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1509
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Db 75877 TGTGCTTCTGCTGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 75936

OY 1510 TTGCGCAGAGAGAGAGAGATTAACACTTTTCAACCCGGGGAGATGGCTGTGTAA 1569
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 75937 TTGCGCAGAGAGAGAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATG 75994

OY 1570 AGAAGACATTAATGCTTTAGACATGTA 1600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 75995 -AAAAAGCGTAAATGCTTTGACAGTGA 76023

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 17:54:48 ; Search time 2169.32 Seconds
(without alignments)
12086.984 Million cell updates/sec

Title: US-09-970-966-211

Sequence: 1619
1 ggcacatttgcgaltgt.....aaaaaaaaaaaaaaaa 1619

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 10

Total number of hits satisfying chosen parameters: 1916787

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
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6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
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23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	571	35.3	888 14	BQ689771 AGENCOURT
2	531	32.8	879 14	BQ689033 AGENCOURT
3	507	31.3	702 14	BQ006545 UI-H-EI-
4	506	31.3	743 10	BE385797
5	467	28.8	676 10	BE385990 601276636
6	466	28.8	696 13	BM547680 AGENCOURT

7	463	28.6	530 12	BF726459	BF726459 by06h03.y
8	461	28.5	537 12	BF594242	BF594242 7n10d03.x
9	437	27.0	457 9	AI459805	AI459805 ap17910.x
10	436	26.9	591 9	AI884686	AI884686 w183d07.x
11	434	26.8	540 12	BF939683	BF939683 nac80b12
12	432	26.7	696 12	BF439382	BF439382 nabc3906
13	429	26.5	538 13	BM667937	BM667937 UI-E-DW1-
14	429	26.5	627 13	BM669397	BM669397 wp69h10.x
15	426	26.3	467 9	AI936826	AI936826 qb53c04.x
16	425	26.3	678 9	AI150931	AI150931 qb53c04.x
17	424	26.2	527 10	AM338938	AM338938 ha68h04.x
18	415	25.6	515 9	AI336858	AI336858 q886g11.x
19	413	25.5	421 14	BM686824	BM686824 UI-E-CR1-
20	412	25.4	500 10	AM075598	AM075598 xb24e07.x
21	411	25.4	551 12	BE858216	BE858216 7919e07.x
22	411	25.4	616 9	AI990500	AI990500 w4d0d07.x
23	411	25.4	649 10	AM590950	AM590950 h951e12.x
24	394	24.3	452 9	AI391683	AI391683 qv93f04.x
25	386	23.8	704 13	BI919074	BI919074 603180881
26	380	23.5	456 9	AI765236	AI765236 w172h08.x
27	379	23.4	821 12	BM981455	BM981455 UI-CF-EN1
28	372	23.0	821 12	BM752229	BM752229 60271372
29	369	22.8	381 12	BP054837	BP054837 7171h01.y
30	368	22.7	371 12	BP054680	BP054680 7169f08.y
31	364	22.5	465 10	AV725028	AV725028 AV725028
32	364	22.5	578 9	AI742092	AI742092 w938h03.x
33	363	22.4	379 9	AA084248	AA084248 zn17f09.x
34	359	22.2	534 10	BE350014	BE350014 h107g12.x
35	355	21.9	573 10	BE395206	BE395206 601309558
36	353	21.8	432 10	AM087372	AM087372 xp19e02.x
37	353	21.8	537 9	AI018769	AI018769 ov32e04.x
38	349	21.6	707 13	BI913989	BI913989 603180565
39	348	21.5	920 9	BE386060	BE386060 601276753
40	347	21.4	933 9	AL538562	AL538562 AL538562
41	338	20.9	368 12	BF935708	BF935708 MR2-WY01.3
42	336	20.8	454 10	AM191974	AM191974 x178a02.x
43	336	20.8	747 13	BI917149	BI917149 603181571
44	334	20.6	540 10	AM954549	AM954549 EST366619
45	328	20.3	690 13	BI669845	BI669845 603293440

ALIGNMENTS

RESULT 1
BQ689771 888 bp mRNA linear EST 15-JUL-2002
LOCUS BQ689771.1 GI.21815087
DEFINITION AGENCOURT_8344092 NIH_MGC_110 Homo sapiens CDNA clone IMAGE:6248684
ACCESSION BQ689771
VERSION BQ689771.1
KEYWORDS EST.
SOURCE human.
ORANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 888)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLT)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNLT at:
http://image.llnl.gov
Plate: LICM2388 row: O column: 21
High quality sequence stop: 665.
Location/Qualifiers
1..888

FEATURES
Source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6248684"
/clone_1ib="NIH_MGC_110"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: pancreas; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

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BASE COUNT      217 a      219 c      264 g      187 t
ORIGIN
Query Match      35.3%; Score 571; DB 14; Length 888;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 691; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 583 AATTGAGCTGACTGAATTTGAGTATGACTTGAAGAGAGGTGAGTGAAGTTCA 642
Db 13 AATTGAGCTGACTGAATTTGAGTATGACTTGAAGAGAGGTGAGTGAAGTTCA 72
QY 643 CCCCCATGCTGTGTACCGGAGTCAAGCCAGCTGCGACAGTCAATTCAGTCA 702
Db 73 CCCCCATGCTGTGTACCGGAGTCAAGCCAGCTGCGACAGTCAATTCAGTCA 132
QY 703 CTGAGGTGGGAGTCCCTTTTGTAAAGCTTCACATTCATCCCTGATGGGGC 762
Db 133 CTGAGGTGGGAGTCCCTTTTGTAAAGCTTCACATTCATCCCTGATGGGGC 192
QY 763 ATAGTTTGAAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 822
Db 193 ATAGTTTGAAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 252
QY 823 TCAGAGCTCCCTCGCTTGTACATTCATTCATTCATTCATTCATTCATTCATTC 882
Db 253 TCAGAGCTCCCTCGCTTGTACATTCATTCATTCATTCATTCATTCATTCATTC 312
QY 883 AATTGAGCTGCTGTGTACCGGAGTCAAGCCAGCTGCGACAGTCAATTCAGTCA 942
Db 313 AATTGAGCTGCTGTGTACCGGAGTCAAGCCAGCTGCGACAGTCAATTCAGTCA 372
QY 943 TAGACTGGGCTCGGCTCGCTCTGAAGAGTCTTAAGAAATCTTCAAGTTCTCT 1002
Db 373 TAGACTGGGCTCGGCTCGCTCTGAAGAGTCTTAAGAAATCTTCAAGTTCTCT 432
QY 1003 CAGAGGAGTGGGCGGCGGAGCGGAGCAAGAGCAAGCGGCGCTGCTCGG 1062
Db 433 CAGAGGAGTGGGCGGCGGAGCGGAGCAAGAGCAAGCGGCGCTGCTCGG 492
QY 1063 TGTGTAGTGTGCTGTACCGGAGTCAAGCCAGCTGCGACAGTCAATTCAGTCA 1122
Db 493 TGTGTAGTGTGCTGTACCGGAGTCAAGCCAGCTGCGACAGTCAATTCAGTCA 552
QY 1123 GGCAGCAGCAGCAGTTCAGCAAGAACCCCGCAAACTGCTGCGAGAGCAACCGTGTACAG 1182
Db 553 GGCAGCAGCAGCAGTTCAGCAAGAACCCCGCAAACTGCTGCGAGAGCAACCGTGTACAG 611
QY 1183 AGCGGAGTGTGACGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1242
Db 612 AGCGGAGTGTGACGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 671
QY 1243 TACGCCCGGAAGTAGAGCTCTGTCAGTCTGTG 1274
Db 672 TACGCCCGGAAGTAGAGCTCTGTCAGTCTGTG 703

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RESULT 2
B0689033
LOCUS      B0689033      879 bp      mRNA      linear      EST 15-JUL-2002

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DEFINITION      AGENCOURT 8063959 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6207625
ACCESSION      B0689033
VERSION      B0689033.1
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 879)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: IL0W2364 row: a column: 02
High quality sequence stop: 555.
Location/Qualifiers
1..879

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FEATURES
source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6207625"
/clone_1ib="NIH_MGC_110"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: pancreas; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."
BASE COUNT      203 a      260 c      241 g      175 t
ORIGIN
Query Match      32.8%; Score 531; DB 14; Length 879;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 531; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 583 AATTGAGCTGACTGAATTTGAGTATGACTTGAAGAGAGGTGAGTGAAGTTCA 642
Db 13 AATTGAGCTGACTGAATTTGAGTATGACTTGAAGAGAGGTGAGTGAAGTTCA 72
QY 643 CCCCCATGCTGTGTACCGGAGTCAAGCCAGCTGCGACAGTCAATTCAGTCA 702
Db 73 CCCCCATGCTGTGTACCGGAGTCAAGCCAGCTGCGACAGTCAATTCAGTCA 132
QY 703 CTGAGGTGGGAGTCCCTTTTGTAAAGCTTCACATTCATCCCTGATGGGGC 762
Db 133 CTGAGGTGGGAGTCCCTTTTGTAAAGCTTCACATTCATCCCTGATGGGGC 192
QY 763 ATAGTTTGAAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 822
Db 193 ATAGTTTGAAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 252
QY 823 TCAGAGCTCCCTCGCTTGTACATTCATTCATTCATTCATTCATTCATTCATTC 882
Db 253 TCAGAGCTCCCTCGCTTGTACATTCATTCATTCATTCATTCATTCATTCATTC 312
QY 883 AATTGAGCTGCTGTGTACCGGAGTCAAGCCAGCTGCGACAGTCAATTCAGTCA 942
Db 313 AATTGAGCTGCTGTGTACCGGAGTCAAGCCAGCTGCGACAGTCAATTCAGTCA 372
QY 943 TAGACTGGGCTCGGCTCGCTCTGAAGAGTCTTAAGAAATCTTCAAGTTCTCTCT 1002

```


[illegible]

RESULT 3	LOCUS	DEFINITION
B0006545/c	702 bp	linear
B0006545	702 bp	linear
UI-H-E11-a2a-n-21-0-U1	si NCI CGAP_E11	Homo sapiens CDNA clone
IMAGE:5846228 3'		mRNA sequence.

VERSION	BOO06545.1	GI:19731445
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 702)	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap .	National Cancer Institute, Cancer Genome Anatomy Project (CGAP)

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Dr. Jose Merchante
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/INL at: <http://image.inl.gov>
Seq primer: M13 FORWARD
POLYA-yes.

FEATURES	Location/Qualifiers
source	1. .702

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/db_xref="taxon:9606"
/clone="IMAGE:5846228"
/clone_11b="NCI_CGAP_E11"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="PH10B (Life Technologies)"
/notes="Organ: Left Pelvis; Vector: p7T73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I
NCI_CGAP_E11 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7T73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is
ACACTTCGAC.
TAG LIB-UI-H-E11
TAG_TISSUE=chondrosarcoma
TAG_SEQ=ACACTTCGAC"

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Query Match	31.3%	Score 507;	DB 14;	Length 702;
Best Local Similarity	99.78;	Pred. No. 0;		
Matches 677;	Conservative	0;	Mismatches	1; Gaps 1
QY 939 GACTTAGACATGGGGGCTCGGCTTCGTGAAGTGTGTTAGAGAAATCTTCACATTCNC	998			

Db	678	GACATTAGCTGGGGGCTGGGACTCCTCTCGAANAATGCTTAAGAANAATCTTCTCACTTC	619
Qy	999	CTTGACAGAGACATGGCCGCCGGAGACCCGAAGACAACGGCGCTGCACAAAGCGGGCCCTG	1058
Db	618	CTTGAGAGGAGCATGGCGCGGGAGCGGAAGAGCAACGGCGCTGCACAAAGCGGGCCCTG	559
Qy	1059	TGCGGTGGGAGTGGCGCATGTACGCGCACGGCGCTTCTGTGGTTGGGCTGCTGCAGGCAC	1118
Db	558	TGCGGTGGGAGTGGCGCATGTACGCGCACGGCGCTTCTGTGGTTGGGCTTCTGCAGGCAC	499
Qy	1119	AGGCGGCAGCACAGCACCTTGACAGAACACC GCCGGAATCTGCTCCAGCACACCGTGT	1178
Db	498	AGGCGGCAGCACAGCACACC -TGACAGAACACC GCCGGAATCTGCTCCAGCACACCGTGT	440
Qy	1179	CAGGAGCGGGTTGATGAGCCGAGCTGAGGTAGAAAACGTCCGAGAAAGGGAGAGAGAT	1238
Db	439	CAGGAGCGGGTTGATGAGCCGAGCTGAGGTAGAAAACGTCTCCGAGAAAGGGAGAGAGAT	380
Qy	1239	CATGTACGCCCGGGAAAGTAGAGACCTTCGTCACAGTCGTCTGGGTGGGCCGAGCCATGAT	1298
Db	379	CATGTACGCCCGGGAAAGTAGAGACCTTCGTCACAGTCGTCTGGGTGGGCCGAGCCATGAT	320
Qy	1299	CCTCCGAATCTGTGTTGGGCATTCAGCATACGGCCAAATTCACAACAATCACGCCCTGGGCA	1358
Db	319	CCTCCGAATCTGTGTTGGGCATTCAGCATACGGCCAAATTCACAACAATCACGCCCTGGGCA	260
Qy	1359	GACAGAGAGAGAGGAGAGAGACAGAGAAAGAAAAACACAGCATGAGAAACACAGTAAATG	1418
Db	259	GACAGAGAGAGAGGAGAGAGAGACAGAGAAAGAAAAACACAGCATGAGAAACACAGTAAATG	200
Qy	1419	AATTAATAACCATTAATATTTAGCCCCCTCTGTTCTGTCTTACTGGCCAGGAATGATACC	1478
Db	199	AATTAATAACCATTAATATTTAGCCCCCTCTGTTCTGTCTTACTGGCCAGGAATGATACC	140
Qy	1479	AATTTTTCAGTTGATGAGACTTGACAGCTTCCTTTGGCACAAGCAAGAGAAATTTAACT	1538
Db	139	AATTTTTCAGTTGATGAGACTTGACAGCTTCCTTTGGCACAAGCAAGAGAAATTTAACT	80
Qy	1539	GTTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTG	1598
Db	79	GTTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTG	20
Qy	1599	TAAAAAAAAAAAAAAAAAAAAA 1617	
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RESULT 4	BE395797	743 bp	mRNA	linear	EST 21-JUL-2000
LOCUS	BE395797				
DEFINITION	BE395797	601310028F1	NIH_MGC_44	Homo sapiens	CDNA clone IMAGE:3631543 5',
ACCESSION	BE395797				
VERSION	BE395797.1	GI:9341162			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					

cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MSC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LMC321 row: h column: 08

High quality sequence stop: 600.

FEATURES
Location/Qualifiers

1..743

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="IMAGE:3631543"

/issue_type="endometrium, adenocarcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Library constructed by Ling Hong

in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-CDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 160 a 189 c 214 g 180 t

ORIGIN

Query Match 31.3%; Score 506; DB 10; Length 743;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

473 CTGAGTGAATTTCTCTCTGGGCTCTCTTTATCTGGGAGGAGGAGTCCGTTCT 532

65 CTGAGTGAATTTCTCTCTGGGCTCTCTTTATCTGGGAGGAGGAGTCCGTTCT 124

533 CTTTGTTCCTGTGCAATTAATGAAGAGCTGTGAAGCATTTGAAATTAATTCAGCT 592

125 CTTTGTTCCTGTGCAATTAATGAAGAGCTGTGAAGCATTTGAAATTAATTCAGCT 184

593 GACTGAATTTTCAGTATGATCTTGAAGAGAGGTGAGTGAAGATTACCCCATGTC 652

185 GACTGAATTTTCAGTATGATCTTGAAGAGAGGTGAGTGAAGATTACCCCATGTC 244

653 TGTGTACCGAGTGAAGGCGGCTGTGAGAGTGTCTTAAGAGTCACTAGAGTGG 712

245 TGTGTACCGAGTGAAGGCGGCTGTGAGAGTGTCTTAAGAGTCACTAGAGTGG 304

713 CATGTGCTTTTGTAAAGCCCTCACTGTCATTCATCCCTGATGAGGGGCAATTTAG 772

305 CATGTGCTTTTGTAAAGCCCTCACTGTCATTCATCCCTGATGAGGGGCAATTTAG 364

773 ACTGAGAGTGAAGTGAAGCTTTTCTAGGGCTGAGGGGCAATTTCCCAAGGCTCC 832

365 ACTGAGAGTGAAGTGAAGCTTTTCTAGGGCTGAGGGGCAATTTCCCAAGGCTCC 424

833 CTGCTGTGACATTTCAATCTCATGCTCTGAAAGCATTTCTGAGAGAGATGGCTGG 892

425 CTGCTGTGACATTTCAATCTCATGCTCTGAAAGCATTTCTGAGAGAGATGGCTGG 484

893 TTTGGCGCTGAGTGGGCTCTAGTACTGAGACTCAATGACTGAGACTTGAAGTGG 952

485 TTTGGCGCTGAGTGGGCTCTAGTACTGAGACTCAATGACTGAGACTTGAAGTGG 544

953 CTGCGCTGCTGTGAAGAGTCTTA 978

545 CTGCGCTGCTGTGAAGAGTCTTA 570

RESULT 5

BE385990 676 bp mRNA linear EST 21-JUL-2000

LOCUS BE385990

DEFINITION mRNA sequence.

BE385990

VERSION BE385990.1 GI:9331355

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 676)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT Robert Strausberg, Ph.D.
COMMENT Email: cgaps-r@mail.nih.gov
Tissue Procurement: ATCC/DCMP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Inceye Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
Plate: LICM285 row: 9 column: 09
High quality sequence stop: 653.

FEATURES
Location/Qualifiers

1..676

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="IMAGE:3617696"

/issue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-CDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 168 a 172 c 199 g 137 t

ORIGIN

Query Match 28.8%; Score 467; DB 10; Length 676;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 587; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

830 TCCCTGCTTGAATTCATCTCATGCTCTGAAAGCATTTCTGAGAGATTTGGC 889

1 TCCCTGCTTGAATTCATCTCATGCTCTGAAAGCATTTCTGAGAGATTTGGC 60

890 TGGTTTGGCGCTGAGTGGGCTCTAGTACTGAGACTCAATGACTGGACTTACGTC 949

61 TGGTTTGGCGCTGAGTGGGCTCTAGTACTGAGACTCAATGACTGGACTTACGTC 120

950 GGGCTGCGCTCTGCTGTGAAGAGTGTCTGAGAGAGTGTCTGCGTGGAGAGA 1009

121 GGGCTGCGCTCTGCTGTGAAGAGTGTCTGAGAGAGTGTCTGCGTGGAGAGA 180

1010 CTGGCGCGGAGGAGCAAGAGCAACGCGGCTGACAAAGCGGCGCTGCGTGGTGA 1069

181 CTGGCGCGGAGGAGCAAGAGCAACGCGGCTGACAAAGCGGCGCTGCGTGGTGA 240

1070 GTGCGGATGACCGGAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1129

241 GTGCGGATGACCGGAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

1130 CAGCACCCTTGACGAGACACCGCGGAACTGCTGCGAGAGACCGGTTACAGAGCGGGT 1189

301 CAGCACCCTTGACGAGACACCGCGGAACTGCTGCGAGAGACCGGTTACAGAGCGGGT 359

1190 TGAATGACGAGCTGAGTGAAGAAAGCTGCTGAGAAAGGAGAGATCATGTACGCC 1249

360 TGAATGACGAGCTGAGTGAAGAAAGCTGCTGAGAAAGGAGAGATCATGTACGCC 419

1250 GGAAGTGAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1309

420 GGAAGTGAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479

1310 GGTGGGATCCAGCATAGAGCCAAATGTCACAAATCAGCCCTGGGAGACAGAGAGC 1369

480 GGTGGGATCCAGCATAGAGCCAAATGTCACAAATCAGCCCTGGGAGACAGAGAGC 539

1370 GAGGAGAGACAGAGAGAGAGAGAGAGATGAGAACTAGTAAT 1417

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Db      540 GAGGAGAGACAGAGAAAAACACAGCATGAGAACAGTAAT 587
|||||
RESULT 6
LOCUS    BM547680                      696 bp  mRNA      linear  EST 20-FEB-2002
DEFINITION AGENCOURT.6507108 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5727798
5', mRNA sequence.
ACCESSION BM547680
VERSION    BM547680.1  GI:18781656
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 696)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgep@bbs-remail.nih.gov
            Tissue Procurement: Invitrogen
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://lmln1.nlm.nih.gov
            Plate: LNL12722 row: h column: 07
            High quality sequence stop: 641.
FEATURES
    source
        1..696
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_image="5727798"
            /clone_1lb="NIH_MGC_124"
            /tissue_type="hippocampus"
            /lab_host="DH10B"
            /note="Organ: brain; Vector: pCMV-SPORT6; Site: 1; EcoRV
            (destroyed); Site: 2; NotI; RNA source male hippocampus,
            age 27. Library is oligo-dT primed and directionally
            cloned (EcoRV site is destroyed upon cloning). Average
            insert size 1.4 kb, insert size range 0.9-4 kb. Library is
            normalized and enriched for full-length clones and was
            constructed by C. Gruber (Invitrogen). Research Genetics
            tracking code 012."
BASE COUNT  188 a      160 c      197 g      134 t      17 others
ORIGIN
Query Match      28.8%; Score 466; DB 13; Length 696;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 636; conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY  931 ATGACTGGAGCTTAGACTGGGCTGGCCCTGCTGTAAGTCTTAAAGAAATCTTCT 990
    |||||||
Db   4  ATGACTGGAGCTTAGACTGGGCTGGCCCTGCTGTAAGTCTTAAAGAAATCTTCT 63
QY  991 CAGTTCTCTCTTCAGAGAGACTGGCCGGGAGCGCAAGAGCAGCGGCTGCACAAAGC 1050
    |||||||
Db   64 CAGTTCTCTCTTCAGAGAGACTGGCCGGGAGCGCAAGAGCAGCGGCTGCACAAAGC 123
QY  1051 GGGCCCTGTCGCTGGTGGAGTGCATGATGAGCGGAGCGGCTTCGTTGGTGGGCTGCT 1110
    |||||||
Db   124 GGGCCCTGTCGCTGGTGGAGTGCATGATGAGCGGAGCGGCTTCGTTGGTGGGCTGCT 183
QY  1111 GCAGCGACAGGGGAGCAGCAGACACTTGCACAGAAACCCGCCGAATGCTGCGAGAGC 1170
    |||||||
Db   184 GCAGCGACAGGGGAGCAGCAGACACTTGCACAGAAACCCGCCGAATGCTGCGAGAGC 242
QY  1171 ACCGCTGTACAGAGAGCGGCTGATGACCGAGCTGAGCTAGAAAAAGCTCTCGAGAGAGG 1230
    |||||||
Db   243 ACCGCTGTACAGAGAGCGGCTGATGACCGAGCTGAGCTAGAAAAAGCTCTCGAGAGAGG 302

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QY  1231 AGAGATCATGTATGAGCCCGGAAGTAGACCTGCTCAGTCTGCTGGTTGGCCGCA 1290
    |||||||
Db   303 AGAGATCATGTATGAGCCCGGAAGTAGACCTGCTCAGTCTGCTGGTTGGCCGCA 362
QY  1291 GCCATGATCTCTCCGAATCTGTTGGGATCCAGCATACGCCCAATGTACACAAATCAGC 1350
    |||||||
Db   363 GCCATGATCTCTCCGAATCTGTTGGGATCCAGCATACGCCCAATGTACACAAATCAGC 422
QY  1351 CCTGGCAGACAGCAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1410
    |||||||
Db   423 CCTGGCAGACAGCAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 482
QY  1411 AGTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1470
    |||||||
Db   483 AGTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 542
QY  1471 ATGTACCAATTTTTCAGTGTGGACTTGCACAGCTTCTTGGCAGAGAGAGAGAGAT 1530
    |||||||
Db   543 ATGTACCAATTTTTCAGTGTGGACTTGCACAGCTTCTTGGCAGAGAGAGAGAGAT 602
QY  1531 TTAACACTGTTTCAACCCCGGGGAGTTGGCTGTGTTA 1568
    |||||||
Db   603 TTAACACTGTTTCAACCCCGGGGAGTTGGCTGTGTTA 640
RESULT 7
LOCUS    BF726459                      530 bp  mRNA      linear  EST 05-JAN-2001
DEFINITION by06h03.y1 Human Lens cDNA (Un-normalized, unamplified): By Homo
sapiens cDNA clone by06h03 5', mRNA sequence.
ACCESSION BF726459
VERSION    BF726459.1  GI:12042370
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 530)
AUTHORS   Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
TITLE     NEIBANK: EST analysis and bioinformatics for ocular genomics
JOURNAL    Invest. Ophthalmol. Vis. Sci. 41, (2000) In press
COMMENT    Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: gfreem@helix.nih.gov
            Plate: 06 row: h column: 03
            Seg primer: M13RPL reverse primer (ABI).
FEATURES
    source
        1..530
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_image="by06h03"
            /clone_1lb="Human Lens cDNA (Un-normalized, unamplified):
            By"
            /tissue_type="lens"
            /dev_stage="Adult"
            /lab_host="EMDH10B"
            /note="Organ: Eye; Vector: pCMVSPORT6; Two human lenses
            from different adults (both approximately 40 years old)
            together yielded 20ug of total RNA and 150ng mRNA for cDNA
            library synthesis. A directionally cloned cDNA library in
            the pCMVSPORT6 vector was constructed at Life Technologies
            , essentially following the protocols of the Superscript
            Plasmid System full details of which are contained in the
            manufacturer's instruction manual
            (http://www.lifetechn.com/). First strand synthesis was
            carried out using a Not I primer-adaptor
            [5'-pGACTGATGTAGATCGGAGCGGCCGCT(7)5'-3']. Not I/Dlunt
            end inserts were cloned into the Not I/EcoR V sites in the

```


TITLE
JOURNAL
COMMENT
J.I., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
Mashu-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

FEATURES
source
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Gibco
High quality sequence stop: 420.
Location/Qualifiers
1. 457
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1955682"
/clone_lib="Schiller oligodendrogloma"
/sex="male"
/tissue_type="oligodendrogloma"
/dev_stage="44 years"
/lab_host="SOLR"

BASE COUNT 125 a 119 c 114 g 99 t
ORIGIN

Query Match 27.0%; Score 437; DB 9; Length 457;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

465 CCACCTCCCTGAGTGGTCTTCTGGGCTCCTTTATTCGGAGGAGCGGAGTC 524
|||||
437 CCACCTCCCTGAGTGGTCTTCTGGGCTCCTTTATTCGGAGGAGCGGAGTC 378
|||||
525 CGTGTCTCTTTTGTCTCTGCAATATGAAGAGCTCGGTAAGCAATCTGAATTA 584
|||||
377 CGTGTCTCTTTTGTCTCTGCAATATGAAGAGCTCGGTAAGCAATCTGAATTA 318
|||||
585 TTCAGCTGACGAAATTTTCATATGTTGAAGAGGAGGAGTGAATTTTACC 644
|||||
317 TTCAGCTGACGAAATTTTCATATGTTGAAGAGGAGGAGTGAATTTTACC 258
|||||
645 CCCATCTCTGTAAACCGAGTCAAGGCGGAGTGGAGAGTCACTTAAATGACT 704
|||||
257 CCCATCTCTGTAAACCGAGTCAAGGCGGAGTGGAGAGTCACTTAAATGACT 198
|||||
705 GAGGTGGGATCTGCTTTTGTAAAGCCTCCAGTCTCCATTCCTGATGGGGCAT 764
|||||
197 GAGGTGGGATCTGCTTTTGTAAAGCCTCCAGTCTCCATTCCTGATGGGGCAT 138
|||||
765 AGTTTGAGACGTCAGAGGAGAGTGGAGTGGTCTTGAAGGCGGAGTGGAGTCC 824
|||||
137 AGTTTGAGACGTCAGAGGAGAGTGGAGTGGTCTTGAAGGCGGAGTGGAGTCC 78
|||||
825 AAGGCTCCCTGCTTGAATTTCAATGCTCTGAAAAACATTCCTGAGACAGAA 884
|||||
77 AAGGCTCCCTGCTTGAATTTCAATGCTCTGAAAAACATTCCTGAGACAGAA 18
|||||
885 TTGGCTGCTTGGCGCC 901
|||||

Db 17 TTGGCTGCTTGGCGCC 1

RESULT 10
AI884686/c
LOCUS
DEFINITION
w183d07.x1 NCI-CGAP Brn25 Homo sapiens cDNA clone IMAGE:2431501 3'
similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GPR39. ; mRNA sequence.
AI884686
VERSION
AI884686.1 GI:5589850
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
Unpublished (1998)
CONTACT: Robert Strausberg, Ph.D.
Email: cga@bbs.fda.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldi, Ph.D.

FEATURES
source
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1462 Std. Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 444.
Location/Qualifiers
1. 591
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2431501"
/clone_lib="NCI-CGAP Brn25"
/tissue_type="anaplastic oligodendrogloma"
/lab_host="DH10B"
/note="Organ: brain; Vector: pTZ19-Pac (Pharmacia) with a
modified polylinker; Site: 1; Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTACCAATCTGAAAGTGGAGCGCGGCGCATAGTCTTTTCTTTTCTTTTCTTTT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pTZ19 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldi."

BASE COUNT 109 a 179 c 147 g 155 t
ORIGIN

Query Match 26.9%; Score 436; DB 9; Length 591;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 556; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

861 TGAACACATCTCTGAGCAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 920
|||||
578 TGAACACATCTCTGAGCAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519
|||||
921 TCGAGCTCAATGACTGGGCTTGAATGAGTGGGCTGCTGCTGCTGCTGCTGCT 980
|||||
518 TCGAGCTCAATGACTGGGCTTGAATGAGTGGGCTGCTGCTGCTGCTGCTGCT 459
|||||
981 AAAATCTTCTCAGTTCTCTGAGAGAGTGGGCGGCGGAGCGAAGAGCAAGGGCG 1040
|||||
458 AAAATCTTCTCAGTTCTCTGAGAGAGTGGGCGGCGGAGCGAAGAGCAAGGGCG 399
|||||
1041 TGCACAAAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1100
|||||


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|||||
DB 360 GACCTGTCACATCGGCTTGGGTTGGCCGAGCATGATCTCCGAATCGTTGGG 301
OY 1318 ATCCAGCATACGCCCAATGTCAACATCAGCCCTGGGCGAGACGAGGAGGAGA 1377
DB 300 ATCCAGCATACGCCCAATGTCAACATCAGCCCTGGGCGAGACGAGGAGGAGA 241
OY 1378 GACAGAGAAAGAAAACACAGCATGAGAACAGTAATGAATTAACCATTAATATT 1437
DB 240 GACAGAGAAAGAAAACACAGCATGAGAACAGTAATGAATTAACCATTAATATT 181
OY 1438 TAGCCCTCTGTTCTGCTTACTGCTGACGAGCAATGTGACCAATTTTTCAGTGTGACT 1497
DB 180 TAGCCCTCTGTTCTGCTTACTGCTGACGAGAAATGTGACCAATTTTTCAGTGTGACT 121
OY 1498 TGACAGCTTCTTTTGGCAGACAGAGAGATTTAACACTGTTTCAAAACCGGGGAGT 1557
DB 120 TGACAGCTTCTTTTGGCAGACAGAGAGATTTAACACTGTTTCAAAACCGGGGAGT 61
OY 1558 TGACCTGTGTTAAAGAAAGACCATTAATGCTTTAGCACTGTAATAAAAAA 1617
DB 60 TGCGTGTGTTAAAGAAAGACCATTAATGCTTTAGCACTGTAATAAAAAA 1

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RESULT 14
BM669397 627 bp mRNA linear EST 27-FEB-2002
LOCUS BM669397
DEFINITION UI-E-DWI-ahd-c-11-0-UI-s1 UI-E-DWI Homo sapiens cDNA clone
VERSION UI-E-DWI-ahd-c-11-0-UI 3', mRNA sequence.
KEYWORDS BM669397.1 GI:18979294
SOURCE EST.
ORGANISM human.

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REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 627)
Normalisation and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Aided by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Forward
POLYA=yes

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FEATURES

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SOURCE Location/Qualifiers
1..627
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-DWI-ahd-c-11-0-UI"
/clone_id="UI-E-DWI"
/tissue_type="lens"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-DWI is a normalized cDNA library containing the
following tissue(s): lens. The library was constructed
according to Ronaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double

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stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (drl)18 tail. The
sequence tag for this library is CGATTAGCA. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI).
TAG-LIB=UI-E-DWI
TAG-RISUB=human lens
TAG_SEQ=CGATTAGCA"
BASE COUNT 118 a 180 c 145 g 183 t 1 others

```

```

Query Match 26.5%; Score 429; DB 13; Length 627;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1138 TGACAGACACCCCGCCGAACCTGTCGAGACACCGGTACAGAGCGGTTATGACC 1197
DB 480 TGACAGACACCCCGCCGAACCTGTCGAGACACCGGTACAGAGCGGTTATGACC 421
OY 1198 GAGCTGAGTAGAAGAAACGCTCCGAGAGGGAGAGATCATGTACGCCGGAATAG 1257
DB 420 GAGCTGAGTAGAAGAAACGCTCCGAGAGGGAGAGATCATGTACGCCGGAATAG 361
OY 1258 GACCTGTCAGTCGTCGCTGGTTGGCCGAGCATGATCCTCCGATCTGTTGGGC 1317
DB 360 GACCTGTCAGTCGTCGCTGGTTGGCCGAGCATGATCCTCCGATCTGTTGGGC 301
OY 1318 ATCCAGCATACGCCCAATGTACACACATCAGCCCTGGCGAGACGAGGAGGAGA 1377
DB 300 ATCCAGCATACGCCCAATGTACACACATCAGCCCTGGCGAGACGAGGAGGAGA 241
OY 1378 GACAGAGAAAGAAAACACAGCATGAGAACAGTAATGAATTAACCATTAATATT 1437
DB 240 GACAGAGAAAGAAAACACAGCATGAGAACAGTAATGAATTAACCATTAATATT 181
OY 1438 TAGCCCTCTGTTCTGCTTACTGCTGACGAGCAATGTGACCAATTTTTCAGTGTGACT 1497
DB 180 TAGCCCTCTGTTCTGCTTACTGCTGACGAGAAATGTGACCAATTTTTCAGTGTGACT 121
OY 1498 TGACAGCTTCTTTTGGCAGACAGAGAGATTTAACACTGTTTCAAAACCGGGGAGT 1557
DB 120 TGACAGCTTCTTTTGGCAGACAGAGAGATTTAACACTGTTTCAAAACCGGGGAGT 61
OY 1558 TGCGTGTGTTAAAGAAAGACCATTAATGCTTTAGCACTGTAATAAAAAA 1617
DB 60 TGCGTGTGTTAAAGAAAGACCATTAATGCTTTAGCACTGTAATAAAAAA 1

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RESULT 15
A1936826 678 bp mRNA linear EST 08-MAR-2000
LOCUS A1936826
DEFINITION w669h10 x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2467075 3'
similar to SW:GP39.HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GPR39.; mRNA sequence.
ACCESSION A1936826
VERSION A1936826.1 GI:5675696
KEYWORDS EST.
SOURCE human.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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REFERENCE NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
1 (bases 1 to 678)

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AUTHORS National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
UNPUBLISHED (1998)

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COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rtmail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

```


Reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 103 a 142 c 119 g 151 t

ORIGIN

Query Match 25.6%; Score 415; DB 9; Length 515;

Best Local Similarity 99.8%; Pred. No. 0; Matches 465; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1138 TGGACGACACACCCCGGGAACCTGCTCCGAGACACCGCTTACAGAGCGGGTTGATACC 1197
 466 TGGACGACACACCCCGGGAACCTGCTCCGAGACACCGCTTACAGAGCGGGTTGATACC 407
 1198 GAGCTAGGTAGAGAAAGCTCCGAGAGGGAGAGAGATCATGATGACCGCGGAATG 1257
 406 GAGCTAGGTAGAGAAAGCTCCGAGAGGGAGAGAGATCATGATGACCGCGGAATG 347
 1258 GAGCTAGGTAGAGAAAGCTCCGAGAGGGAGAGATCATGATGACCGCGGAATG 1317
 346 GAGCTAGGTAGAGAAAGCTCCGAGAGGGAGAGAGATCATGATGACCGCGGAATG 287
 1318 ATCCAGCATACGCGCAATGCAACATCAGCCCTGGGAGACAGACAGAGAGAGAGA 1377
 286 ATCCAGCATACGCGCAATGCAACATCAGCCCTGGGAGACAGACAGAGAGAGAGA 227
 1378 GACAGAGAAAGAAAGAAACACAGATGAGAACAGTAATGATTAATTAATTAATTAAT 1437
 226 GACAGAGAAAGAAAGAAACACAGATGAGAACAGTAATGATTAATTAATTAATTAAT 167
 1438 TACCCCTCTGTTCTGCTGCTTACTGCGAGAAATGTAACAAATTTTTCAGTTGGACT 1497
 166 TACCCCTCTGTTCTGCTGCTTACTGCGAGAAATGTAACAAATTTTTCAGTTGGACT 107
 1498 TGCACAGCTCTTTTGGCAAGAGAGAAATTAACAGCTTTTCAACCCGGGGAGT 1557
 106 TGCACAGCTCTTTTGGCAAGAGAGAAATTAACAGCTTTTCAACCCGGGGAGT 47
 1558 TGCCTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGTAAA 1603
 46 TGCCTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGTAAA 1

RESULT 19
 BM686824 421 bp mRNA linear EST 28-FEB-2002
 LOCUS UI-E-CRI-sec-b-10-0-UI.r1 UI-E-CRI Homo sapiens cDNA clone
 ACCESSION BM686824
 VERSION BM686824.1 GI:19000082
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 421)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 JOURNAL 97044477
 MEDLINE
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
 Seq primer: M13 Reverse.
 Location/Qualifiers

FEATURES
 source 1..421

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-E-CRI-sec-b-10-0-UI"
 /clone_1bp="UI-E-CRI"
 /issue_type="eye anterior segment"
 /dev_stage="adult"
 /note="Host: DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: eye; Vector: pRT3-Pac (Pharmacia) with a modified polylinker. Site.1: EcoR I; Site.2: Not I; UI-E-CRI is a normalized cDNA library containing the following tissue(s): eye anterior segment. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AATGCCCAT. This library was created for the program Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 96 a 99 c 118 g 108 t

ORIGIN

Query Match 25.5%; Score 413; DB 14; Length 421;

Best Local Similarity 100.0%; Pred. No. 0; Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

564 CGGTAAAGCATTTGTAATTAATTCAGCTGATTAATTTTCAATGATGATGAAAGAG 623
 9 CGGTAAAGCATTTGTAATTAATTCAGCTGATTAATTTTCAATGATGATGAAAGAG 68
 624 GAGGAGAGTAAAGTTCACCCCATGCTGCTTAACCCGAGTAAAGCCAGGTGCGAG 683
 69 GAGGAGAGTAAAGTTCACCCCATGCTGCTTAACCCGAGTAAAGCCAGGTGCGAG 128
 684 AGTCACTCTTAGAAGTACAGTACAGTGGGATGCTGCTTTTGAACCTCCAGTGTCA 743
 129 AGTCACTCTTAGAAGTACAGTACAGTGGGATGCTGCTTTTGAACCTCCAGTGTCA 188
 744 TTCCATCCCTGATGGGGCATAGTTTGAAGTGCAGAGTGAAGTGAAGTGTCTTAA 803
 189 TTCCATCCCTGATGGGGCATAGTTTGAAGTGCAGAGTGAAGTGAAGTGTCTTAA 248
 804 CTGGAGGGCCAGTCCCACTCAAGGCTCCCTGCTTACATTCAAACTTATGCTCTGA 863
 249 CTGGAGGGCCAGTCCCACTCAAGGCTCCCTGCTTACATTCAAACTTATGCTCTGA 308
 864 AAACCATCTCTGAGAGAGAAATTTGGTGGTTCCGGCTAGTGGGCTTAGTGAATCG 923
 309 AAACCATCTCTGAGAGAGAAATTTGGTGGTTCCGGCTAGTGGGCTTAGTGAATCG 368
 924 AGACTCAATGACTGGAGCTTAGTACTGGGGCTGGCTCTGAAAAAGTCT 976
 369 AGACTCAATGACTGGAGCTTAGTACTGGGGCTGGCTCTGAAAAAGTCT 421

RESULT 20
 AM075598/c 500 bp mRNA linear EST 13-OCT-1999
 LOCUS XM24607.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:257752.3
 DEFINITION similar to SW:GP39 HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
 ACCESSION AM075598
 VERSION AM075598.1 GI:6030596
 KEYWORDS EST.

Source	Organism	Human
1	(bases 1 to 500)	
ADPHOS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
JOURNAL	Tumor Gene Index	
COMMENT	Unpublished (1997)	
	Contact: Robert Strausberg, Ph.D.	
	Email: cge@bbs-remail.nih.gov	
	Tissue Procurement: Chris Moskalko, M.D., Ph.D., Michael R.	
	Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life	
	Technologies, Inc. cDNA Library Arrayed by: Christina Prange, The	
	I.M.A.G.E. Consortium DNA Sequencing by: Washington University	
	Genome Sequencing Center	
	Clone distribution: NCI-CGAP clone distribution information can be	
	found through the I.M.A.G.E. Consortium/MLW at:	
	www-bio.lnl.gov/bdrp/image/image.html	
FEATURES	Possible reversed clone: similarity on wrong strand	
Source	Seq primer: -40UP from Gibco	
	High quality sequence stop: 413.	
	Location/Qualifiers	
	1..500	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:2577252"	
	/clone_lib="NCI CGAP Kid13"	
	/tissue_type="2, pooled Wilms' tumors, one primary and one	
	metastatic to brain"	
	/lab_host="DH10B"	
	/note="Organ: Kidney; Vector: pCMV-Sport6; Site:1: SalI;	
	Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.	
	Library constructed by Life Technologies."	
BASE COUNT	99 a 139 c 114 g 148 t	
ORIGIN		
Query Match	25.4%	Score 412; DB 10; Length 500;
Best Local Similarity	99.8%;	Pred. No. 0;
Matches 462; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
OY 1138	TGCACGACACCCGCCGGAACACTGTCGCGAGACACCGTGTACAGGAGCGGTGTGATGACC	1197
DB 463	TGCACGACACCCGCCGGAACACTGTCGCGAGACACCGTGTACAGGAGCGGTGTGATGACC	404
OY 1198	GAGCTGAGGTAGAAAAACGCTCTCGAGAGAGGGAGAGAGATCATGTACGCCCGGAAGTAG	1257
DB 403	GAGCTGAGGTAGAAAAACGCTCTCGAGAGAGGGAGAGAGATCATGTACGCCCGGAAGTAG	344
OY 1258	GACCTGCTCCACTGCTGCTGGCTTGGCGCGAGCGATCATGATCTCCGAATCTGGTGGGC	1317
DB 343	GACCTGCTCCACTGCTGCTGGCTTGGCGCGAGCGATCATGATCTCCGAATCTGGTGGGC	284
OY 1318	ATCCAGCATATCCGCCCAATGTCAACAACAATCAGCCCTGGGCAGACAGCAGAGAGGAGA	1377
DB 283	ATCCAGCATATCCGCCCAATGTCAACAACAATCAGCCCTGGGCAGACAGCAGAGAGGAGA	224
OY 1378	GACACAGAAAAAACAACACACGATGAGAGAACACAGTAATGAAATAAACCATAAATAATT	1437
DB 223	GACACAGAAAAAACAACACACGATGAGAGAACACAGTAATGAAATAAACCATAAATAATT	164
OY 1438	TAGCCCTCTGCTTGTCTGTCTACTGGCCAGAAATGGTACCAATTTTTCAGTGTGGACT	1497
DB 163	TAGCCCTCTGCTTGTCTGTCTACTGGCCAGAAATGGTACCAATTTTTCAGTGTGGACT	104
OY 1498	TGACAGACTTCTTTTGGCACACAGCAGAGAGAAATTTTACACTGTTCGAACCCCGGGAGT	1557
DB 103	TGACAGACTTCTTTTGGCACACAGCAGAGAGAAATTTTACACTGTTCGAACCCCGGGAGT	44
OY 1558	TGGCTGTGTTAAGAAAGACCATTTAATGCTTTAGACAGTGA 1600	
DB 43	TGGCTGTGTTAAGAAAGACCATTTAATGCTTTAGACAGTGA 1	

RESULT 21	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
BE858216/c	551 bp	mRNA	linear	EST 29-SEP-2000								
BE858216	7919907.x1	NCI_CGAP_Brn23 Homo sapiens CDNA clone IMAGE:3306972 3'										
		similar to SW:G939_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR										
		GP39.1; mRNA sequence.										
		BE858216										
		BE858216										
		EST.										
		human.										
		Homo sapiens										
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;										
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.										
		1 (bases 1 to 551)										
		NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .										
		National Cancer Institute / National Institute of Neurological										
		Disorders and Stroke, Brain Tumor Genome Anatomy Project										
		(CGAP/BRGAP), Tumor Gene Index										
		Unpublished (1998)										
		Contact: Robert Strausberg, Ph.D.										
		Email: cgapbs-r@mail.nih.gov										
		Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfield M.D.,										
		Ph.D.										
		CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima										
		Bonaldo, Ph.D.										
		CDNA Library Arrayed by: Greg Lennon, Ph.D.										
		DNA sequencing by: Washington University Genome Sequencing Center										
		Clone distribution: NCI-CGAP clone distribution information can be										
		found through the I.M.A.G.E. Consortium/LLNL, send email to:										
		info@image.llnl.gov										
		Seq primer: -40UP from Glibco										
		High quality sequence stop: 490.										
FEATURES	source	location/Qualifiers										
		1..551										
		/organism="Homo sapiens"										
		/db_xref="taxon:9606"										
		/clone="IMAGE:3306972"										
		/clone_lib="NCI_CGAP_Brn23"										
		/tissue_type="gliblastoma (pooled)"										
		/lab_host="DH10B"										
		/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a										
		modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st										
		strand CDNA was primed with a Not I - oligo(dT) primer [5										
		TGTTCACATCTGAAGTGGAGCGCGCGGCAATATCTTTTCTTTTCTTTTCTTTT										
		T 3']; double-stranded CDNA was ligated to Eco RI										
		adaptors (Pharmacia), digested with Not I and cloned into										
		the Not I and Eco RI sites of the modified pT7T3 vector.										
		Library is normalized, and was constructed by Bento										


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/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/Note="Vector: pRT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI-CGAP_G4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneids
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      132 a      189 c      155 g      173 t
ORIGIN
Query Match      25.4%; Score 411; DB 10; Length 649;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 461; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1138 TGCAGAACACCCGCCGAACTGTCGAGACACCGTGTACAGAGCGGGTGTATGACC 1197
|
|
|
Db 462 TGCAGAACACCCGCCGAACTGTCGAGACACCGTGTACAGAGCGGGTGTATGACC 403
QY 1198 GAGCTGAGTAGAAAAACGCTCCGAGAGGAGAGAGATCATGTACGCCCGAAGTAG 1257
|
|
|
Db 402 GAGCTGAGTAGAAAAACGCTCCGAGAGGAGAGAGATCATGTACGCCCGAAGTAG 343
QY 1258 GACCTGTCACAGTCGTGTTGGGTTGGCCGACGACATCATCTCCGAATCTGTTGGCC 1317
|
|
|
Db 342 GACCTGTCACAGTCGTGTTGGGTTGGCCGACGACATCATCTCCGAATCTGTTGGCC 283
QY 1318 ATCCAGCATACGCCCAATGTACAAACATCAGCCCTGGGCGACAGCAGAGAGAGAGA 1377
|
|
|
Db 282 ATCCAGCATACGCCCAATGTACAAACATCAGCCCTGGGCGACAGCAGAGAGAGAGA 223
QY 1378 GACAGAGAAAAAAGACAGCATGAGAACACAGTAAATGAATAAACCATTAATATT 1437
|
|
|
Db 222 GACAGAGAAAAAAGACAGCATGAGAACACAGTAAATGAATAAACCATTAATATT 163
QY 1438 TAGCCCTCTCTTCTGTCTTACTGCGCAGAGAAATGTTACCAATTTTTCAGTGTGACT 1497
|
|
|
Db 162 TAGCCCTCTCTTCTGTCTTACTGCGCAGAGAAATGTTACCAATTTTTCAGTGTGACT 103
QY 1498 TGACAGCTCTTCTTGGCACAAGAGAGAAATTAACATCTGTTCAACCCGGGGAGT 1557
|
|
|
Db 102 TGACAGCTCTTCTTGGCACAAGAGAGAAATTAACATCTGTTCAACCCGGGGAGT 43
QY 1558 TGCGCTGTGTTAAAGAAACCATTAATGCTTTAGACAGTGT 1599
|
|
|
Db 42 TGCGTGTGTTAAAGAAACCATTAATGCTTTAGACAGTGT 1

```

```

RESULT 24
AI391683/c 452 bp mRNA linear EST 17-MAR-1999
LOCUS AI391683
DEFINITION AI391683.1 NCI-CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2019583.3'
sequence.
similar to SW:NTRL_RAT P20789 NEUROTENSIN RECEPTOR TYPE 1; mRNA
sequence.
ACCESSION AI391683
VERSION AI391683.1 GI:4217687
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 452)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

```

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FEATURES
source
1..452
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2019583"
/clone_lib="NCI-CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/Note="Organ: Brain; Vector: pRT73D-Pac (Pharmacia) with a
modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTATCCATCTGCAAGTGGAGCGCGCCGATGCTTTTGTGTTTTTTTTTTT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT      94 a      122 c      99 g      137 t
ORIGIN
Query Match      24.3%; Score 394; DB 9; Length 452;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1155 AAATGCTCGAGAGACCGTGTACAGAGCGGGTGTATGACCGAGCTGAGTAAAAA 1214
|
|
|
Db 445 AAATGCTCGAGAGACCGTGTACAGAGCGGGTGTATGACCGAGCTGAGTAAAAA 386
QY 1215 CGTCTCCGAGAAAGGAGAGAGATCATGTACGCCCGAAGTAGACCTCTGCTGCTG 1274
|
|
|
Db 385 CGTCTCCGAGAAAGGAGAGAGATCATGTACGCCCGAAGTAGACCTCTGCTGCTG 326
QY 1275 CTTGGGTTGGCGGACCGATGATCTCCGATCTGTTGGGATCCAGCATACGCCCAA 1334
|
|
|
Db 325 CTTGGGTTGGCGGACCGATGATCTCCGATCTGTTGGGATCCAGCATACGCCCAA 266
QY 1335 TGTCAACAAATCAGCCCTGGGCGACAGCAGAGCAGAGAGAGAGAGAGAGAGAG 1394
|
|
|
Db 265 TGTCAACAAATCAGCCCTGGGCGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 206
QY 1395 CACAGCATGAGAGACAGTAAATGAATTAACATTAATTAATTAATTAATTAATTA 1454
|
|
|
Db 205 CACAGCATGAGAGACAGTAAATGAATTAACATTAATTAATTAATTAATTAATTA 146
QY 1455 GCTTACTGGCCAGAGAAATGTTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1514
|
|
|
Db 145 GCTTACTGGCCAGAGAAATGTTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 86
QY 1515 ACAAGCAGAGAGAAATTAACAGTGTTCAAACCCGGGGAGTGTGTTAAAGAA 1574
|
|
|
Db 85 ACAAGCAGAGAGAAATTAACAGTGTTCAAACCCGGGGAGTGTGTTAAAGAA 26
QY 1575 GACCATTAATGCTTTAGACAGTGT 1599
|
|
|
Db 25 GACCATTAATGCTTTAGACAGTGT 1

```

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RESULT 25
B1919074 704 bp mRNA linear EST 16-OCT-2001
LOCUS B1919074
DEFINITION B0318088.F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5244956.5',
mRNA sequence.

```


ACCESSION B1919074
 VERSION B1919074.1 GI:16200128
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 704)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
 Plate: L16M1618 row: a column: 21
 High quality sequence start: 4
 High quality sequence stop: 702.
 Location/Qualifiers
 1..704
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5244956"
 /clone_1lb="NIH-MGC_121"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; site_1: NotI; site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH-MGC Library."
 BASE COUNT 132 a 237 c 204 g 131 t
 ORIGIN
 Query Match 23.8%; Score 386; DB 13; Length 704;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GGCACTTTTGGGATGTTCTTCTTCAGGCTTTGGCTGCAATCCAGTCTACCA 60
 Db 318 GGCACTTTTGGGATGTTCTTCTTCAGGCTTTGGCTGCAATCCAGTCTACCA 377
 Oy 61 GGTGAGAAATTCAGAGTCAACAGAGCTGCTCCCGGCGATTCATTTGTAATGGAC 120
 Db 378 GTGTGAGAAATTCAGAGTCAACAGAGCTGCTCCCGGCGATTCATTTGTAATGGAC 437
 Oy 121 GGTGAGCTTCAAGACATGTCAGAAAGAGTGAATGAGCAATGCCGGGATCATGTA 180
 Db 438 GGTGAGCTTCAAGACATGTCAGAAAGAGTGAATGAGCAATGCCGGGATCATGTA 497
 Oy 181 CGGCAAGTCTTGATCATATCAGCGGCTGTCTATCGCTTGC CGGGTACAGTCTCT 240
 Db 498 CGGCAAGTCTTGATCATATCAGCGGCTGTCTATCGCTTGC CGGGTACAGTCTCT 557
 Oy 241 CTGCTCCCGAGGAAAGTCAATCAAGTTGATCGAGTCTCAACACCCCTTTGTA 300
 Db 558 CTGCTCCCGAGGAAAGTCAATCAAGTTGATCGAGTCTCAACACCCCTTTGTA 617
 Oy 301 CGGGCCCAAGGCCCAAGAAAGGGGAATTTCTGCTCGGCTTCAGGCCAAGGGCTCCGAC 360
 Db 618 CGGGCCCAAGGCCCAAGAAAGGGGAATTTCTGCTCGGCTTCAGGCCAAGGGCTCCGAC 677
 Oy 361 CACCATCTCTGTTCTCAATTAGCC 386
 ||||||||||||||||||||||||||||

Db 678 CACCATCTCTGTTCTCAATTAGCCC 703
 RESULT 26
 LOCUS A1765236/c 456 bp mRNA linear EST 21-DEC-1999
 DEFINITION w172108.x1 NCI-CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2398911 3' similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39. ; mRNA sequence.
 ACCESSION A1765236
 VERSION A1765236.1 GI:5231745
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 456)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.dio.llnl.gov/dbrr/image/image.html
 Insert length: 961 Std Error: 0.00
 Seq primer: -400P from Gibco
 High quality sequence stop: 453.
 Location/Qualifiers
 1..456
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2398911"
 /clone_1lb="NCI-CGAP_K1d12"
 /tissue_type="2 pooled tumors (clear cell type)"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: p7T73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP_K1d5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo "
 BASE COUNT 93 a 122 c 99 g 142 t
 ORIGIN
 Query Match 23.5%; Score 380; DB 9; Length 456;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 430; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1149 CGCGGAAACTGCTGCGAGACACCGTGTACAGAGCGGGTTGATGACCGAGCTGAGTA 1208
 Db 456 CGCGGAAACTGCTGCGAGACACCGTGTACAGAGCGGGTTGATGACCGAGCTGAGTA 397
 Oy 1209 GAAAAGCTCCGAGAGAGGAGAGATCATGTACGCCCGGAAGTAGACCTCGTCA 1268
 Db 396 GAAAAGCTCCGAGAGAGGAGAGATCATGTACGCCCGGAAGTAGACCTCGTCA 337
 Oy 1269 GTCTGCTTGGGTTGGCGCAGCATGATCTCCGATCTGTTGGGCAATCCAGCATAC 1328
 Db 336 GTCTGCTTGGGTTGGCGCAGCATGATCTCCGATCTGTTGGGCAATCCAGCATAC 277
 Oy 1329 GGCCATTCACAAATCAGCCCTGGGCGACACGAGCAGAGGAGAGACAGAGAAA 1388
 ||||||||||||||||||||||||||||

Db 276 GGGCAATGTCACAAATCAGCCCTGGGACAGACAGGAGGAGAGACAGAGAAAA 217
 QY 1389 GAAAAACACAGCATGGAACACAGTAATGATTAATAACCATTAATTTACCCCTCTG 1448
 Db 216 GAAAAACACAGCATGGAACACAGTAATGATTAATAACCATTAATTTACCCCTCTG 157
 QY 1449 TTCTGTGCTTACTGGCCAGGAATGTACCAATTTTTCAGTGTGGACTTGACACTTCT 1508
 Db 156 TTCTGTGCTTACTGGCCAGGAATGTACCAATTTTTCAGTGTGGACTTGACACTTCT 97
 QY 1509 TTTCGCCACAGCAAGAGAGATTTTAACACTGTTTCAACCCGGGAGTGTGGCTGTGA 1568
 Db 96 TTTCGCCACAGCAAGAGAGATTTTAACACTGTTTCAACCCGGGAGTGTGGCTGTGA 37
 QY 1569 AAGAAAGACCA 1579
 Db 36 AAGAAAGACCA 26

RESULT 27 738 bp mRNA linear EST 21-MAR-2002
 LOCUS BM981455
 DEFINITION UI-CF-EN1-adh-b-10-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
 ACCESSION BM981455
 VERSION BM981455.1 GI:19603962
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 738)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source location/Qualifiers
 1..738
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-CF-EN1-adh-b-10-0-UI"
 /clone_lib="UI-CF-EN1"
 /tissue_type="Primary Lung Cystic Fibrosis Epithelial
 Cells"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker. Site_1: EcoR I; Site_2: Not I;
 UI-CF-EN1 is a normalized cDNA library containing the
 following tissue(s): Primary Lung Cystic Fibrosis
 Epithelial Cells. The library was constructed according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was ligated to an EcoR I adaptor, digested with Not
 I, and cloned directionally into pT73-Pac vector. The
 oligonucleotide used to prime the synthesis of

first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is CTGCTCAGGT.
 TAG-LIB=UI-CF-EN1
 TAG-TISSUE=Human Lung Epithelial Cell lines untreated LPS
 6hr to LPS 24h
 TAG-SFO=CTGCTCAGGT"
 BASE COUNT 151 a 199 c 164 g 221 t 3 others
 ORIGIN

Query Match 23.4%; Score 379; DB 14; Length 738;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 GGAATCATGATACCGAAGTCTGTGATCATACAGGCTGTCTCATGCTTGGCGGG 229
 Db 290 GGGATCATGATACCGAAGTCTGTGATCATACAGGCTGTCTCATGCTTGGCGGG 349
 QY 230 TACAGTCTTGTGATACCGAAGTCTGTGATCATACAGGCTGTCTCATGCTTGGCGGG 289
 Db 350 TACAGTCTTGTGATACCGAAGTCTGTGATCATACAGGCTGTCTCATGCTTGGCGGG 409
 QY 290 CCTCTTTGTAACGGGCGCAAGGCGCCAGAAAAAGGGAAGTTCTGCTCTGCGCTCAGGCA 349
 Db 410 CCTCTTTGTAACGGGCGCAAGGCGCCAGAAAAAGGGAAGTTCTGCTCTGCGCTCAGGCA 469
 QY 350 GGGCTCCGACACACACATCCTGCTTCAATTTAGCCCTCTTCTGCGCACACTCTGAAG 409
 Db 470 GGGCTCCGACACACACATCCTGCTTCAATTTAGCCCTCTTCTGCGCACACTCTGAAG 529
 QY 410 TGAAGGAGATGCGCCGCCCTGCTGATTTTTCAGGCTGCGCCGCCACCCGAC 469
 Db 530 TGAAGGAGATGCGCCGCCCTGCTGATTTTTCAGGCTGCGCCGCCACCCGAC 589
 QY 470 TCCCTGAGTGAATTTCTTCTGAGTCTCTTATTCGAGTGAAGGAGGAGTCCGTGT 529
 Db 590 TCCCTGAGTGAATTTCTTCTGAGTCTCTTATTCGAGTGAAGGAGGAGTCCGTGT 649
 QY 530 TCTCTTTTGTCTCTGCTGCA 548
 Db 650 TCTCTTTTGTCTCTGCTGCA 668

RESULT 28 821 bp mRNA linear EST 15-MAY-2001
 LOCUS BG752229
 DEFINITION 602731372F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4875113 5',
 mRNA sequence.
 ACCESSION BG752229
 VERSION BG752229.1 GI:14062882
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 821)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ULNL at:
 http://image.jnl.gov
 plate: LLCMI755 row: O column: 18
 High quality sequence stop: 770.
 Location/Qualifiers
 1..821
 /organism="Homo sapiens"

FEATURES

source location/Qualifiers
 1..821
 /organism="Homo sapiens"

/db_xref="taxon:9606"
 /clone="IMAGE:487513"
 /clone_lib="NIH_MGC_43"
 /tissue_type="normal pigmented retinal epithelium"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pORF7; Site: 1; XhoI; Site: 2; EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"

BASE COUNT

194 a 201 c 248 g 178 t

ORIGIN

Query Match 23.0%; Score 372; DB 12; Length 821;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

555 GAAGAGCTCGGTAAAGCAATTCGATAATTAATTCAGCTGACTGAATTTTCAGTATGACT 614
 |||||||
 2 GAAGAGCTCGGTAAAGCAATTCGATAATTAATTCAGCTGACTGAATTTTCAGTATGACT 61
 |||||||
 615 TGAAGAGAGAGCTGAGTGAAGTCAACCCCATGCTGCTGACGAGTCAAGGCCA 674
 |||||||
 62 TGAAGAGAGAGCTGAGTGAAGTCAACCCCATGCTGCTGACGAGTCAAGGCCA 121
 |||||||
 675 GGCTGGCAGAGTCACTGCTTGAAGTCACTGAGTGGGATCTGCTTTTGAAGCCCTC 734
 |||||||
 122 GGCTGGCAGAGTCACTGCTTGAAGTCACTGAGTGGGATCTGCTTTTGAAGCCCTC 181
 |||||||
 735 CAGTGTCAATTCATCCCTGATGAGGGGCAATTTGAGACTCAAGTACAGTACGTT 794
 |||||||
 182 CAGTGTCAATTCATCCCTGATGAGGGGCAATTTGAGACTCAAGTACAGTACGTT 241
 |||||||
 795 TTCTTGGCTGGAGGGGAGTTCCTCAAGGCTCCCTGCTTGAATTAACCTCA 854
 |||||||
 242 TTCTTGGCTGGAGGGGAGTTCCTCAAGGCTCCCTGCTTGAATTAACCTCA 301
 |||||||
 855 TGCTCTGAAAACCATTTCTGCGACAGAAATGGCTGTTTGGCGCTGAGTTGGGCTCT 914
 |||||||
 302 TGCTCTGAAAACCATTTCTGCGACAGAAATGGCTGTTTGGCGCTGAGTTGGGCTCT 361
 |||||||
 915 AGTGAAGTCAAG 926
 |||||||
 362 AGTGAAGTCAAG 373

RESULT 29

BP054837 381 bp mRNA linear EST 16-OCT-2000
 LOCUS 7171h01.y1 NCI_CGAP_Brn20 Homo sapiens cDNA clone IMAGE:3340177 5'
 DEFINITION similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
 GPR39. ; mRNA sequence.

ACCESSION BP054837
 VERSION BP054837.1 GI:10808733
 KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 381)
 AUTHORS NCI/NIH-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BRGAP), Tumor Gene Index
 JOURNAL Unpublished (1998)
 COMMENT Other ESTs: 7171h01.x1
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Robert Jenkins, M.D., Mark Israel, M.D., Jim
 Jacobson, Ph.D.

cDNA Library Preparation: David B. Kitzman, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
 info@image.llnl.gov
 Putative full length read
 The vector to vector length is 382
 Seq primer: -40RP from Gluco.
 Location/Qualifiers
 1. 381
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3340177"
 /clone_lib="NCI_CGAP_Brn20"
 /tissue_type="oligodendroglioma"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: Brain; Vector: PAMPI; mRNA made from
 oligodendroglioma tissue, cDNA made by oligo-dT priming.
 Directionally cloned. Size selected on agarose gel,
 average insert size 500 bp. Primary library,
 non-amplified."

FEATURES

source

BASE COUNT 123 a 81 c 83 t

ORIGIN

Query Match 22.8%; Score 369; DB 12; Length 381;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1229 GGAGAGAGATCATGAGCCCGGAGTAGAGACTGTCAGTCTGCTGGTGGCCG 1288
 |||||||
 1 GGAGAGAGATCATGAGCCCGGAGTAGAGACTGTCAGTCTGCTGGTGGCCG 60
 |||||||
 1289 CAGCATATCTCTCCGATCTGCTGGGATCCAGCATAGGCCCATGTCACAAATCA 1348
 |||||||
 61 CAGCATATCTCTCCGATCTGCTGGGATCCAGCATAGGCCCATGTCACAAATCA 120
 |||||||
 1349 GCCCTGGCAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1408
 |||||||
 121 GCCCTGGCAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 |||||||
 1409 ACAGTAAATGAATTAACCATTAATTTAGCCCTCTGTTCTGCTTCTGCGCCAG 1468
 |||||||
 181 ACAGTAAATGAATTAACCATTAATTTAGCCCTCTGTTCTGCTTCTGCGCCAG 240
 |||||||
 1469 AATGTACCAATTTTTCAGTGTGACTGACAGCTCTTTTGCACAAAGAGAGA 1528
 |||||||
 241 AATGTACCAATTTTTCAGTGTGACTGACAGCTCTTTTGCACAAAGAGAGA 300
 |||||||
 1529 ATTAACTGTTTCAAAACCCGGGAGTGGCTGTAAAGAAAGCAATTAATGCT 1588
 |||||||
 301 ATTAACTGTTTCAAAACCCGGGAGTGGCTGTAAAGAAAGCAATTAATGCT 360
 |||||||
 1589 TTAGACAGT 1597
 |||||||
 361 TTAGACAGT 369

RESULT 30

BP054680 371 bp mRNA linear EST 16-OCT-2000
 LOCUS 7169f08.y1 NCI_CGAP_Brn20 Homo sapiens cDNA clone IMAGE:3339975 5'
 DEFINITION similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
 GPR39. ; mRNA sequence.

ACCESSION BP054680
 VERSION BP054680.1 GI:10808576
 KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 371)

PROTEIN-COUPLED RECEPTOR GPR39. ; mRNA sequence.
 AT142092
 VERSION AT142092.1 GI:5110380
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 578)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nlm.nih.gov
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert length: 806 Std Error: 0.00
 Seq primer: -400p from Glibco
 High quality sequence stop: 460.
 Location/Qualifiers
 1..578
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2367413"
 /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pF73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clones: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares ND2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares ND2HF8-9W pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NBHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Falina Bernaldo."
 BASE COUNT 102 a 176 c 142 g 158 t
 ORIGIN
 Query Match 22.5%; Score 364; DB 9; Length 578;
 Best local Similarity 99.6%; Pred. No. 0;
 Matches 534; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 Db 873 TCTGCACGACAATTCGCTGCTTCCGCGCTGAGTGGCTCTAGTACCTGACACTCAAT 932
 |||||||
 574 TCTGCACGACAATTCGCTGCTTCCGCGCTGAGTGGCTCTAGTACCTGACACTCAAT 515
 |||||||
 933 GACTGGACTTACGACTGGGCTCGGCTCGCTCTGAAAAGCTTAAAGAAATCTTCTCA 992
 |||||||
 514 GACTGGACTTACGACTGGGCTCGGCTCGCTCTGAAAAGCTTAAAGAAATCTTCTCA 455
 |||||||
 993 GTTCTCTTTCAGAGACAGTGGCGCGGAGCGCAAGAGCAAGCGGCGCTGCAAAAGCGG 1052
 |||||||
 454 GTTCTCTTTCAGAGACAGTGGCGCGGAGCGCAAGAGCAAGCGGCGCTGCAAAAGCGG 395
 |||||||
 1053 GCGGTCTCGGTGGTGGAGTGGCGCATGTACGCGCAGCGCTTCTCGTGGTGGCGTCTGC 1112
 |||||||
 394 GCGGTCTCGGTGGTGGAGTGGCGCATGTACGCGCAGCGCTTCTCGTGGTGGCGTCTGC 335
 |||||||
 1113 AGCAGACAGGCGGAGCAGACACCTTCACAGACACCCCGGAACTGCTGCGAGCAGAC 1172
 |||||||
 334 AGCAGACAGGCGGAGCAGACACCTTCACAGACACCCCGGAACTGCTGCGAGCAGAC 276
 |||||||
 1173 CGTGTACAGGAGCGGCTTGTAGTACGAGCGTGTAGTAAAGCTCCGAGAGGAGGAG 1232
 |||||||
 275 CGTGTACAGGAGCGGCTTGTAGTACGAGCGTGTAGTAAAGCTCCGAGAGGAGGAG 216

1233 GAGGATCATGTACGCCCGGAAGTAGACCTCTCCAGTGTGCTTGGGCTGCCAGC 1292
 |||||||
 Db 215 GAGGATCATGTACGCCCGGAAGTAGACCTCTCTGCTTGGGCTTGGCGCAGC 156
 |||||||
 1293 CATGATCTCCGGAATCTGTTGGCATCAGCATACGCCCAATGTCAACAATCAGCCC 1352
 |||||||
 Db 155 CATGATCTCCGGAATCTGTTGGCATCAGCATACGCCCAATGTCAACAATCAGCCC 96
 |||||||
 1353 TGGCAGACAGCAGCAGGAGGAGAGACAGCAAGAAACACAGCATGAGAAC 1408
 |||||||
 Db 95 TGGCAGACAGCAGCAGGAGGAGAGACAGCAAGAAACACAGCATGAGAAC 40
 |||||||
 RESULT 33
 AA084248 379 bp mRNA linear EST 31-JUL-1997
 LOCUS 2117109.r1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens
 DEFINITION CDNA clone IMAGE:547721 5', mRNA sequence.
 ACCESSION AA084248
 VERSION AA084248.1 GI:1626368
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 379)
 AUTHORS Hallier, L., Lennon, G., Becker, M., Bernaldo, M.F., Chiappelli, B., Chissee, S., Dietrich, N., Dubuque, T., Favell, A., Gish, N., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Maris, E., Moore, B., Morris, M., Parsons, J., Prange, C., Riklin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierly-Meg, J., Trevas, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 TITLE JOURNAL MEDLINE
 CONTACT: Wilson RK
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert length: 980 Std Error: 0.00
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 357.
 Location/Qualifiers
 1..379
 /organism="Homo sapiens"
 /db_xref="GDB:3926237"
 /db_xref="taxon:9606"
 /clone="IMAGE:547721"
 /clone_lib="Stratagene neuroepithelium NT2RAM1 937234"
 /dev_stage="Ntera-2/RH+MI neuroepithelial cells"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Precursor cells induced with Retinoic acid for 1 week, followed by 3 weeks in mitotic inhibitors (Replate #2). Average insert size: 1.1 kb; Uni-ZAP XR vector; ~5' adaptor sequence: 5' GAAATTCGCGCAGAG 3' -3' adaptor sequence: 5' CTCGATGTTTCTTTTCTTTT 3'."
 BASE COUNT 77 a 95 c 114 g 93 t
 ORIGIN
 Query Match 22.4%; Score 363; DB 9; Length 379;
 Best local Similarity 100.0%; Pred. No. 0;
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 720 CTTTGTAAAGCTCCAGTGTCCATTCATCCCTGATGGGCGCATAGTTGAGACTGAG 779
 |||||||
 17 CTTTGTAAAGCTCCAGTGTCCATTCATCCCTGATGGGCGCATAGTTGAGACTGAG 76

QY 780 ACTGACAGTACGCTTTTCTTAGGGCTGAGGGCCAGTTCACATCAGGCTCCCTGCT 839
 DB 77 ACTGAGAGTACGCTTTTCTTAGGGCTGAGGGCCAGTTCACATCAGGCTCCCTGCT 136
 QY 840 GACATTCAAACTTCACTGCTCCCTGAGAAACCACTTCTGACAGCAGAAATGCTGTTCCG 899
 DB 137 GACATTCAAACTTCACTGCTCCCTGAGAAACCACTTCTGACAGCAGAAATGCTGTTCCG 196
 QY 900 CCTGAGTTGGGCTCTAGTACTCGAGACATGACTGGGACTTGGAGTGGGCTGGCC 959
 DB 197 CCTGAGTTGGGCTCTAGTACTCGAGACATGACTGGGACTTGGAGTGGGCTGGCC 256
 QY 960 TCGCTCTGAAAAGTCTTAAGAAAATCTTCTGAGTTCTCTGACAGAGACTGGCGCCG 1019
 DB 257 TCGCTCTGAAAAGTCTTAAGAAAATCTTCTGAGTTCTCTGACAGAGACTGGCGCCG 316
 QY 1020 GACGGAGAGCAGGGGGCGTGCACAAAGGGGGCGCTGTGGTGGTGGAGTGGCGCATGT 1079
 DB 317 GACGGAGAGCAGGGGGCGTGCACAAAGGGGGCGCTGTGGTGGTGGAGTGGCGCATGT 376
 QY 1080 ACG 1082
 DB 377 ACG 379

RESULT 34
 BE350014/c 534 bp mRNA linear EST 18-JUL-2000
 LOCUS h107912.x1 NCI-CGAP Kid13 Homo sapiens cDNA clone IMAGE:3146086 3'
 DEFINITION similar to SW:GP39.HUMAN 043194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
 GP39 ; mRNA sequence.

ACCESSION BE350014
 VERSION BE350014.1 GI:9261867
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 534)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapds-remail.nih.gov
 Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
 Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
 InfoImage.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 408.

FEATURES
 source
 1.534
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3146086"
 /clone_1b="NCI-CGAP Kid13"
 /tissue_type="2 pooled Wilms' tumors, one primary and one
 metastatic to brain"
 /lab_host="DH10B"
 /note="Organ: Kidney; Vector: PCMV-SPORE6; Site: 1: SalI;
 Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies."

BASE COUNT 98 a 172 c 143 g 121 t

Query Match 22.2%; Score 359; DB 10; Length 534;
 Best Local Similarity 99.6%; Pred. No. 0;

Matches 529; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 852 TCATGCTCTGAAAACCATTCCTGACAGCAATTTGGCTGTTCCGCGCTGATGGGC 911
 DB 530 TCATGCTCTGAAAACCATTCCTGACAGCAATTTGGCTGTTCCGCGCTGATGGGC 471
 QY 912 TCTAGTACTCGAGACATCATGACTGGGACTTACATGCGGCTCGGCTCTGAAA 971
 DB 470 TCTAGTACTCGAGACATCATGACTGGGACTTACATGCGGCTCGGCTCTGAAA 411
 QY 972 GTGCTTAAGAAAATCTTCTGATTCCTCTGACAGAGACTGGCGGGAGCGGAAGAC 1031
 DB 410 GTGCTTAAGAAAATCTTCTGATTCCTCTGACAGAGACTGGCGGGAGCGGAAGAC 351
 QY 1032 AAGGGCGCTGCAAAAAGCGGGCGCTGTGGTGGTGGAGTGGCATGTACGGCAGCGC 1091
 DB 350 AAGGGCGCTGCAAAAAGCGGGCGCTGTGGTGGTGGAGTGGCATGTACGGCAGCGC 291
 QY 1092 TTCTCGTGTGGCGTGTGCTGACGAGCGCGGCGGACACAGACCTTGCACAGACCCG 1151
 DB 290 TTCTCGTGTGGCGTGTGCTGACGAGCGCGGCGGACACAGACCTTGCACAGACCCG 232
 QY 1152 CCGAACTGCTGCGAGACACCGCTGTACAGAGCGGTTGATGACCGAGCTGAGTAGAA 1211
 DB 231 CCGAACTGCTGCGAGACACCGCTGTACAGAGCGGTTGATGACCGAGCTGAGTAGAA 172
 QY 1212 AACGCTCTCGAAGAGGAGAGATCATGTACCGCCGGAAGTAGACCTGTCAGTC 1271
 DB 171 AACGCTCTCGAAGAGGAGAGATCATGTACCGCCGGAAGTAGACCTGTCAGTC 112
 QY 1272 GTGCTGTGGTGGCGCGGACCATGATCTCGAATCTGTTGGGCAATCCACATACGCG 1331
 DB 111 GTGCTGTGGTGGCGCGGACCATGATCTCGAATCTGTTGGGCAATCCACATACGCG 52
 QY 1332 CAATGTACACATACGCGCTGGCGAGACAGACAGAGAGAGAGAGAG 1382
 DB 51 CAATGTACACATACGCGCTGGCGAGACAGACAGAGAGAGAGAGAGAG 1

RESULT 35
 BE395206 573 bp mRNA linear EST 21-JUL-2000
 LOCUS 601309558F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631047 5',
 DEFINITION mRNA sequence.
 ACCESSION BE395206
 VERSION BE395206.1 GI:9340571
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 573)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapds-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://Image.llnl.gov
 Plate: LICM320 row: C column: 16
 High quality sequence stop: 573.

FEATURES
 source
 1.573
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3631047"
 /clone_1b="NIH_MGC_44"
 /tissue_type="endometrium, adenocarcinoma cell line"

/lab_host="DH10B (phage-resistant)"
 /note="Organ: uterus; Vector: pORF7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 119 a 192 c 154 g 108 t
 ORIGIN

Query Match 21.9%; Score 355; DB 10; Length 573;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

82 CAACGACCTCTCTCCCGGAGTTCATTTGATGACAGGTAACGTTCAAGACATGTG 141
 1 CAACGACCTCTCTCCCGGAGTTCATTTGATGACAGGTAACGTTCAAGACATGTG 60
 142 TCAGAAAGATGATGAGCAAAAGTCCGGATCATGTACCCGAAGTCTCTGCATCATC 201
 61 TCAGAAAGATGATGAGCAAAAGTCCGGATCATGTACCCGAAGTCTCTGCATCATC 120
 202 AGCGGCTCTCTCATGCGCTCTGCGGGTACCAAGTCTCTGCTCCCGAGGAAGTGA 261
 121 AGCGGCTCTCTCATGCGCTCTGCGGGTACCAAGTCTCTGCTCCCGAGGAAGTGA 180
 262 CTCAGTTTCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCCAAGCCCAAGAAG 321
 181 CTCAGTTTCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCCAAGCCCAAGAAG 240
 322 GGAAGTTTGGCTCGGGCCCTCAGGGCAGGGCTCCGACACCATCTGTTCTCAAAAT 381
 241 GGAAGTTTGGCTCGGGCCCTCAGGGCAGGGCTCCGACACCATCTGTTCTCAAAAT 300
 382 AGCCCTCTCTCGGACACACTGCTGAAGCTGAAGAGATGCCACCCCTCTGCAT 436
 301 AGCCCTCTCTCGGACACACTGCTGAAGCTGAAGAGATGCCACCCCTCTGCAT 355

RESULT 36
 AM087372 432 bp mRNA linear EST 15-OCT-1999
 LOCUS x019602.x1 NCI-CGAP Kid13 Homo sapiens cDNA clone IMAGE:2576786 3'
 DEFINITION similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
 GPR39, mRNA sequence.

ACCESSION AM087372 GI:6043177
 VERSION EST.
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 432)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
 Technologies, Inc. cDNA Library Arrayed by: Christa Pirange, The
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/dbp/image/image.html

FEATURES
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40UP from Gibco
 High quality sequence stop: 306.
 Location/Qualifiers

source

1..432
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2576786"
 /clone_1b="NCI-CGAP Kid13"
 /tissue_type="2 pooled Wilms' tumors, one primary and one
 metastatic to brain"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pCMV-Sport6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies."
 BASE COUNT 92 a 116 c 89 g 134 t 1 others
 ORIGIN

Query Match 21.8%; Score 353; DB 10; Length 432;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1252 AAGTAGACCTCTCTCCCGGAGTTCATTTGATGACAGGTAACGTTCAAGACATGTG 1311
 353 AAGTAGACCTCTCTCCCGGAGTTCATTTGATGACAGGTAACGTTCAAGACATGTG 294
 1312 TTGGGCATCCAGCATACGCGCAATGTCAACAATACACCTCTGGGACAGACAGCAGGA 1371
 293 TTGGGCATCCAGCATACGCGCAATGTCAACAATACACCTCTGGGACAGACAGCAGGA 234
 1372 GGGAGACAGAGAAAACAAAACACAGCATGACAGACAGTAATGATTAATACATTA 1431
 233 GGGAGACAGAGAAAACAAAACACAGCATGACAGACAGTAATGATTAATACATTA 174
 1432 AATATTTAGCCCTCTGTTGCTGTGCTTACTGCGCCAGGAATGTACCAATTTTCACTGT 1491
 173 AATATTTAGCCCTCTGTTGCTGTGCTTACTGCGCCAGGAATGTACCAATTTTCACTGT 114
 1492 TCGACTTGACACTCTTTTGGCAACAAGAGAGATTTACACTGTTCAACCCGG 1551
 113 TCGACTTGACACTCTTTTGGCAACAAGAGATTTACACTGTTTCAACCCGG 54
 1552 GGGAGTTGGCTGTGTTAAAGAACATTAATGCTTTAGCAGTGTAAAA 1604
 53 GGGAGTTGGCTGTGTTAAAGAACATTAATGCTTTAGCAGTGTAAAA 1

RESULT 37
 A1018769 537 bp mRNA linear EST 27-AUG-1998
 LOCUS A1018769/c
 DEFINITION ov32e04.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1639038
 3' similar to SW:NTBL_RAT P20789 NEUROGENIN RECEPTOR TYPE 1 ;

ACCESSION A1018769 GI:3232567
 VERSION EST.
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 537)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
 , Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/dbp/image/image.html
 Insert length: 1394 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 452.

FEATURES
source

Location/Qualifiers
1. .537
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1639038"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories Inc. and primed with a Not I - oligo(dT) primer [5']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cots, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 105 a 147 c 126 g 139 t

ORIGIN

Query Match 21.8%; Score 353; DB 9; Length 537;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 453; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1138 TGCAGAACACCCCGGAACTGCTGCAGAGACACCGTGTACAGAGAGCGGGTGTATGACC 1197
|||||
DB 475 TGCAGAACACCCCGGAACTGCTGCAGAGACACCGTGTACAGAGAGCGGGTGTATGACC 416
|||||

QY 1198 GAGCTGAGTGAAGAAAGAGTCTCCGAGAGAGGAGAGATCATGTACCGCCGGAATAG 1257
|||||
DB 415 GAGCTGAGTGAAGAAAGAGTCTCCGAGAGAGGAGAGATCATGTACCGCCGGAATAG 356
|||||

QY 1258 GACCTGCTGCAGTGTGCTGGTGGTGGCGGACCATGATCTCCGAACTGTGGTGGC 1317
DB 355 GACCTGCTGCAGTGTGCTGGTGGTGGCGGACCATGATCTCCGAACTGTGGTGGC 296
|||||

QY 1318 ATCCAGCATATGACCAATGTACAAACATGACCCCTGGGAGACAGACAGAGAGAGAGA 1377
DB 295 ATCCAGCATATGACCAATGTACAAACATGACCCCTGGGAGACAGACAGAGAGAGAGA 236
|||||

QY 1378 GACGAG 1437
DB 235 GACGAG 176
|||||

QY 1438 TAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1497
DB 175 TAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 116
|||||

QY 1498 TGACAGCTCTTTTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1557
DB 115 TGACAGCTCTTTTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 56
|||||

QY 1558 TGGCTGTGTAAAGAAAGACATTAAATGCTTAA 1592
DB 55 TGGCTGTGTAAAGAAAGACATTAAATGCTTAA 21
|||||

RESULT 38
LOCUS B1913989 707 bp mRNA linear EST 16-OCT-2001
DEFINITION 60318056F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5244569 5',
ACCESSION B1913989
VERSION B1913989.1 GI:16178286
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgi.mcl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
http://image.lnl.gov
Plate: L16M1617 row: a column: 18
High quality sequence stop: 698.

FEATURES
source

Location/Qualifiers
1. .707
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5244569"
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH-MGC Library."

BASE COUNT 133 a 233 c 209 g 132 t

ORIGIN

Query Match 21.6%; Score 349; DB 13; Length 707;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACATTTTGGGAGTGTCTTGTCCAGGCTTGGCTGCAATTCAGTGTACCA 60
DB 286 GGCACATTTTGGGAGTGTCTTGTCCAGGCTTGGCTGCAATTCAGTGTACCA 345
|||||

QY 61 GGTGAGAGATTCAGCTGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 346 GGTGAGAGATTCAGCTGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
|||||

QY 121 GGTGAGAGATTCAGCTGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 406 GGTGAGAGATTCAGCTGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
|||||

QY 181 CGGCAAGTCTGTGATCATTCAGCGGCTGTCTATGCGCTTGGCGGGATCAAGTCTT 240
DB 466 CGGCAAGTCTGTGATCATTCAGCGGCTGTCTATGCGCTTGGCGGGATCAAGTCTT 525
|||||

QY 241 CTGCTCCCGAGGAGAAAGTCACTGTTGATCATGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 526 CTGCTCCCGAGGAGAAAGTCACTGTTGATCATGCTGCTGCTGCTGCTGCTGCTGCTG 585
|||||

QY 301 CGGGCCAAAGGCCCAAGAAAGGGAGATTGCTGCGCTGCGCTCAGGCCA 349
DB 586 CGGGCCAAAGGCCCAAGAAAGGGAGATTGCTGCGCTGCGCTCAGGCCA 634
|||||

RESULT 39
LOCUS BE386060 593 bp mRNA linear EST 21-JUL-2000
DEFINITION 601276753F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617749 5',
ACCESSION BE386060
VERSION BE386060.1 GI:9331425
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 593)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DRP
 DNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: image.llnl.gov
 Plate: L1CM285 row: 1 column: 14
 High quality sequence stop: 593.

FEATURES

source

1..593
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="3617749"
 /clone_1lb="NIH-MGC_20"
 /tissue_type="melanocytic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pOB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 139 a 166 c 183 g 105 t
 ORIGIN

Query Match 21.5%; Score 348; DB 10; Length 593;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 AGCGTTTGGCGTCAATCCAGTGTACAGTGTGAAGATTCAGTCAACAGACTG 90
 DB 246 AGCGTTTGGCGTCAATCCAGTGTACAGTGTGAAGATTCAGTCAACAGACTG 305
 QY 91 CTTCCCTCCCGGATTCATGTGAATTCGACGGTGAACGTTCAAGCATGTGTCAAGAA 150
 DB 306 CTTCCCTCCCGGATTCATGTGAATTCGACGGTGAACGTTCAAGCATGTGTCAAGAA 365
 QY 151 AGTGAATGAGCAAGTGCAGGATCATGTATGACGCAAGTCCGTGATCATGAGCGGCTG 210
 DB 366 AGTGAATGAGCAAGTGCAGGATCATGTATGACGCAAGTCCGTGATCATGAGCGGCTG 425
 QY 211 TCTCATCGCTTGCAGGATCATGTATGACGCAAGTCCGTGATCATGAGCGGCTG 270
 DB 426 TCTCATCGCTTGCAGGATCATGTATGACGCAAGTCCGTGATCATGAGCGGCTG 485
 QY 271 CATCACTGCTGACACACCCCTCTTTTGAACGGGCAAGGCCCAAGAAAGGGAAGTTC 330
 DB 486 CATCACTGCTGACACACCCCTCTTTTGAACGGGCAAGGCCCAAGAAAGGGAAGTTC 545
 QY 331 TGCCTCGGCGCTCAGGCGGAGGCTCCGACCACTCCGTTCCCA 378
 DB 546 TGCCTCGGCGCTCAGGCGGAGGCTCCGACCACTCCGTTCCCA 593

RESULT 40
 LOCUS AL538562 920 bp mRNA linear EST 16-FEB-2001
 DEFINITION AL538562.LT1.FL013.FBn1 Homo sapiens cDNA clone CS0DF024Y004.5
 ACCESSION AL538562
 VERSION AL538562.1 GI:12866967
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 920)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polyes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

1..920
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="CS0DF024Y004"
 /clone_1lb="LT1.FL013.FBn1"
 /dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
 /lab_host="DH10B"
 /note="Organ: Fetal brain; Vector: PCWVSport 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCWVSport 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax : (1) 301 610 8371 Email : liang@lifetech.com URL : <http://fulllength.invitrogen.com>"
 BASE COUNT 172 a 285 c 257 g 199 t 7 others
 ORIGIN

Query Match 21.4%; Score 347; DB 9; Length 920;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGCGAATGTTCTTGCCTCCAGGCTTTGCGTCAATCCAGTGTACCA 60
 DB 279 GGCACCTTTTGGCGAATGTTCTTGCCTCCAGGCTTTGCGTCAATCCAGTGTACCA 338
 QY 61 GTGGAAGAAATTCACGTCGAACACGACTGCTCCCGGAGTTCATTTGAAATTCAC 120
 DB 339 GTGGAAGAAATTCACGTCGAACACGACTGCTCCCGGAGTTCATTTGAAATTCAC 398
 QY 121 GGTGAAGTTCAGACATGTCGAGAAAGAGTATGAGCAAGTCCGCGGATCATGTA 180
 DB 399 GGTGAAGTTCAGACATGTCGAGAAAGAGTATGAGCAAGTCCGCGGATCATGTA 458
 QY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCTTGCAGGATTCACAGTCTT 240
 DB 459 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCTTGCAGGATTCACAGTCTT 518
 QY 241 CTGCTCCCGAAGGAAATCAATCAATGTTGATGATGCTGCAACACCCCTCTTTGTA 300
 DB 519 CTGCTCCCGAAGGAAATCAATCAATGTTGATGATGCTGCAACACCCCTCTTTGTA 578
 QY 301 CGGCGCAAGGCGCAAGAAAGGGAAGTTTCGCTCGGCGCTCAGGC 347
 DB 579 CGGCGCAAGGCGCAAGAAAGGGAAGTTTCGCTCGGCGCTCAGGC 625

RESULT 41
 LOCUS BF935708/c 368 bp mRNA linear EST 22-JAN-2001
 DEFINITION BF935708 NR2-NT0138-281200-008-f08 NT0138 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF935708
 VERSION BF935708.1 GI:12353032
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 368)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bai, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
-------	--

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
DOI: 10.1073/pnas.0000000

**JOURNAL
MEDLINE
COMMENT**

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP
Brazil
Tel.: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=WR2stt2=WR2-NR0138.281200-008-108&t3=2000-12-28&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 368

FEATURES	Location/Qualifiers
source	1. .368

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0138"
/dev_stage="Adult"
/notice="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      88 a      109 c      96 g      75 t
ORIGIN

```

Query Match	20.9%	Score 338	DB 12	Length 368
Best Local Similarity	100.0%	Pred. No. 0		
Matches 338	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	CCATCCCTGATGGGGGACATGTTTGAGACGTGAGAGTGAAGTGAAGTTCCTTAAGGCT	805		
Db	352 CCATCCCTGATGGGGGACATGTTTGAGACGTGAGAGTGAAGTGAAGTTCCTTAAGGCT	293		
QY	GGAGGGCCAGTTCACCACTCAAGGCTCCCTCGCTTACATTCAAAGTTCATGCTCCGAAA	865		
Db	292 GGAGGGCCAGTTCACCACTCAAGGCTCCCTCGCTTACATTCAAAGTTCATGCTCCGAAA	233		
QY	ACCAATTCCTGACAGAGAAATGGCTGGTTTCGAGCTGAGTTGGGCTCTAATGACTCGAG	925		
Db	232 ACCAATTCCTGACAGAGAAATGGCTGGTTTCGAGCTGAGTTGGGCTCTAATGACTCGAG	173		
QY	ACTCAATGACTGAGGACTTAGACTGGGGGCTCGGCTCTGCTCTGAAAAAGTCTTAAGAAAT	985		
Db	172 ACTCAATGACTGAGGACTTAGACTGGGGGCTCGGCTCTGCTCTGAAAAAGTCTTAAGAAAT	113		
QY	CTTTCACAGTTCCTTCGACAGAGACTGGGCGGGGACGCGAAGACCAACGGGCGCTGCAC	1045		
Db	112 CTTTCACAGTTCCTTCGACAGAGACTGGGCGGGGACGCGAAGACCAACGGGCGCTGCAC	53		
QY	AAAGGGGGGCTGTCGGGTGGAGTGGGCGCAATGACGC	1083		
Db	52 AAAGGGGGGCTGTCGGGTGGAGTGGGCGCAATGACGC	15		

RESULT 42	AM191974/c	LOCUS	DEFINITION
	AM191974	454 bp	mRNA
	x178a02.x1	Homo sapiens	clone IMAGE:2680778 3'
		NCI_CGAP_Pan1	linear EST 29-NOV-1996

ACCESSION similar to SW:GP39_HUMAN 043194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
 VERSION GP39.1, mRNA sequence.
 KEYWORDS AW191974
 AW191974.1 GI:6470673
 EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 454)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE Tumor Gene Index
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Unpublished (1997)
Contact: Robert Strusberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Possible reversed clone: similarly on wrong strand
Possible reversed clone: poly^r not found
Seq primer: ~400P from Gibco
High quality sequence stop: 195.

FEATURES	SOURCE
Location/Qualifiers	1. .454
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone IMAGE:2680778"	
/clone_11b="NCL CGAP_Pan1"	
/tissue_type="adenocarcinoma"	
/lab_host="DH10B"	
/note="Organ: pancreas; Vector: pCMV-Sport6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: oligo dr..	
Average insert size 1.72 kb. Life Technologies catalog #:	
11548-013"	
BASE COUNT	96 a 123 c 95 g 138 t 2 others
ORIGIN	

```
Query Match      20.8%; Score 336; DB 10; Length 454;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

OY	1165	GAGGACACCGTGTACAGGAGCGGGTTGATGACCGAGCTGAGGTTAGAAAAACGTCGCCAG	1224
Db	438	GAGGACACCGTGTACAGGAGCGGGTTGATGACCGAGCTGAGGTTAGAAAAACGTCGCCAG	379
OY	1225	AAGGGAGAGAGATCATGTACGCCCGGAAGTAGACCTTCGTCACTGTCCTTGGGTTTG	1284
Db	378	AAGGGAGAGAGATCATGTACGCCCGGAAGTAGACCTTCGTCACTGTCCTTGGGTTTG	319
OY	1285	GCCGCACCCATGATCCTCCGAATCTTGTTGGGCATCCAGCATACGCCCATGTCTCAACA	1344
Db	318	GCCGCACCCATGATCCTCCGAATCTTGTTGGGCATCCAGCATACGCCCATGTCTCAACA	259
OY	1345	ATCAGCCCTGGGCAACACACGAGCAGAGGAGGAGACACAGAAAAAACAACACACATAGA	1404
Db	258	ATCAGCCCTGGGCAACACACGAGCAGAGGAGGAGACAGAAAAAACAACACACATAGA	199
OY	1405	GAAACAGTAAATGATTAANAACATAAAAATTTAGCCCTCTGTCTGTGCTTACTGGC	1464
Db	198	GAAACAGTAAATGATTAANAACATAAAAATTTAGCCCTCTGTCTGTGCTTACTGGC	139
OY	1465	CAGGAAATGATCCAAATTTTCAGTGTGGACTTACACAGCTCTTTGCGCACACACAAGA	1524
Db	138	CAGGAAATGATCCAAATTTTCAGTGTGGACTTACACAGCTCTTTGCGCACACACAAGA	79
OY	1525	GAGAAATTAACACTGTCTCAAAACCGGGGAGATGGCTGTGTTAAAGAAAGCACTTAAA	1584
Db	78	GAGAAATTAACACTGTCTCAAAACCGGGGAGATGGCTGTGTTAAAGAAAGCACTTAAA	19

QY 1585 TCCTTAGACAGTGTAA 1602
DB 18 TCGTTAGACAGTGTAA 1

RESULT 43
BI917149 747 bp mRNA linear EST 16-OCT-2001
LOCUS 60318157.F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5245648 5',
DEFINITION mRNA sequence.
ACCESSION BI917149
VERSION BI917149.1 GI:16181111
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 747)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M1619 row: n column: 17
High quality sequence stop: 737.
Location/Qualifiers
1..747
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5245648"
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: PCMV-SPORE6; Site:1; NotI;
Site:2; EcoRV (destroyed): RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

BASE COUNT 140 a 245 c 216 g 146 t
ORIGIN

Query Match 20.8%; Score 336; DB 13; Length 747;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACATTTTGGCGATGTTCTGCTTCCAGGCTTGGCTGCAATTCAGTCTACCA 60
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QY 61 GTGTGAAGATTCACAGTGAACAACAGCTGCTCTCCCGAGATTCTGTGAATTGCAC 120
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QY 121 GGTGACGTTTAAAGACATGTCAGAAAGAGATGAGAGCAAGTCCGGGATCATGTA 180
DB 445 GGTGACGTTTAAAGACATGTCAGAAAGAGATGAGAGCAAGTCCGGGATCATGTA 504

QY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCTTCCGCGGTACACAGTCTT 240
DB 505 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCTTCCGCGGTACACAGTCTT 564

QY 241 CTGCTCCCAAGGAACTGAACCTAGTTTGCATGCTGCTGCAACACCCCTTTGTAA 300

DB 565 CTGCTCCCAAGGAACTGAACCTAGTTTGCATGCTGCTGCAACACCCCTTTGTAA 624

QY 301 CCGGCCAAGGCCCAAGAAAGGGAAGTCTGCTC 336
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LOCUS EST366619 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
DEFINITION AW954549
ACCESSION AW954549
VERSION AW954549.1 GI:8144232
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 540)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspar, R., Gay, C., Holt,
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 65
Seq primer: Reverse.
Location/Qualifiers
1..540
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGE"
/note="Vector: pBluescriptSM"

BASE COUNT 122 a 150 c 134 g 134 t
ORIGIN

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Best Local Similarity 99.5%; Pred. No. 0;
Matches 434; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 56 ATGAGCAAGTCCGCGATCATGTACCGCAAGTCTGTGCATCATCAGCGCTGTCTC 115

QY 215 ATGCGCTTCCCGGATACAGTCTTCTGCTCCCGAGGAATGACATCATGTTGCATC 274
DB 116 ATGCGCTTCCCGGATACAGTCTTCTGCTCCCGAGGAATGACATCATGTTGCATC 175

QY 275 AGCTGCTGCAACACCCCTCTTGTACGGGCGCAAGGCCCAAGAAAGGGAAGTTGCGC 334
DB 176 AGCTGCTGCAACACCCCTCTTGTACGGGCGCAAGGCCCAAGAAAGGGAAGTTGCGC 235

QY 335 TCGGCGCTGAGGCGAGGCTCCGACACACATCTGTTCTCAATTAAGCCCTCTTTCG 394
DB 236 TCGGCGCTGAGGCGAGGCTCCGACACACATCTGTTCTCAATTAAGCCCTCTTTCG 295

QY 395 GCACATGCTGAGGCGAGGAGATGCCACACCCCTCTGATGTTCTTCTCCAGCCCTGCG 454
DB 296 GCACATGCTGAGGCGAGGAGATGCCACACCCCTCTGATGTTCTTCTCCAGCCCTGCG 355

QY 455 CCGCAACCCCGACCTCTCTGATGAGTTTCTTCTGCTGCTTTTATTCGGGTAGGG 514
DB 356 CCGCAACCCCGACCTCTCTGATGAGTTTCTTCTGCTGCTTTTATTCGGGTAGGG 415

QY 515 AGCGGAGTCCGTCTCTTTTGTCTGTGCAATTAAGAGCTCGGTAAAGCAT 574
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Db 416 AGCGGAGTCCCTGTTCTTTTCTTCTGCAAAATGAAGAGCTCGTAAGCAT 475
 Oy 575 TCTGAATAATTTCAGC 590
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RESULT 45

BI669845

LOCUS 603293440F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:531289 5',
 DEFINITION mRNA sequence.

ACCESSION

BI669845
 BI669845.1 GI:15584078

KEYWORDS

EST.

SOURCE

ORGANISM

human.

REFERENCE

1 (bases 1 to 690)

NIH-MGC http://mgs.nci.nih.gov/.

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshlyukl and Piero Carninci (RIKEN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM1792 row: p column: 10
 High quality sequence stop: 690.

FEATURES

source

Location/Qualifiers

1..690

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/note="Organ: brain; Vector: pBluescriptPR (modified

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); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',

size-selected for average insert size 2.3 kb and

normalized to ROP 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIH/NHGRI, National

Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT

ORIGIN

127 a 231 c 202 g 130 t

Query Match

Best Local Similarity 100.0%; Pred. No. 0;

Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 61 GTGTGAAGATTCAGCTGACCAACAGACTGCTCTCCCGAGTTCATTTGAATTGCAC 120

Db 363 GTGTGAAGATTCAGCTGACCAACAGACTGCTCTCCCGAGTTCATTTGAATTGCAC 422

Oy 121 GGTGAACGTTCAAGCATGTGTGCAAGAAAGATGTGAGCAAAAGTCCGGATCATGTA 180

Db 423 GGTGAACGTTCAAGCATGTGTGCAAGAAAGATGTGAGCAAAAGTCCGGATCATGTA 482

Oy 181 CCGCAAGTCCTGTGCATCATCAGCGGCTGTCTCATGCTGCGGGGTACAGTCTT 240

Db 483 CCGCAAGTCCTGTGCATCATCAGCGGCTGTCTCATGCTGCGGGGTACAGTCTT 542

Oy 241 CTGCTCCCGAGGAACTGAACCTCAGTTGCATCAGCTGTCACAACCCCTTTTGTA 300

Db 663 CACCATCTCTTCTCTCAATTAAGCCCTC 690

Db 543 CTGCTCCCGAGGAACTGAACCTCAGTTGCATCAGCTGTCACAACCCCTTTTGTA 602
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Search completed: November 7, 2002, 23:08:04
 Job time: 2196.32 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:50:02 ; Search time 318.774 Seconds

(Without alignments)
11437.514 Million cell updates/sec

Title: US-09-970-966-211

Perfect score: 1619
Sequence: 1 ggcacatttcgcgattgt.....aaaaaaaaaaaaaaaa 1619

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1619	100.0	1619	24	ABT03277
2	1619	100.0	1619	24	ABT03281
3	1619	100.0	1619	24	ABT03284
4	1619	100.0	1619	24	ABT03284
5	1606.2	99.2	1897	24	ABT03284
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7	1574.2	97.2	1956	22	AAF64188
8	1574.2	97.2	1956	22	AAF64188
9	1548.8	95.7	1890	22	AAF93845

10	1395	86.2	1608	24	ABQ54231	Human ovarian anti
11	1373	84.8	1524	24	ABK33543	CDNA encoding huma
12	1310.4	80.9	2528	22	AAD18690	Human G protein co
13	613	37.9	625	24	ABT03280	Human ovarian carc
14	613	37.9	625	24	ABL40348	Ovarian carcinoma
15	613	37.9	625	24	ABL87898	Ovarian carcinoma
16	497.6	30.7	1362	24	ABT03279	Human ovarian carc
17	497.6	30.7	1362	24	ABL40347	Human ovarian carc
18	474.6	29.3	587	22	AAF94186	Ovarian carcinoma
19	424.2	26.2	558	24	ABL79397	Primer specific fo
20	413.4	25.5	444	22	AAH50766	Human ovarian carc
21	396.4	24.5	409	24	ABL81262	Human tumour assoc
22	388.4	24.0	1010	24	ABT03282	Human ovarian carc
23	388.4	24.0	1010	24	ABL40350	Ovarian carcinoma
24	377.4	23.3	430	24	ABL81273	Human ovarian carc
25	365.4	22.6	369	22	AAF95007	Human ovarian carc
26	365.4	22.6	369	24	ABT03274	Human ovarian carc
27	365.4	22.6	369	24	ABL48956	Human ovarian carc
28	362	22.4	373	24	ABL78538	Ovarian carcinoma
29	362	22.4	396	22	AAF94818	Human ovarian carc
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31	362	22.4	396	24	ABL48768	Human ovarian carc
32	354	21.9	390	24	ABL78554	Human ovarian carc
33	330.8	20.4	381	24	ABL84848	Human ovarian carc
34	310.2	19.2	349	24	ABL79431	Human ovarian carc
35	285	17.6	591	22	AAF94044	Human ovarian carc
36	197.8	12.2	480	24	ABT03283	Human ovarian carc
37	197.8	12.2	480	24	ABL40351	Human ovarian carc
38	175.4	10.8	468	22	AAK54063	Human ovarian carc
39	171.2	10.6	201	24	ABL85916	Human ovarian carc
40	60	3.7	60	24	ABN1977	Human ovarian carc
41	52.4	3.2	1254	17	AAI33127	Human spliced tran
42	52.4	3.2	1257	23	ABT03007	Human neurotensin
43	52.4	3.2	1249	23	AAI33127	Non-endogenous hum
44	52.4	3.2	1419	23	AAI33127	DNA encoding novel
45	51.6	3.2	3609	22	AAK94581	Human full-length

ALIGNMENTS

RESULT 1	ABT03277	standard; CDNA; 1619 BP.
ID	ABT03277	
AC	ABT03277	
XX		
DT	05-SEP-2002	(first entry)
DE		Human ovarian carcinoma associated coding sequence SEQ ID NO: 205.
XX		
KW		Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
KW		cytostatic; gene; ss.
XX		
OS		Homo sapiens.
XX		
PN	WO200239885-A2.	
XX		
PD	23-MAY-2002.	
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PF	13-NOV-2001; 2001WO-US45395.	
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PR	14-NOV-2000; 2000US-0713550.	
XX		
PR	03-APR-2001; 2001US-0825294.	
XX		
PR	02-OCT-2001; 2001US-0970966.	
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PA	(CORI-) CORIXA CORP.	
XX		
PI	Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;	
XX		
DR	WPI; 2002-500186/53.	
XX		
PT	Novel ovarian cancer polypeptide and polynucleotide, useful for	

PT detecting the presence of ovarian cancer in a patient, and in
PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
PT
PS
XX Claim 2: Page 189-190, 197pp: English.

XX The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention.

XX Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other:

Query Match 100.0%; Score 1619; DB 24; Length 1619;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

ABT03281
ID ABT03281 standard; cDNA: 1619 BP.

XX ABT03281:

AC 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 211.

XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KW cytosolic; gene; ss.

XX Homo sapiens.

OS WO200239885-A2.

XX 23-MAY-2002.

PF 13-NOV-2001; 2001MO-US45395.

XX 14-NOV-2000: 2000US-0713550.
PR 03-APR-2001: 2001US-0825294.
PR 02-OCT-2001: 2001US-0970966.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Stolk JA, Algate PA, Fling SP, Molash DA:
XX WPI: 2002-500186/53.
XX
XX Novel ovarian cancer polypeptide and polynucleotide, useful for
XX detecting the presence of ovarian cancer in a patient, and in
XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
XX
XX
XX Claim 2: Page 195; 197pp: English.
XX
XX The present invention provides human ovarian cancer associated proteins
XX and coding sequences. The sequences can be used in the diagnosis and
XX treatment of ovarian cancers. The present sequence is a coding sequence
XX of the invention.
XX
XX Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other:

Query Match 100.0%; Score 1619; DB 24; Length 1619;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACATTTTGGCGATGTTCTTCTGCTCCAGGCTTGGCGCTGCAATTCAGTCTACCA 60
DB 1 GGCACATTTTGGCGATGTTCTTCTGCTCCAGGCTTGGCGCTGCAATTCAGTCTACCA 60
QY 61 GTGTGAAGATTCACCTGACACAGACAGTCTCTCCCGAGGTTATTTGTGATTCAC 120
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QY 661 CGAGTCAAGGCCAGGCTGCGAGATCAGTCTTTCAGATCTGAGTGGCATCTGCC 720
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QY 1081 GCGGAGGCGCTTCTGAGTGGTGGGCTGCTGAGGAGAGGCGGAGAGTGGCTTGC 1140
DB 1081 GCGGAGGCGCTTCTGAGTGGTGGGCTGCTGAGGAGAGGCGGAGAGTGGCTTGC 1140
QY 1141 ACGAAGACCCCGGAACTGCTGCGAGAGACCGTGTACAGAGAGCGGTTGATGACCGAG 1200
DB 1141 ACGAAGACCCCGGAACTGCTGCGAGAGACCGTGTACAGAGAGCGGTTGATGACCGAG 1200
QY 1201 CTGAGAGTGAAGAAACGCTCCGAGAGAGGAGAGAGTACATGACCGGCAATGAGAC 1260
DB 1201 CTGAGAGTGAAGAAACGCTCCGAGAGAGGAGAGAGTACATGACCGGCAATGAGAC 1260
QY 1261 CTGCTCAGTCTGCTGAGTGGTGGGCTGCGCAGCAGTATCTCCGATGCTGGTGGCATC 1320
DB 1261 CTGCTCAGTCTGCTGAGTGGTGGGCTGCGCAGCAGTATCTCCGATGCTGGTGGCATC 1320
QY 1321 CAGCATACGCGCAATGTCAACAATCAAGCCCTGGGAGAGACGAGGAGGAGAC 1380
DB 1321 CAGCATACGCGCAATGTCAACAATCAAGCCCTGGGAGAGACGAGGAGGAGAC 1380
QY 1381 AAGAGAAAGAAAGAAACAGCAATGAGACAGTAAATGATTAATTAATTAATTAAT 1440
DB 1381 AAGAGAAAGAAAGAAACAGCAATGAGACAGTAAATGATTAATTAATTAATTAAT 1440
QY 1441 CCCCTCTGCTGCTGCTTACTGCGCAGGAAATGATACCAATTTTTCAGTGTGAGTGA 1500
DB 1441 CCCCTCTGCTGCTGCTTACTGCGCAGGAAATGATACCAATTTTTCAGTGTGAGTGA 1500
QY 1501 CAGCTTCTTTTGCACACAGAGAGAAATTAACACTGTTTCAACCCGGGGAGTTGG 1560
DB 1501 CAGCTTCTTTTGCACACAGAGAGAAATTAACACTGTTTCAACCCGGGGAGTTGG 1560
QY 1561 CTGTGTTAAGAAAGCACTTAATGCTTTAGACAGTGTAAAAAATTAATTAATTAAT 1619
DB 1561 CTGTGTTAAGAAAGCACTTAATGCTTTAGACAGTGTAAAAAATTAATTAATTAAT 1619

RESULT 3
ABLA0345
ID ABLA0345 standard; cDNA; 1619 BP.
XX ABLA0345;
AC
XX
DT 28-JUN-2002 (first entry)
XX


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Db 901 CTGAGTGGGCTCTAGTGAAGTCACTGAGACTGAGTGGAGCTTAGCTGGGCTGGCCT 960
Qy 961 CGGCTGGAAGAGTCTTAAAGAAATCTTCTCACTTCTCTTGCAGAGACTGGCCGGG 1020
Db 961 CGGCTGGAAGAGTCTTAAAGAAATCTTCTCACTTCTCTTGCAGAGACTGGCCGGG 1020
Qy 1021 ACGCGAAGAGCAAGCGGCGCTGCACAAAGCGGCGCTGTCCGGTGGTGGAGTGCAGTGA 1080
Db 1021 ACGCGAAGAGCAAGCGGCGCTGCACAAAGCGGCGCTGTCCGGTGGTGGAGTGCAGTGA 1080
Qy 1081 CGGCGAAGCGCTTCTCTGCTTGGCTGCTGCTGAGCGAGCGGCGGAGCAACACCTTTC 1140
Db 1081 CGGCGAAGCGCTTCTCTGCTTGGCTGCTGCTGAGCGAGCGGCGGAGCAACACCTTTC 1140
Qy 1141 ACGAAGACCGCGGAGAAAGTGTGCGAGGACCGCTGTACAGAGGCGGTGATGACCGAG 1200
Db 1141 ACGAAGACCGCGGAGAAAGTGTGCGAGGACCGCTGTACAGAGGCGGTGATGACCGAG 1200
Qy 1201 CTGAGGTAGAAAAACGCTTCCGAGAGAGGAGAGATCATGTACGCCCGGAAGTAGAGAC 1260
Db 1201 CTGAGGTAGAAAAACGCTTCCGAGAGAGGAGAGATCATGTACGCCCGGAAGTAGAGAC 1260
Qy 1261 CTGCTCCAGTCTGCTTGGGCTTGGCGCGAGCCATGATCTCCGAATCTGTTGGGCAATC 1320
Db 1261 CTGCTCCAGTCTGCTTGGGCTTGGCGCGAGCCATGATCTCCGAATCTGTTGGGCAATC 1320
Qy 1321 CAGCATACGCGCAATGTCTCAACAAATCAAGCCCTGGGCGAGACGAGGAGGAGAGAC 1380
Db 1321 CAGCATACGCGCAATGTCTCAACAAATCAAGCCCTGGGCGAGACGAGGAGGAGAGAC 1380
Qy 1381 AAGAGAAAGAAACACAGCATGAGAACACAGTAATGATTAATTAATTAATTAATTAAT 1440
Db 1381 AAGAGAAAGAAACACAGCATGAGAACACAGTAATGATTAATTAATTAATTAATTAAT 1440
Qy 1441 CCCCTCTGCTTGTCTTACTGCTGAGGAAATGTGACAAATTTTTCAGTGTGACTTGA 1500
Db 1441 CCCCTCTGCTTGTCTTACTGCTGAGGAAATGTGACAAATTTTTCAGTGTGACTTGA 1500
Qy 1501 CAGCTTCTTGTGCGACAGCAAGAGAGATTTTACACTGTTTCAAAACCCGGGAGATTGG 1560
Db 1501 CAGCTTCTTGTGCGACAGCAAGAGAGATTTTACACTGTTTCAAAACCCGGGAGATTGG 1560
Qy 1561 CTGCTTAAAGAAAGACATTAATGCTTTAGACAGTGAATTAATTAATTAATTAATTAAT 1619
Db 1561 CTGCTTAAAGAAAGACATTAATGCTTTAGACAGTGAATTAATTAATTAATTAATTAAT 1619

```

RESULT 5
 ABT03284
 ID ABT03284 standard; cDNA; 1897 BP.
 XX

```

AC ABT03284;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.
XX
KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
XX
KW cytosolic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200239885-A2.
XX
PD 23-MAY-2002.
XX
PF 13-NOV-2001; 2001WO-US45395.
XX
PR 14-NOV-2000; 2000US-0713550.
XX
PR 03-APR-2001; 2001US-0825294.
XX
PR 02-OCT-2001; 2001US-0970966.
XX
PA (CORI-) CORIXA CORP.

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XX
PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX
DR WPI: 2002-500186/53.
XX
PT Novel ovarian cancer polypeptide and polynucleotide, useful for
PT detecting the presence of ovarian cancer in a patient, and in
PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
PT
XX
PS Claim 2; Page 196; 197pp; English.
XX
CC The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention.
XX
SQ Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other;
XX
Query Match 99.2%; Score 1606.2; DB 24; Length 1897;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1616; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
Qy 1 GCGAAGTCTTGGGAGTGTCTTGTCTTCCAGGCTTGGCGCTGCAAAATCCAGTCTACCA 60
Db 280 GCGAAGTCTTGGGAGTGTCTTGTCTTCCAGGCTTGGCGCTGCAAAATCCAGTCTACCA 339
Qy 61 GTTGAAGAAATCCAGCTGAACAAGCACTGCTCTCCCGGAGTTCATTTGAATTCAC 120
Db 340 GTTGAAGAAATCCAGCTGAACAAGCACTGCTCTCCCGGAGTTCATTTGAATTCAC 399
Qy 121 GGTGAAGTTCAGACATGTGTGAGAAAGAGTATGAGCAAAAGTCCGGATCATGTA 180
Db 400 GGTGAAGTTCAGACATGTGTGAGAAAGAGTATGAGCAAAAGTCCGGATCATGTA 459
Qy 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCTCTGCGGGATCAGTCTT 240
Db 460 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCTCTGCGGGATCAGTCTT 519
Qy 241 CTGTCTCCCGAGGAAGTCACTGATTTGTCATCAGCTGCTGCAACACCTCTTGTAA 300
Db 520 CTGTCTCCCGAGGAAGTCACTGATTTGTCATCAGCTGCTGCAACACCTCTTGTAA 579
Qy 301 CGGCGCAAGGCCCAAGAAAGGGAAGTCTGCTGGGCGCTGACGCGAGGCTCCGAC 360
Db 580 CGGCGCAAGGCCCAAGAAAGGGAAGTCTGCTGGGCGCTGACGCGAGGCTCCGAC 639
Qy 361 CACCATCTGTCTCTCAAAATTAAGCCCTCTTCTGCGACACTGCTGAAGCTGAAGAGATG 420
Db 640 CACCATCTGTCTCTCAAAATTAAGCCCTCTTCTGCGACACTGCTGAAGCTGAAGAGATG 699
Qy 421 CCAACCCCTCCTGATGTTCTTCCAGCCCTGCGCCCAACCCCGACCTCCCTGAGTGA 480
Db 700 CCAACCCCTCCTGATGTTCTTCCAGCCCTGCGCCCAACCCCGACCTCCCTGAGTGA 759
Qy 481 GTTCTTCTGAGGCTCTTCTTATCTGAGGTAGGAGCGGAGTCCGCTTCTTGTGT 540
Db 760 GTTCTTCTGAGGCTCTTCTTATCTGAGGTAGGAGCGGAGTCCGCTTCTTGTGT 819
Qy 541 CCTGTGCAAAATTAAGAAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGATGAT 600
Db 820 CCGTGCAGAAATTAAGAAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGATGAT 879
Qy 601 TTTCAATATGACTTGAAGAGAGGAGTGAAGATTCACCCCATGTCTGTGTAC 660
Db 880 TTTCAATATGACTTGAAGAGAGGAGTGAAGATTCACCCCATGTCTGTGTAC 939
Qy 661 CGGAGTCAAGGCGAGGCTGCGAGAGTCAAGTCTTGAAGTCACTGAGTGGGATCTGCC 720
Db 940 CGGAGTCAAGGCGAGGCTGCGAGAGTCAAGTCTTGAAGTCACTGAGTGGGATCTGCC 999
Qy 721 TTTTGAAGGCTCCAGTGTCCATTCATCCCTGATGGGGGATAGTTGAGACTGACAGA 780

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Qy	241	CTGCTCCCCAGGAAACTGAACCTACGATTTGGATCGACGTGCTGCACAACACCCCTCTTTGTAA	300
Db	520	CTGCTCCCCAGGAAACTGAACCTACGATTTGGATCGACGTGCTGCACAACACCCCTCTTTGTAA	579
Qy	301	CGGGCCAAAGGCCCAAGAAAAAGGGGAAGTTCCTGCTCGGCCCTCCAGGCGAGGGATCCGCAC	360
Db	580	CGGGCCAAAGGCCCAAGAAAAAGGGGAAGTTCCTGCTCGGCCCTCCAGGCGAGGGATCCGCAC	639
Qy	361	CACCATCTGTTTCTCCAAATTTAGCCCTCTCTCGGCACACTGCTGAAGCTGAAGAGATG	420
Db	640	CACCATCTGTTTCTCCAAATTTAGCCCTCTCTCGGCACACTGCTGAAGCTGAAGAGATG	699
Qy	421	CCACCCCTCTCGCATTTGTTCTTCCAGCCCTCGCCCCAACCCCCCACTCCCTGAGTGA	480
Db	700	CCACCCCTCTCGCATTTGTTCTTCCAGCCCTCGCCCCAACCCCCCACTCCCTGAGTGA	759
Qy	481	GTTTCTCTGGGGTGTCCTTTTATTTCTGGGTAGGACGGGAGTCCGTGTTCTCTTTGTT	540
Db	760	GTTTCTCTGGGGTGTCCTTTTATTTCTGGGTAGGAGGGGGAGTCCGTGTTCTCTTTGTT	819
Qy	541	CCTGTGCAATTAATGAAAGAGCTCGGTAAACCATTTGAAATTAATTAAGCTCGACGAAT	600
Db	820	CCGTGTCAATTAATGAAAGAGCTCGGTAAACCATTTGAAATTAATTAAGCTCGACGAAT	879
Qy	601	TTTTCACTATGCTCTTGAAGAGAGAGGTGAGGTGAATTAATTAAGCTCGACGAAT	660
Db	880	TTTTCACTATGCTCTTGAAGAGAGAGGTGAGGTGAATTAATTAAGCTCGACGAAT	939
Qy	661	CGGAGTCAAGGCCAGAGCTGGGAGAGTCACTGCTTAGAAGTCACTGAGGTGGGATCTGGC	720
Db	940	CGGAGTCAAGGCCAGAGCTGGGAGAGTCACTGCTTAGAAGTCACTGAGGTGGGATCTGGC	999
Qy	721	TTTTGTAAAGCTCCAGTGTCCATTTCCATCCCTGATGGGGGCATAGTTTGACACTGCAGA	780
Db	1000	TTTTGTAAAGCTCCAGTGTCCATTTCCATCCCTGATGGGGGCATAGTTTGACACTGCAGA	105
Qy	781	GTTGAGAGTACATTTTCTTGAAGGCTGGAGGGCCAGTCCACATCAAGGCCTCGCTGG	840
Db	1060	GTTGAGAGTACATTTTCTTGAAGGCTGGAGGGCCAGTCCACATCAAGGCCTCGCTGG	111
Qy	841	ACATTCAAACTTCATGCTCTCGAANAACCATTTCTCGCAGACAGAAATTTGGCTGTTTGGCC	900
Db	1120	ACATTCAAACTTCATGCTCTCGAANAACCATTTCTCGCAGACAGAAATTTGGCTGTTTGGCC	117
Qy	901	CTGAGTGGGGCTAGTAGTACTCGAGACTGCATAATGACATGGGACTTAAGCTGGGCTCGGCT	960
Db	1180	CTGAGTGGGGCTAGTAGTACTCGAGACTGCATAATGACATGGGACTTAAGCTGGGCTCGGCT	1239
Qy	961	CGCTCTGAAAAGTCTTAAGAAAAATTTCTTCAGTTCTCTCTCGACAGAGACTGGCGCGGG	1020
Db	1240	CGCTCTGAAAAGTCTTAAGAAAAATTTCTTCAGTTCTCTCTCGACAGAGACTGGCGCGGG	129
Qy	1021	ACGGCAAGAGCAAGGGGCGCTGCACAAGGGGGCGCTGTCGGTGGTGGAGTCCGATGTA	1080
Db	1300	ACGGCAAGAGCAAGGGGCGCTGCACAAGGGGGCGCTGTCGGTGGTGGAGTCCGATGTA	135
Qy	1081	CGCGCAGGCGCTTCTCGTGGTTGGCGTGTGACAGCAAGGGGCGAGCAGACACTGGC	1144
Db	1360	CGCGCAGGCGCTTCTCGTGGTTGGCGTGTGACAGCAAGGGGCGAGCAGACACTGGC	1418
Qy	1141	ACGAACACCCGCCGAATCTGCTCGAGAGACACCGTGTACAGAGCGGCTTGAATGAACGAG	1200
Db	1419	ACGAACACCCGCCGAATCTGCTCGAGAGACACCGTGTACAGAGCGGCTTGAATGAACGAG	1478
Qy	1201	CTGAGGTGAAAAACGTCCTCGAAGAGGGGAGAGGATCATTTACGGCCCGGAAGTAGAGAC	1260
Db	1479	CTGAGGTGAAAAACGTCCTCGAAGAGGGGAGAGGATCATTTACGGCCCGGAAGTAGAGAC	1538
Qy	1261	CTCGTCCAGTGTGCTTGGGTTTGGCCGACAGCCATGATCCTCCGAATGTGTTGGGCAATC	1320
Db	1539	CTCGTCCAGTGTGCTTGGGTTTGGCCGACAGCCATGATCCTCCGAATGTGTTGGGCAATC	1598
Qy	1321	CAGGATACGGGCAATGTCAACAACATTCAGCCCTGGGCGACACGAGCAGAGAGAGAGAC	1380

Db	1539	CAGCATACGGCCATGTGCACAACTAGCCCTGGCCAGACACAGAGCAGGAGCAGAC	1658
Qy	1381	AGAGAAAAGAAAACACAGCATGGAAACACAGTAATGAAATAAACCATAAATTTTAC	1440
Db	1659	AGAGAAAAGAAAACACAGCATGGAAACACAGTAATGAAATAAACCATAAATTTTAC	1718
Qy	1441	CCCCTGTGTTGTGCTTACTGGCCAGGAATGTAACAAATTTTCAGTGTGGACTTGA	1500
Db	1719	CCCCTGTGTTGTGCTTACTGGCCAGGAATGTAACAAATTTTCAGTGTGGACTTGA	1778
Qy	1501	CAGCTTCCTTTGGCACAAGACAAGAAATTTAACCTGTTTCAAAACCGGGGGAGTTGG	1560
Db	1779	CAGCTTCCTTTGGCACAAGACAAGAAATTTAACCTGTTTCAAAACCGGGGGAGTTGG	1838
Qy	1561	CTGTGTTAAAGAAAGACCATTAATGCTTATAGACAGTGTAAAAAATTTTTAAAAA	1619
Db	1839	CTGTGTTAAAGAAAGACCATTAATGCTTATAGACAGTGTAAAAAATTTTTAAAAA	1897

RESULT 7

XX	AAE22400/C	
ID	AAE22400	standard; cDNA; 1953 BP.
XX	AC	
XX	AAE22400;	
DT	26-MAR-2001	(first entry)
XX		
DE	Human secreted protein gene 28	SEQ ID NO:38.
XX		
KW	Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;	
KW	antirheumatic; antiproliferative; cytosolic; cardiant; vasotropic;	
KW	cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;	
KW	fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;	
KW	rhumatoid arthritis; hyperproliferative disorder; cardiac arrest;	
KW	cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;	
KW	angiogenesis; nervous system disorder; Alzheimer's disease; infection;	
KW	ocular disorder; corneal infection; wound healing; skin aging;	
KW	food additive; preservative; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WC0200061629-A1.	
XX		
PD	19-OCT-2000.	
XX		
PF	06-APR-2000; 2000WO-US09071.	
XX		
PR	09-APR-1999; 99US-0128694.	
XX	20-JAN-2000; 2000US-0176931.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
PA	(ROSE/) ROSEN C A.	
XX		
PI	Ruben SM, Komatsoulis G;	
XX		
DR	WPI: 2000-647420/62.	
XX		
DR	P-PsDB; AAB63161.	
XX		
PT	Isolated nucleic acid molecule encoding a human secreted protein is	
PT	used in preventing, treating or ameliorating a medical condition -	
XX		
PS	Claim 1, Page 440; 533pp; English.	
XX		
XX	AAE22373 to AAE22421 encode the human secreted proteins given in AAB63113	
CC	to AAB63182. AAB63183 to AAB63231 represent more human secreted proteins	
CC	and polypeptides homologous to them. Human secreted proteins have	
CC	activities based on the tissues and cells the genes are expressed in.	
CC	Examples of activities include: immunosuppressive; antiarthritic;	
CC	antirheumatic; antiproliferative; cytosolic; cardiant; vasotropic;	
CC	cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;	
CC	fungicide; and ophthalmological. The polynucleotides and proteins can be	
CC	used to prevent, treat or ameliorate a medical condition in e.g. humans.	

CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are
 CC also used in diagnosing a pathological condition or susceptibility to a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular
 CC disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral
 CC ischemia, angiodysplasia, nervous system disorders e.g. Alzheimer's
 CC disease, infections caused by bacteria, viruses and fungi and also
 CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis. The polypeptides can also be used as a food additive or
 CC preservative to increase or decrease storage capabilities. AAF22364 to
 CC AAF22372 and AAB63133 represent sequences used in the exemplification of
 CC the present invention.

XX Sequence 1953 BP; 428 A; 540 C; 524 G; 458 T; 3 other;

Query Match 97.2% Score 1574.2; DB 21; Length 1953;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1993; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 GGCACATTTTTCGCGATTTCTTCTTCAGGCTTTCGCTGCAATTCAGTCTACCA 60
 DB 1674 GGCACATTTTTCGCGATTTCTTCTTCAGGCTTTCGCTGCAATTCAGTCTACCA 1615
 QY 61 GTGTGAAGATTCAGCTACACAGCAGCTGCTTCCTCCCGAGTTTCAATGTAATGAC 120
 DB 1614 GTGTGAAGATTCAGCTACACAGCAGCTGCTTCCTCCCGAGTTTCAATGTAATGAC 1555
 QY 121 GGTGAAGATTCAGCTACACAGCAGCTGCTTCCTCCCGAGTTTCAATGTAATGAC 180
 DB 1554 GGTGAAGATTCAGCTACACAGCAGCTGCTTCCTCCCGAGTTTCAATGTAATGAC 1495
 QY 181 CCGCAAGTCTGTCATCATCAGGCTGCTCTCATGCTCTGCGGGTACCAATGCTT 240
 DB 1494 CCGCAAGTCTGTCATCATCAGGCTGCTCTCATGCTCTGCGGGTACCAATGCTT 1435
 QY 241 CTGCTCCCAAGGAACTGATGATGATGATGATGATGATGATGATGATGATGATG 300
 DB 1434 CTGCTCCCAAGGAACTGATGATGATGATGATGATGATGATGATGATGATGATG 1375
 QY 301 CCGGCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
 DB 1374 CCGGCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1316
 QY 361 CACCATCTGCTGCTCAATTAAGCTCTTCTGCGACACTGCTGAAGTGAAGATG 420
 DB 1315 CACCATCTGCTGCTCAATTAAGCTCTTCTGCGACACTGCTGAAGTGAAGATG 1256
 QY 421 CCAACCCCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 DB 1255 CCAACCCCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1196
 QY 481 GTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 DB 1195 GTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1136
 QY 541 CCGTGCATTAATGAAGAGCTGCTGAAGCAATTCGAATTAATGACCTGACGAT 600
 DB 1135 CCGTGCATTAATGAAGAGCTGCTGAAGCAATTCGAATTAATGACCTGACGAT 1076
 QY 601 TTTTCAGTATGATGATGAAGAGAGGAGTGAAGCAATTCACCCCATGCTGTGAAC 660
 DB 1075 TTTTCAGTATGATGATGAAGAGAGGAGTGAAGCAATTCACCCCATGCTGTGAAC 1016
 QY 661 CGAGTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 DB 1015 CGAGTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 956
 QY 721 TTTTGTAAAGCTTCAAGTGTCAATCCCTGATGGGGCATAGTTTGAAGCTGAGA 780
 DB 1111 TTTTGTAAAGCTTCAAGTGTCAATCCCTGATGGGGCATAGTTTGAAGCTGAGA 780

DB 955 TTTTGTAAAGCTTCAAGTGTCAATCCCTGATGGGGCATAGTTTGAAGCTGAGA 896
 QY 781 GTGAGTGAAGCTTCTTGAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
 DB 895 GTGAGTGAAGCTTCTTGAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 836
 QY 841 ACATTTCAACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 DB 835 ACATTTCAACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 776
 QY 901 CTGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 DB 775 CTGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 716
 QY 961 CGCTCTGAAAAGTCTTGAAGAAATCTTTCAGTCTTCTTCTGCTGCTGCTGCTGCT 1020
 DB 715 CGCTCTGAAAAGTCTTGAAGAAATCTTTCAGTCTTCTTCTGCTGCTGCTGCTGCT 656
 QY 1021 ACAGGAGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
 DB 655 ACAGGAGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 596
 QY 1081 CGCGCAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 DB 595 CGCGCAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 537
 QY 1141 ACAGAACCCCGCAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
 DB 536 ACAGAACCCCGCAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 477
 QY 1201 CTGAGTGAAGAAACGCTCTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
 DB 476 CTGAGTGAAGAAACGCTCTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
 QY 1261 CTGCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 DB 416 CTGCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 357
 QY 1321 CAGCATACGCGCAATGTCAACAATACGCTGAGGAGGAGGAGGAGGAGGAGGAG 1380
 DB 356 CAGCATACGCGCAATGTCAACAATACGCTGAGGAGGAGGAGGAGGAGGAGGAG 297
 QY 1381 AGAGAAAGAAAGAAAGCAAGCATGAGACACAGTAAATTAATTAATTAATTAAT 1440
 DB 296 AGAGAAAGAAAGAAAGCAAGCATGAGACACAGTAAATTAATTAATTAATTAAT 237
 QY 1441 CCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 DB 236 CCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 117
 QY 1501 CAGCTTCTTTCGCAAGCAAGAGAGAAATTAACACTGTTTCAAAACCCGGGAGTTGG 1560
 DB 176 CAGCTTCTTTCGCAAGCAAGAGAGAAATTAACACTGTTTCAAAACCCGGGAGTTGG 117
 QY 1561 CTGTGTAAAGAAAGCAATTAATGCTTTAGACAGTGA 1600
 DB 116 CTGTGTAAAGAAAGCAATTAATGCTTTAGACAGTGA 77

RESULT 8
 AAF64188/c
 ID AAF64188 standard; cdna; 1956 BP.
 XX
 AC AAF64188;
 XX
 DT 06-APR-2001 (first entry)
 XX
 DE Human secreted protein gene 13 SEQ ID NO:23.
 XX
 XX Human: secreted protein; immunosuppressive; antiarthritic; antirheumatic;
 KW antiproliferative; cardiac; vasodilator; cerebroprotective;
 KW neurotrophic; neuroprotective; antibacterial; virucide; fungicide;
 KW optical; immunological; vulnary; autoimmune disease; cardiovascular disorder;

hyperproliferative disorders; cerebrovascular disorder; wound healing;
nervous system disorder; ocular disorder; skin ageing; chemotaxis;
food additive; ss.

OS Homo sapiens.

PN WO200077026-A1.

PD 21-DEC-2000

01-JUN-2000; 2000WO-US14973.

PR 11-JUN-1999; 99US-0138630.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
PA (DOE) POSTAL

2 XX
3
4
5
6
7
8
9

PI Rosen CA, Ruben SM, Komatsoulls GA;
 VY

DR WPI; 2001-071258/08.

DK P-PSDB; AAB75518.
XY

PT Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -

PS Claim 1; Page 443-444; 542pp; English.

human secreted proteins AAB75506 - AAB75554 are encoded by polynucleotide sequences AAF64176 - AAF64224. The specification includes amino acid sequences AAB75555 - AAB75606 which represent fragments of the human secreted proteins, and protein sequences with which they share homology. The proteins and polynucleotides, their agonists and antagonists have activities dependent on the tissues and cells in which they are expressed, examples of these activities include, immunosuppressive; antitumoric; antirheumatic; antiproliferative; cytostatic; cardiac; vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; and vulnerary. The proteins, polynucleotides, agonists and antagonists can be used to treat or detect or diagnose various diseases and disorders including, autoimmune diseases e.g. Rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angioneuromas, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. Included in the invention are polynucleotide sequences AAF64167 - AAF64175 and peptide AAB75505 which are used in the isolation, identification and characterisation of the proteins of the invention.

Sequence 1956 BP; 430 A; 543 C; 524 G; 456 T; 3 other;

Query Match	97.28;	Score 1574.2;	DB 22;	Length 1956;
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Matches 1595; Conservative 2; Mismatches 1; Indels 2; Gaps 2

[illegible]

QY	181	CCGCAAGTCCTTGGATGATATAGGAGGCGCTGTCATACGCGCTCGCGGGTACCACTCCTT	240
Db	1494	CGCGAAGTCCTTGCATATATACGAGGCGCTGCTCATACGCTCTGCGCGGGTACCACTCCTT	14353
QY	241	CTGCTCCCGAGGGAATCGAACTCAGTTTGATCAGCTGCTGCACACCCCTCTTTGTAA	300
Db	1434	CTTGCTCCCGAGGGAATCGAACTCAGTTTGATCAGCTGCTGCACACCCCTCTTTGTAA	1375
QY	301	CGGGCCAAAGGCCCAAGAAAGGGGAATTCTGCGCTGGCGCTCAGGCCAGGGCTCCGCAC	360
Db	1374	CGGGCCAAAGGCCCAAGAAAGGGGAATTCTGCGCTGGCGCTCAGGCCAGGGCTCCGCAC	1316
QY	361	CACCATTCCTGTTCCCAATTAATAGCCCTCTTCTCGGACACTGCTGAAGCTGAAGAGATG	420
Db	1315	CACCATTCCTGTTCCCAATTAATAGCCCTCTTCTCGGACACTGCTGAAGCTGAAGAGATG	1256
QY	421	CCACCCCTCTCGCATTTGTTCTTCAGCCCTCGCCCCCAACCCCCACCTCCCTGATGA	480
Db	1255	CCACCCCTCTCGCATTTGTTCTTCAGCCCTCGCCCCCAACCCCCACCTCCCTGATGA	1196
QY	481	GTTTCCTCCGGGGTGCCCTTTATCTCGGGTAGGGACGGGAGTCCGTGTTCTTTTGT	540
Db	1195	GTTTCCTCCGGGGTGCCCTTTATCTCGGGTAGGGACGGGAGTCCGTGTTCTTTTGT	1136
QY	541	CCTGTGCAAAATTAATGAAAGAGCTCGGTAAAGCATTCCTGATTAATTAATCAGCTGAT	600
Db	1135	CCTGTGCAAAATTAATGAAAGAGCTCGGTAAAGCATTCCTGATTAATTAATCAGCTGAT	1076
QY	601	TTTTCACTTTGTAATGAAAGAGAGGTGGAGTGAAGATTACCCCACTGTTCTGTATAC	660
Db	1075	TTTTCACTTTGTAATGAAAGAGAGGTGGAGTGAAGATTACCCCACTGTTCTGTATAC	1016
QY	661	CGGAGTCAAGGCCCAAGCGTGGCAGAGTCAAGTCCCTTAGAATCACTAGATGGGAGTGGC	720
Db	1015	CGGAGTCAAGGCCCAAGCGTGGCAGAGTCAAGTCCCTTAGAATCACTAGATGGGAGTGGC	956
QY	721	TTTTTTAAAGCCTCACTGTTCCATTCCTCATCCTGATGGGGCATAGTTTGAAGACTGCAGA	780
Db	955	TTTTTTAAAGCCTCACTGTTCCATTCCTCATCCTGATGGGGCATAGTTTGAAGACTGCAGA	896
QY	781	GTCGAGTGAAGCTTTTCTTAGGGCTGGAGGGCCAGTCTCCCACTCAAGGCTCCCTGGCTG	840
Db	895	GTCGAGTGAAGCTTTTCTTAGGGCTGGAGGGCCAGTCTCCCACTCAAGGCTCCCTGGCTG	836
QY	841	ACATTCAAACTTCACTGCTCCTGAAANCAATTCCTGCAAGCAGAAATGGCTGTTCCGCG	900
Db	835	ACATTCAAACTTCACTGCTCCTGAAANCAATTCCTGCAAGCAGAAATGGCTGTTCCGCG	776
QY	901	CTGAGTTGGGCTTAGAGACTCGAGACTCAATGACGTGGAGACTTAGACGTGGGGCTGGGCT	960
Db	775	CTGAGTTGGGCTTAGAGACTCGAGACTCAATGACGTGGAGACTTAGACGTGGGGCTGGGCT	716
QY	961	CGCTCTGAAAAGTGCCTTAAGAAAATCTTCTCAGTTCTCCTTGCAGAGAGACTGGCGCGGG	1020
Db	715	CGCTCTGAAAAGTGCCTTAAGAAAATCTTCTCAGTTCTCCTTGCAGAGAGACTGGCGCGGG	656
QY	1021	ACGGGAAGAGCAACGGGGCGCTGCAACAACGGGGCGCTCGGTGGTGAATGGCATGTGA	1080
Db	655	ACGGGAAGAGCAACGGGGCGCTGCAACAACGGGGCGCTCGGTGGTGAATGGCATGTGA	596
QY	1081	CGCGCAGGCGCTTCTCGTGGTTGGGCTGCTGTCAGAGCAAGAGCGCGCACAGCAACCTTGC	1140
Db	595	CGCGCAGGCGCTTCTCGTGGTTGGGCTGCTGTCAGAGCAAGAGCGCGCACAGCAACCTTGC	537
QY	1141	ACGGAACACCCCGCGGAATCTGTCCGAGGACACCGGTGTACAGAGCGGGTTGATACCGAG	1200
Db	536	ACGGAACACCCCGCGGAATCTGTCCGAGGACACCGGTGTACAGAGCGGGTTGATACCGAG	477
QY	1201	CTGAGGTAGAAAAAGCTCTCCGACAAGGGGAGAGAGATCATGTACGGCCGGGAAGTTAGAG	1260
Db	476	CTGAGGTAGAAAAAGCTCTCCGACAAGGGGAGAGAGATCATGTACGGCCGGGAAGTTAGAG	417
QY	1261	CTGTGTCAGTGTGTTGGGTTTGGCCGACCATGTAGTCTCCGAATCTGTTGGGCAATC	1320


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|||||
Db 416 CTCGTCAGTGTGCTTGGCTTGGCCCGACCATGATCTCCGAAATCTGTTGGGATC 357
Oy 1321 CAGCATAGGCGCAATGTGACAAACATCAGCCCTGGGAGACAGGAGGAGAGAC 1380
Db 336 CAGCATAGGCGCAATGTGACAAACATCAGCCCTGGGAGACAGGAGGAGAGAC 297
Oy 1381 AGAGAAAAGAAAACACAGCATGAGAACACAGTAATGATTAACATAATATTATTAG 1440
Db 296 AGAGAAAAGAAAACACAGCATGAGAACACAGTAATGATTAACATAATATTATTAG 237
Oy 1441 CCCCTCTGTTCTGTGCTTACTGCGCCAGGAAATGTTACCAATTTTCACTGTGAGCTTGA 1500
Db 236 CCCCTCTGTTCTGTGCTTACTGCGCCAGGAAATGTTACCAATTTTCACTGTGAGCTTGA 177
Oy 1501 CAGCTTCTTTTGGCCAGCAAGAGAGAAATTAACATCTGTTCAACCCCGGGAGATTGG 1560
Db 176 CAGCTTCTTTTGGCCAGCAAGAGAGAAATTAACATCTGTTCAACCCCGGGAGATTGG 117
Oy 1561 CTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTGA 1600
Db 116 CTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTGA 77

```

RESULT 9
AA93845 standard; cDNA; 1890 BP.

AA93845:

23-MAY-2001 (first entry)

Human cDNA encoding a membrane or secretory protein clone PSEC0181.

Human; secretory protein; membrane or secretory protein; vaccine; gene therapy;
rheumatoid arthritis; diabetes; ss.

Homo sapiens.

EP1067182-A2.

10-JAN-2001.

07-JUL-2000; 2000EP-0114090.

08-JUL-1999; 99JP-0194179.

11-JAN-2000; 2000JP-0118775.

02-MAY-2000; 2000JP-0183766.

(HELI-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

WPI: 2001-093989/11.

P-PSDB: AAB88418.

Nucleic acids encoding secretory proteins/membrane proteins, useful in
gene therapy or as candidate target molecules in drug development -

Claim 1: SEQ ID 203; 609bp + CD ROM; English.

This invention relates to nucleic acid sequences AAF93744 - AAF93916

which encode human secretory or membrane proteins represented by

AA93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the

cDNA sequences of the invention. The invention also includes methods for

the production of antibodies directed against the proteins, and cDNA

sequences, which can be used in vaccines. The polynucleotide sequences

can be used in gene therapy. The polynucleotide sequences and the

proteins they encode may be used in the prevention, treatment and

diagnosis of diseases associated with inappropriate secretory

protein/membrane protein expression. The nucleic acids and complementary

sequences may also be used as DNA probes in diagnostic assays

(e.g. polymerase chain reactions (PCR)) to detect and quantitate the
presence of similar nucleic acid sequences in samples. They may also be
used to study the expression and function of secretory proteins/membrane
polypeptides and their role in metabolism. The polypeptides may be used
as antigens in the production of antibodies against them and in assays to
identify modulators (agonists and antagonists) of expression and
activity. The antibodies and antagonists may also be used as therapeutic
agents to down regulate expression and activity. The antibodies may also
be used as diagnostic agents for detecting the presence of the
polypeptides in samples (e.g. by enzyme linked immunosorbent assay
(ELISA). Examples of diseases which may be treated include rheumatoid
arthritis and diabetes.

Sequence 1890 BP; 419 A; 528 C; 533 G; 410 T; 0 other;

Query Match 95.7%; Score 1548.8; DB 22; Length 1890;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1594; Conservative 0; Mismatches 2; Indels 4; Gaps 4;

1 GGCACCTTTTGGCGATGTTCTGCTTCCAGGCTTGGCCGCAATCCAGTCAACCA 60

294 GGCACCTTTTGGCGATGTTCTGCTTCCAGGCTTGGCCGCAATCCAGTCAACCA 353

61 GTGTGAAGAAATTCAGCTGAACAACGACCTCTCCGCCGAGTTCATTGTGATTCAC 120

354 GTGTGAAGAAATTCAGCTGAACAACGACCTCTCCGCCGAGTTCATTGTGATTCAC 413

121 GGTGAAGCTTCAAGACATGTCGTGAGAAAGAGTGAAGAGCAAAAGTCCGGGATCATGTA 180

414 GGTGAAGCTTCAAGACATGTCGTGAGAAAGAGTGAAGAGCAAAAGTCCGGGATCATGTA 473

181 CCGCAAGTCTGTGTCATCATCAGGCGCTGTCTCATCGCTGCGGGATCAGTCTT 240

474 CCGCAAGTCTGTGTCATCATCAGGCGCTGTCTCATCGCTGCGGGATCAGTCTT 533

241 CTGCTCCCAAGGAACTGAACTGATTCATGATGCTGCAACACCCCTTTGTAA 300

534 CTGCTCCCAAGGAACTGAACTGATTCATGATGCTGCAACACCCCTTTGTAA 593

301 CGGCGCAAGGCGCAAGAAAGGGGAAGTTGCTGCGGCCCTGAGCGAGGCTCCGGCAC 360

594 CGGCGCAAGGCGCAAGAAAGGGGAAGTTGCTGCGGCCCTGAGCGAGGCTCCGGCAC 653

361 CACCATCTGTTCTCAATTAAGCCCTTCTCGGACACATGCTGAAGCTGAAGAGATG 420

654 CACCATCTGTTCTCAATTAAGCCCTTCTCGGACACATGCTGAAGCTGAAGAGATG 711

421 CCACCCCTCTCGATTTGTTCTTCAGCCCTGCGCCCAACCCCCACCTCCCTGAGTGA 480

712 CCACCCCTCTCGATTTGTTCTTCAGCCCTGCGCCCAACCCCCACCTCCCTGAGTGA 771

481 GTTCTCTTGGGTCCTCTTTATTTCTGGGTAGGAGGAGGAGTCCGTTCTTTTGT 540

772 GTTCTCTTGGGTCCTCTTTATTTCTGGGTAGGAGGAGGAGTCCGTTCTTTTGT 811

541 CCTGCAAAATGAAGAGAGCTGCTGAAGAGAGTTCGATTAATTAATTCAGCTGAGT 600

832 CCTGCAAAATGAAGAGAGCTGCTGAAGAGAGTTCGATTAATTAATTCAGCTGAGT 891

601 TTTGATATGTTACTTGAAGAGAGAGTTCGATTAATTAATTCAGCTGAGT 660

892 TTTGATATGTTACTTGAAGAGAGAGTTCGATTAATTAATTCAGCTGAGT 951

661 CGGAGTCAAGGCGCGCTGCGAGAGTCAAGTCTTAGAAGTCACTGAGGTGGATCTGCC 720

952 CGGAGTCAAGGCGCGCTGCGAGAGTCAAGTCTTAGAAGTCACTGAGGTGGATCTGCC 1011

721 TTTGTAAGGCTCAATGTCATTCATCCATGATGGGAGATGTTAGAGTCAAGTCAAG 780

1012 TTTGTAAGGCTCAATGTCATTCATCCATGATGGGAGATGTTAGAGTCAAGTCAAG 1071

781 GTGAGATGACGTTTCTTAGGGCTGAGGAGGACGTTCCACATCAAGCTCCCTGCTG 840

Db 1072 GTGAGAGTACGCTTTTCTTAGGGCTGAGGGCCAGTCCCACTCAAGGCTCCCTCGTTG 1131
 QY 841 ACATTCAAACTTCATGCTCCTGAAAAACATTCCTGCGAGCAAAATTCGCTGTTCCGGC 900
 Db 1132 ACATTCAAACTTCATGCTCCTGAAAAACATTCCTGCGAGCAAAATTCGCTGTTCCGGC 1191
 QY 901 CTGAGTTGGGCTCTAGTGAATGAGACTCAATGACTGGGACTTAGACTGGGCTCGGCT 960
 Db 1192 CTGAGTTGGGCTCTAGTGAATGAGACTCAATGACTGGGACTTAGACTGGGCTCGGCT 1251
 QY 961 CGCTCTGAAAAATGCTTAAAGAAAATCTTCTCACTTCT-CTTTCAGAGAGACTGCGCCGG 1019
 Db 1252 CGCTCTGAAAAATGCTTAAAGAAAATCTTCTCACTTCTCGAGAGAGACTGCGCCGG 1311
 QY 1020 GACGGCAAGAGACGAGGGGCTGCACAAAGGGGGCTGTGGTGGTGGAGGGCCATGT 1079
 Db 1312 GACGGCAAGAGACGAGGGGCTGCACAAAGGGGGCTGTGGTGGTGGAGGGCCATGT 1371
 QY 1080 AGCGCGAGGCGCTTCTCGTGGTGGCGCTGACAGCAGAGGCGGCGACAGCACTTGG 1139
 Db 1372 AGCGCGAGGCGCTTCTCGTGGTGGCGCTGACAGCAGAGGCGGCGACAGCACTTGG 1430
 QY 1140 CACGAACACCCCGCAAACTGCTGCGAGAGACCGCTGTACAGAGAGCGGGTGTATACCGA 1199
 Db 1431 CACGAACACCCCGCAAACTGCTGCGAGAGACCGCTGTACAGAGAGCGGGTGTATACCGA 1490
 QY 1200 GCTGAGGTGAAAAAGCTCCGAGAGGGAGAGAGTCAATGATCGGCCGCAACTAGCA 1259
 Db 1491 GCTGAGGTGAAAAAGCTCCGAGAGGGAGAGAGTCAATGATCGGCCGCAACTAGCA 1550
 QY 1260 CCTGCTCAGTGTGCTTGGGTTGGCGCAGCAGTGAATCTCCGAAATCTGTTGGGAT 1319
 Db 1551 CCTGCTCAGTGTGCTTGGGTTGGCGCAGCAGTGAATCTCCGAAATCTGTTGGGAT 1610
 QY 1320 CCAGCATACGGGCATATGTCACACATACAGCCCTGGCGAGACAGCAGAGAGAGAGA 1379
 Db 1611 CCAGCATACGGGCATATGTCACACATACAGCCCTGGCGAGACAGCAGAGAGAGAGA 1670
 QY 1380 CAGAGAAAAAGAAAACACAGCATGAGAACACAGTAATGAATAAACATTAATATTTA 1439
 Db 1671 CAGAGAAAAAGAAAACACAGCATGAGAACACAGTAATGAATAAACATTAATATTTA 1730
 QY 1440 GCCCCTCTGTTCTGCTTACTGCGCAGAGAAATGTTACCAATTTTTCAGTTGGACTTG 1499
 Db 1731 GCCCCTCTGTTCTGCTTACTGCGCAGAGAAATGTTACCAATTTTTCAGTTGGACTTG 1790
 QY 1500 ACAGCTTCTTTTCCCAAGCAAGAGAGATTAATTAACATCTTTTCAACCCCGGGAGTTG 1539
 Db 1791 ACAGCTTCTTTTCCCAAGCAAGAGAGATTAATTAACATCTTTTCAACCCCGGGAGTTG 1850
 QY 1560 GCTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGT 1599
 Db 1851 GCTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGT 1890
 RESULT 10
 AB054231.
 ID AB054231 standard; cDNA: 1608 BP.
 XX
 AC AB054231;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HVCAG04 cDNA, SEQ ID NO:111.
 XX
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;

KW antibody preparation; cytosolic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynecological; reproductive; chromosome 2q21-22;
 KW gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200200677-A1.
 XX
 PD 03-JAN-2002.
 XX
 PF 07-JUN-2001; 2001WO-US18569.
 XX
 PR 07-JUN-2000; 2000US-209467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX
 DR WPI: 2002-147878/19.
 XX
 DR P-PSDB; ABP41154.
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.
 PT ovarian cancer), immune disorders, cardiovascular disorders and
 PT neurological diseases -
 XX
 PS Claim 1; SEQ ID NO 111; 2922pp; English.
 XX
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents cDNA encoding a human ovarian antigen of the
 CC invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIFO
 CC at ftp.wipo.int/pub/published_pcl-sequences.
 XX
 SQ Sequence 1608 BP; 402 A; 402 C; 417 G; 381 T; 6 other;
 XX
 Query Match 86.2%; Score 1395; DB 24; Length 1608;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1428; Conservative 2; Mismatches 2; Indels 3; Gaps 3;
 QY 166 TGCCGGATCATGTACCGCAAGTCTGTGCATCATAGCGGCTGTCTCATGCGCTCTGC 225
 Db 101 TCCAGATATATATACCGCAAGTCTGTGCATCATAGCGGCTGTCTCATGCGCTCTGC 160
 QY 226 CGGGTACCACTCTTCTGCTCCCGAGGAAAGTGAAGTCAATGATGATGATGATGATG 285
 Db 161 CGGGTACCACTCTTCTGCTCCCGAGGAAAGTGAAGTCAATGATGATGATGATGATG 220

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Qy 286 CACCCCTCTTTTAAAGGCGCCAGGCGCCAGAAAGGGAGATGCTGCGCCCTGAG 345
    |||
Db 221 CACCCCTCTTTTAAAGGCGCCAGGCGCCAGAAAGGGAGATGCTGCGCCCTGAG 279
Qy 346 GCGAGGGGCTCGGACACACATCCTGTCTCTCAAAATAGCCCTCTCTGGGACACTGCTG 405
    | |||
Db 280 G-CAGGGGCTCGGACACACATCCTGTCTCTCAAAATAGCCCTCTCTGGGACACTGCTG 338
Qy 406 AAGCTGAAGAGATGCGACACCCCTCTGCAATGTTCTTCCAGCCCTCGCCCAACCCCC 465
    |||
Db 339 AAGCTGAAGAGATGCGACACCCCTCTGCAATGTTCTTCCAGCCCTCGCCCAACCCCC 398
Qy 466 CACCTCCCTGAGTGAATTTCTTCTGGGTCTCTTTTATTTCTGGTGAAGGCGGAGTCC 525
    |||
Db 399 CACCTCCCTGAGTGAATTTCTTCTGGGTCTCTTTTATTTCTGGTGAAGGCGGAGTCC 458
Qy 526 GTTGTCTCTTTGCTGCTGCAATTAATGAAGAGCTCGGTAAGCAATTCGATTAAT 585
    |||
Db 459 GTTGTCTCTTTGCTGCTGCAATTAATGAAGAGCTCGGTAAGCAATTCGATTAAT 518
Qy 586 TCAGCCTGACTGAATTTTCTAGTATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 645
    |||
Db 519 TCAGCCTGACTGAATTTTCTAGTATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 578
Qy 646 CCATGCTCTGTGAACCGAGAGTCAAGGCGAGGCTGGCAGAGTCACTTGAAGTCACTG 705
    |||
Db 579 CCATGCTCTGTGAACCGAGAGTCAAGGCGAGGCTGGCAGAGTCACTTGAAGTCACTG 638
Qy 706 AAGTGGGCACTGCGCTTTTGTAAAGCTCCATGTCATTCATCCCTGATGGGGGCAATA 765
    |||
Db 639 AAGTGGGCACTGCGCTTTTGTAAAGCTCCATGTCATTCATCCCTGATGGGGGCAATA 698
Qy 766 GTTTGAGACTGAGAGAGTGAAGTCACTTTTCTTGGGCTGGAGGGGCAATTCACCACTCA 825
    |||
Db 699 GTTTGAGACTGAGAGAGTGAAGTCACTTTTCTTGGGCTGGAGGGGCAATTCACCACTCA 758
Qy 826 AAGCTCCCTGCTTACATTTCAACTTCACTGCTCTGTAAGAAACCATTTCTGACAGAGAT 885
    |||
Db 759 AAGCTCCCTGCTTACATTTCAACTTCACTGCTCTGTAAGAAACCATTTCTGACAGAGAT 818
Qy 886 TGGCTGGTTTGGCGGCTAGTTGGGCTCTAGTACTCGAGACTCAATGACGTGGAGCTTAG 945
    |||
Db 819 TGGCTGGTTTGGCGGCTAGTTGGGCTCTAGTACTCGAGACTCAATGACGTGGAGCTTAG 878
Qy 946 ACTGGGGGCTCGGCTCTGCTGTAAGAAAGCTTCAAGAAATCTTCAAGTTCCTTGGAG 1005
    |||
Db 879 ACTGGGGGCTCGGCTCTGCTGTAAGAAAGCTTCAAGAAATCTTCAAGTTCCTTGGAG 938
Qy 1006 AAGACTGCGCGGCGGAGCGGAAAGCAACGGGCGCTGCAACAAGCGGGCGCTGTCGCTGG 1065
    |||
Db 939 AAGACTGCGCGGCGGAGCGGAAAGCAACGGGCGCTGCAACAAGCGGGCGCTGTCGCTGG 998
Qy 1066 TGGAGTGGGCAATGACGGGCGAGGCGCTTCTGCTGGTGGCGTCTGACAGCGACGCGGCG 1125
    |||
Db 999 TGGAGTGGGCAATGACGGGCGAGGCGCTTCTGCTGGTGGCGTCTGACAGCGACGCGGCG 1058
Qy 1126 AAGCAGACGACTTGGACGAAACCGCGGAAACCTGCTGAGAGAACCGGTGACAGGAGCG 1185
    |||
Db 1059 AAGCAGACGACCTGCAACGAAACCGCGGAAACCTGCTGAGAGAACCGGTGACAGGAGCG 1117
Qy 1186 GGGTTGATGACGAGCTAGGTAGAAAAACGTTCTCGAAGAGGGAGAGAGATCATGTATC 1245
    |||
Db 1118 GGGTTGATGACGAGCTAGGTAGAAAAACGTTCTCGAAGAGGGAGAGAGATCATGTATC 1177
Qy 1246 GCGCGGAAGTGAAGACTGCTGCTGAGTCTGCTTGGGTTGGCGGACGCAATGATCTCCGA 1305
    |||
Db 1178 GCGCGGAAGTGAAGACTGCTGCTGAGTCTGCTTGGGTTGGCGGACGCAATGATCTCCGA 1237
Qy 1306 ATCTGTTGGGATCAGAGATACGCGCAATGTCACAAACATAGCCCGGGGAGAGACAGAGA 1365
    |||
Db 1238 ATCTGTTGGGATCAGAGATACGCGCAATGTCACAAACATAGCCCGGGGAGAGACAGAGA 1297
Qy 1366 GCAGGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACATTAATGAATAAAA 1425
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Db 1298 GCAGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACAGTAAATRAATAAA 1357
Qy 1426 CCATTAATATATTTAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1485
    |||
Db 1358 CCATTAATATATTTAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1417
Qy 1486 CAGTGTGAGACTGACAGCTCTTGTGCAACAGCAGAGAGAGAAATTAACAGTGTTCAA 1545
    |||
Db 1418 CAGTGTGAGACTGACAGCTCTTGTGCAACAGCAGAGAGAGAAATTAACAGTGTTCAA 1477
Qy 1546 ACCCGGGGAGTGGCTGTGTAAAGAAAGCAATTAATGCTTTAGACAGTGA 1600
    |||
Db 1478 ACCCGGGGAGTGGCTGTGTAAAGAAAGCAATTAATGCTTTAGACAGTGA 1532

RESULT 11
ABK33543
ID ABK33543 standard; cDNA; 1524 BP.
XX
AC ABK33543;
XX
DT 08-MAY-2002 (first entry)
XX
DE cDNA encoding human PRO protein, Seq ID NO 15.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; gene; ss.
XX
OS Homo sapiens.
XX
PN WC0200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US21066.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
PR 25-JUL-2000; 2000US-220644P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.
PR 28-JUL-2000; 2000WO-US20710.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-000000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-253646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.

(GETH ) GENENTECH INC.
XX
PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Gritmalid JG, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2002-172001/22.
XX P-PSDB; AA083599.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour -
```


FT /product- "Human GPCR 4941"
ET /note- "The CDS is specifically claimed in claim 1 of
FT the specification"
XX
XX MO200181634-A2.
XX
XX 01-NOV-2001.
XX
XX 25-APR-2001; 2001WO-US13788.
XX
XX 26-APR-2000; 2000US-199908P.
PR 09-AUG-2000; 2000US-0635521.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX GalvIn KA, Rudolph-owen LA;
XX
XX WPI, 2001-611743/70.
DR P-PSDB; ABE11751.
XX
XX Identifying nucleic acids for the diagnosis and treatment of
PT cardiovascular and tumorigenic disorders, comprises identifying G
PT protein coupled receptor (GPCR)-4941 -
XX
XX Example 1; Fig 1; 118pp; English.
XX
XX The present invention relates to a method for identifying a nucleic acid
CC molecule (G protein coupled receptor gene, GPCR 4941) associated with a
CC cardiovascular or tumorigenic disorder. The method comprising contacting
CC a sample containing a nucleic acid molecule with a hybridisation probe or
CC amplification primers and detecting the presence. The invention is used
CC in gene therapy. The method of the invention is used for identifying
CC nucleic acids or polypeptides associated with a cardiovascular or
CC tumorigenic disorder such as aberrant angiogenesis, aberrant
CC vasculisation, arteriosclerosis, or ovarian cancer, ischaemia/
CC reperfusion injury, hypertension, restenosis, arterial inflammation,
CC endothelial cell disorders, diabetic retinopathy, psoriasis, myocardial
CC infarction, Grave's disease and Leukaemia. The methods can also detect
CC mRNA or genomic DNA in a sample. The present sequence is G protein
CC coupled receptor (GPCR) 4941 cDNA.
XX
XX Sequence 2528 BP; 516 A; 766 C; 677 G; 567 T; 2 other:
SQ
Query Match 80.9%; Score 1310.4; DB 22; Length 2528;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1325; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Db 1859 TTCTGGCAGACAGCTGAGCTGAGAGATGCCACCCCTCTGATGTTCTTCACG 1800
Qy 449 CCTGGCCCCCAACCCACCACCTCCCTGAGTGAATTTCTTGGGTCCTTTATTCTGG 508
Db 1799 CCTGGCCCCCAACCCACCACCTCCCTGAGTGAATTTCTTGGGTCCTTTATTCTGG 1740
Qy 509 GTAGGAGCGGAGTCCGTGTTCTTTTGGTCTGCAATTAATGAAGACCTCGGA 568
Db 1739 GTAGGAGCGGAGTCCGTGTTCTTTTGGTCTGCAATTAATGAAGACCTCGGA 1680
Qy 569 AAGATTCTGATAATTAATTAACCTGACTGAATTTTCACTGTTAGTGAAGAGAGGT 628
Db 1679 AAGATTCTGATAATTAATTAACCTGACTGAATTTTCACTGTTAGTGAAGAGAGGT 1620
Qy 629 GGAGTGAAGTTACCCCACTGCTGTGTACCGGAGTCAAGGCCAGGCTGGCAGATCA 688
Db 1619 GGAGTGAAGTTACCCCACTGCTGTGTGTACCGGAGTCAAGGCCAGGCTGGCAGATCA 1560
Qy 689 GTCTTGAAGTCACTGAGTGGGATCTGCTTTTGTAAAGCCTCCAGTTCATTTCA 748
Db 1559 GTCTTGAAGTCACTGAGTGGGATCTGCTTTTGTAAAGCCTCCAGTTCATTTCA 1500
Qy 749 TCCCTGATGGGGCATAGTTTGAAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 808
Db 1499 TCCCTGATGGGGCATAGTTTGAAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1440
Qy 809 GGGCAGATCCCACTCAAGGCTCCCTGCTTGAATTCATTAAGTTCATTCGTAAGAAC 868
Db 1439 GGGCAGATCCCACTCAAGGCTCCCTGCTTGAATTCATTAAGTTCATTCGTAAGAAC 1380
Qy 869 ATTCTGTCAGACAGAAATTTGGTGTTCGGGCTTGAAGTTCATTCGTAAGAAC 928
Db 1379 ATTCTGTCAGACAGAAATTTGGTGTTCGGGCTTGAAGTTCATTCGTAAGAAC 1320
Qy 929 CAATGACTGGGACTTAACATGAGGCTCGGCTCTGTAAGTTCATTCGTAAGAAC 988
Db 1319 CAATGACTGGGACTTAACATGAGGCTCGGCTCTGTAAGTTCATTCGTAAGAAC 1260
Qy 989 CTCAGTCTCTCTTCAAGAGGAGTGGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 1048
Db 1259 CTCAGTCTCTCTTCAAGAGGAGTGGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 1200
Qy 1049 GCGGGCGCTGTGGTGTGAGTGGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG 1108
Db 1199 GCGGGCGCTGTGGTGTGAGTGGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG 1140
Qy 1109 CTGCAAGGAGAGCGGCGGAGCAGACACCTTGCACGAACACCCCGGAATCTGTCGAGG 1168
Db 1139 CTGCAAGGAGAGCGGCGGAGCAGACACCTTGCACGAACACCCCGGAATCTGTCGAGG 1081
Qy 1169 ACACCGTGTACAGAGCGGAGTGTGATGACCGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1228
Db 1080 ACACCGTGTGTACAGAGCGGAGTGTGATGACCGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1021
Qy 1229 GGAGGAGGATCATGACGCCCGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1288
Db 1020 GGAGGAGGATCATGACGCCCGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 961
Qy 1289 CAGGATGATCTCTCCGAATCTGTTGGGATCCAGCATAGGCGCAATGATCAACAATCA 1348
Db 960 CAGGATGATCTCTCCGAATCTGTTGGGATCCAGCATAGGCGCAATGATCAACAATCA 901
Qy 1349 GCCCTGGGAGCA 1360
Db 900 GCCCTGGGAGCA 889
RESULT 13
ABT03280
ID ABT03280 standard; cDNA; 625 BP.
XX
XX AC ABT03280;
XX

Dt	xx	05-SEP-2002	(first entry)
DE	xx	Human ovarian carcinoma associated coding sequence SEQ ID NO: 210.	
KW	xx	Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;	
KM	xx	cytostatic; gene; ss.	
OS	xx	Homo sapiens.	
XX	xx	WO200239885-A2.	
PN	xx	23-MAY-2002.	
PD	xx	13-NOV-2001; 2001WO-US45395.	
PE	xx	14-NOV-2000; 2000US-0713550.	
PR	xx	03-APR-2001; 2001US-0825294.	
PR	xx	02-OCT-2001; 2001US-0970966.	
XX	xx	(CORI-) CORIXA CORP.	
PA	xx	Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;	
PI	xx	WPI; 2002-500186/53.	
DR	xx	Novel ovarian cancer polypeptide and polynucleotide, useful for	
XX	xx	detecting the presence of ovarian cancer in a patient, and in	
PT	xx	pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer	
PS	xx	-	
CC	xx	Claim 2; Page 194; 197pp; English.	
CC	xx	The present invention provides human ovarian cancer associated proteins	
CC	xx	and coding sequences. The sequences can be used in the diagnosis and	
CC	xx	treatment of ovarian cancers. The present sequence is a coding sequence	
CC	xx	of the invention.	
SO	xx	Sequence 625 BP; 182 A; 144 C; 182 G; 116 T; 1 other;	
		Query Match 37.9%; Score 613; DB 24; Length 625;	
		Best Local Similarity 99.7%; Pred. No. 4.6e-164;	
		Matches 624; Conservative 0; Mismatches 1; Indels 1; Gaps 1	
Oy	992	AGTTTCCTCTTGACAGAGACTGGCGCCGCGGACCGGAAGACAACGGCGCTGCACAAAGC 1051	
Dd	1	AGTTTCTCTTGAGAGAGACTGGCGCCGCGGACCGGAAGACAACGGCGCTGCACAAAGC 60	
Oy	1052	GCGCGTGCAGGTGGAGTAGTGCATGTACGGCAAGCGGCTTCTGCGTGGTGGCGTGTG 1111	
Dd	61	GCGCGTGCAGGTGGAGTAGTGCATGTACGGCAAGCGGCTTCTGCGTGGTGGCGTGTG 120	
Oy	1112	CAGCAGACAGGGCGGACAGCACAGCACCCTTGACACACACCAGCGGAAACTGCTCGAGGACA 1171	
Dd	121	CAGCAGACAGGGCGGACAGCACAGCACC-TGACAGAACAACCCGCCGAACCTGCTCGAGGACA 179	
Oy	1172	CCGTTACAGAGCGCGGTTGATGACCGAGCTGAGGTAGAAAAAGCTCTCCGAGAAAGGGA 1231	
Dd	180	CCGTTACAGAGCGCGGTTGATGACCGAGCTGAGGTAGAAAAAGCTCTCCGAGAAAGGGA 239	
Oy	1232	GGAGATCATGTAGCGCCCGGAAGTGGAGACCTGTCAGTCGCGTGGTGGTGGCGCGAG 1291	
Dd	240	GGAGATCATGTAGCGCCCGGAAGTGGAGACCTGTCAGTCGCGTGGTGGTGGCGCGAG 299	
Oy	1292	CCATGATCCTCCGAACTGTGGTGGGCAATCAGCATACGGCCAATGTCACAATCAGCC 1351	
Dd	300	CCATGATCCTCCGAACTGTGGTGGGCAATCAGCATACGGCCAATGTCACAATCAGCC 359	
Oy	1352	CTGGCGACAGACAGCAGCAGAGAGGAGAGACAGAGAAAAGAAAAACACAGCATGAGAACACA 1411	
Dd	360	CTGGCGACAGACAGCAGCAGAGAGGAGAGACAGAGAAAAGAAAAACACAGCATGAGAACACA 419	
Oy	1412	GTAATGAATAAAACCATTAATAATTATTAGCCCCCTGTGTTCTGCTTACTGGCCAGGAAA 1471	

Db	420	GTAATGATTAAGCAATTAATAATTATTTAGCCCTCTGTTCTGTGCTTACTGGCCAGGAA	479
Oy	1472	TGTTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGGCCACAAGCAGAGAAT	1531
Db	480	TGTTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGGCCACAAGCAGAGAAT	539
Oy	1532	TAAACAGTTTCAAAACCCGGGAGTGGCTGTGTAAAGAAAGCAATTAATGCTTA	1591
Db	540	TAAACAGTTTCAAAACCCGGGAGTGGCTGTGTAAAGAAAGCAATTAATGCTTA	599
Oy	1592	GACAGTGTAAATTT	1617
Db	600	GACAGTGTAAATTT	625
RESULT 14			
ABL0348	ABL0348	standard; cDNA; 625 BP.	
AC	ABL0348;		
XX	28-JUN-2002	(first entry)	
XX	Ovarian carcinoma O1034C EST clone nucleotide sequence.		
XX	Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;		
KW	expressed sequence tag; EST; ss.		
XX	Homo sapiens.		
XX	US2002004491-A1.		
XX	10-JAN-2002.		
XX	03-APR-2001; 2001US-0825294.		
XX	10-SEP-1999; 99US-0394374.		
PR	01-MAY-2000; 2000US-0561778.		
PR	15-AUG-2000; 2000US-0640173.		
PR	07-SEP-2000; 2000US-0656668.		
PR	14-NOV-2000; 2000US-0713550.		
XX	(XUJ/) XU J.		
PA	(STOL/) STOLK J A.		
PA	(ALGA/) ALGATE P A.		
PA	(FLIN/) FLING S P.		
XX	Xu J, Stolk JA, Algate PA, Fling SP;		
XX	WPI; 2002-171027/22.		
XX	Ovarian tumour polypeptide and polynucleotide useful in diagnosis,		
XX	prevention and/or treatment of cancer, especially ovarian cancer		
XX	Claim 1a; Page 125; 131pp; English.		
XX	The invention relates to ovarian tumour polynucleotides and polypeptides		
XX	that may be utilised in cancer therapy, for example in a vaccine or		
XX	gene therapy. Polypeptides and polynucleotides of the invention are		
XX	useful for detecting a cancer in a patient, for stimulating and/or		
XX	expanding T-cells specific for a tumour protein, and for inhibiting the		
XX	development of a cancer in a patient. They are also useful for		
XX	stimulating an immune response in a patient, and for treating a cancer		
XX	a patient and for determining the presence of a cancer in a patient.		
XX	The isolated polynucleotides of the invention are useful for their		
XX	ability to selectively form duplex molecules with complementary stretches		
XX	of the entire desired gene or gene fragments, and for designing and		
XX	preparing ribozyme molecules for inhibiting expression of tumour		
XX	polypeptides in tumour cells. Polypeptides and polynucleotides of the		
XX	invention are also useful in recombinant DNA molecules to direct		
XX	expression of a polypeptide in appropriate host cells. The current		
XX	sequence represents the ovarian carcinoma O1034C EST clone nucleotide		
XX	sequence.		

992

```

QY 1472 TGGTACCAATTTTCAGGTGTGGACTTGACAGCTTCTTTGGCCACAGCAGAGAGAAAT 1531
    |||||||
DB 480 TGGTACCAATTTTCAGGTGTGGACTTGACAGCTTCTTTGGCCACAGCAGAGAGAAAT 539
    |||||||
QY 1532 TAACACTGTTTCAACCCGGGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTTTA 1591
    |||||||
DB 540 TAACACTGTTTCAACCCGGGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTTTA 599
    |||||||
QY 1592 GACAGTGTAAAAA 1617
    |||||||
DB 600 GACAGTGTAAAAA 625
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Search completed: November 7, 2002, 10:10:30
 Job time : 329.774 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:53:42 ; Search time 60.6676 Seconds
(without alignments)
8184.096 Million cell updates/sec

Title: US-09-970-966-211

Perfect score: 1619
Sequence: 1 ggcacatttcgcatgtt.....aaaaaaaaaaaaaaaaaa 1619

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/lna/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/Dackfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50.4	3.1	7218	1	US-08-232-463-14
2	50	3.1	1872	1	US-08-153-848-39
3	50	3.1	1872	3	US-09-299-843A-39
4	50	3.1	1872	4	US-09-088-337B-39
5	50	3.1	1872	5	PCT-US93-11153-39
6	48.2	3.0	7218	1	US-08-232-463-14
7	46	2.8	289	4	US-09-007-005-17
8	46	2.8	289	4	US-09-244-796-17
9	44	2.7	1176	4	US-09-200-090-3
10	44	2.7	1342	3	US-08-832-399-1
11	43	2.7	1342	4	US-09-372-498-1
12	43	2.7	1575	3	US-08-858-876A-1
13	43	2.7	1575	4	US-09-472-880-1
14	41.4	2.6	1233	4	US-09-200-090-1
15	39	2.4	6379	1	US-08-499-215-1
16	38	2.3	1417	4	US-09-199-737-3
17	38	2.3	1417	4	US-09-058-333A-3
18	37.2	2.3	1951	4	US-08-922-865-1
19	37.2	2.3	1951	4	US-09-510-949-1
20	36	2.2	2205	4	US-08-687-590-59
21	35.6	2.2	1600	4	US-09-029-027B-1
22	35.4	2.2	1063	4	US-09-077-675A-1
23	35.2	2.2	735	3	US-09-003-287-7
24	35.2	2.2	1535	4	US-09-668-680-12
25	35	2.2	1137	3	US-09-082-088-1
26	35	2.2	1137	4	US-09-546-117-1
27	35	2.2	1555	4	US-08-809-802-11

28	34.8	2.1	1210	4	US-09-443-041A-29	Sequence 29, Appl
29	34.8	2.1	3946	3	US-09-083-351-1	Sequence 1, Appl
30	34.8	2.1	3946	4	US-09-083-352-1	Sequence 1, Appl
31	34.6	2.1	1164	4	US-08-993-088A-6	Sequence 6, Appl
32	34.6	2.1	1164	4	US-08-993-424B-6	Sequence 6, Appl
33	34.6	2.1	3390	4	US-08-993-088A-5	Sequence 5, Appl
34	34.6	2.1	3390	4	US-08-993-424B-5	Sequence 5, Appl
35	34.4	2.1	924	4	US-08-775-882-3	Sequence 3, Appl
36	34.4	2.1	1024	2	US-08-411-607A-1	Sequence 1, Appl
37	34.4	2.1	1122	3	US-08-927-433-2	Sequence 2, Appl
38	34.4	2.1	1201	4	US-08-276-600-1	Sequence 5, Appl
39	34.4	2.1	1201	4	US-08-931-999-4	Sequence 1, Appl
40	34.2	2.1	6755	3	US-08-785-420-1	Sequence 4, Appl
41	34.2	2.1	15378	3	US-07-704-288C-2	Sequence 1, Appl
42	34	2.1	1151	1	US-07-704-288C-2	Sequence 2, Appl
43	34	2.1	1151	1	US-08-093-372-1	Sequence 1, Appl
44	34	2.1	1151	1	US-08-379-259-2	Sequence 2, Appl
45	34	2.1	1248	2	US-08-897-340-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEITLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)863-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
US-08-232-463-14
Query Match 3.1%; Score 50.4; DB 1; Length 7218;

Best Local Similarity 2.4%; Pred. No. 0.00032;
Matches 9; Conservative 221; Mismatches 152; Indels 0; Gaps 0

[illegible]

RESULT 2
US-08-153-848-39/c

Sequence 39, Application US/08153848
Patent No. 5759804

GENERAL INFORMATION:

APPLICANT: Godtska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Ricknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 202..1341
;
US-08-153-848-39

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Query Match	3.1%	Score 50:	DB 1:	Length 1872:
Best Local Similarity	52.4%	Pred. No. 0.00019:		
Matches 110; Conservative	0;	Mismatches 100;	Indels 0;	Gaps 0;

QY	1143	GAAACACCCGCCGAACCTGCTGTGCCAGAGACACCGTGTCACAGACCGGGATTGATATCCGACACT	1202
Db	1141	GCAGGCCCTGGCGAAGAGGGGGGGGTTCGAAAAAGCGATAGAGAAAGGGGTTTAGGCACACTGT	1102
QY	1203	GAGGTAGAAAAACGTCCTCCGAGAAAGGGAGAGAGATCATGTATACGCCCGGAAAGTAGACCT	1263
Db	1101	GACCTAGCTGTATGCACAGGTGCAGTAGTAGGGGAAGATGTTCTATGATGAGAAAGAGGTCAAAGTCA	1042
QY	1263	CGTCCACATCGTGGCTTGGGGTTTGGGCGGACGCATGATCCCTCCCAATCTGGTTGGGCATCA	1322
Db	1041	GGGCGCAGTGCAGCAGCGCTGCCACGACATGTACACACGCTTTCACACAGGTGGTAGGCATCA	982
QY	1323	GCATACGGCCATGTCCACACATCAACGACC	1352
Db	981	GCACAGGGCAAGGTCAACCAACCAACCAAC	952

RESULT 3
US-09-299-843A-39/C

Sequence 39, Application US/092399843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schmelzart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/259,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jll E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27666/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448

TELEX:
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 202..1341
US-09-299-843A-39

Query Match 3.1%; Score 50; DB 3; Length 1872;
Best Local Similarity 52.4%; Pred. No. 0.00019;
Matches 110; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 1143 GAAACCCCGGCGAAGCTGTCGAGAGACCGGTGATGACCGAGCT 1202
DB 1161 GCAGGCTGGCGGAGGCGGGGTGAAAAAGCATAGAGGAGGTTGAGGACCTGT 1102
QY 1203 GAGGTAGAAAAAGCTCTCCGAGAGGAGAGATGATACGCCCGAAGTAGACCT 1262
DB 1101 GAGGTAGCTGATGACGAGTGTAGGAGAGATGTTTCATGAGAGAGAGTCAAACTCACA 1042
QY 1263 GGTCCAGTGTCTGTTGGTGTGGCCGAGCATGATCCTCCGAATGTTGGGATCCA 1322
DB 1041 GGGCCAGTGCAGCAGGCTGCCAGCATGTACAGCTTTACACAGAGTGTAGGCGATCCA 982
QY 1323 GCATACGGCCATGTCAACAATACAGCC 1352
DB 981 GCACAGGGCAAGTCAACCAAGCAGCAC 952

RESULT 4

US-09-088-337B-39/c

Sequence 39, Application US/09088337B

Patent No. 6348574

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald

Gray, Patrick W.

TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/088.337B

FILING DATE: 01-Jun-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/153.848

FILING DATE: 17-NOV-1993

APPLICATION NUMBER: US 07/977.452

FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 6348574and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 202..1341
US-09-088-337B-39

Query Match 3.1%; Score 50; DB 4; Length 1872;
Best Local Similarity 52.4%; Pred. No. 0.00019;
Matches 110; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 1143 GAAACCCCGGCGAAGCTGTCGAGAGACCGGTGATGACCGAGCT 1202
DB 1161 GCAGGCTGGCGGAGGCGGGGTGAAAAAGCATAGAGGAGGTTGAGGACCTGT 1102
QY 1203 GAGGTAGAAAAAGCTCTCCGAGAGGAGAGATGATACGCCCGAAGTAGACCT 1262
DB 1101 GAGGTAGCTGATGACGAGTGTAGGAGAGATGTTTCATGAGAGAGAGTCAAACTCACA 1042
QY 1263 GGTCCAGTGTCTGTTGGTGTGGCCGAGCATGATCCTCCGAATGTTGGGATCCA 1322
DB 1041 GGGCCAGTGCAGCAGGCTGCCAGCATGTACAGCTTTACACAGAGTGTAGGCGATCCA 982
QY 1323 GCATACGGCCATGTCAACAATACAGCC 1352
DB 981 GCACAGGGCAAGTCAACCAAGCAGCAC 952

RESULT 5

PCT-US93-11153-39/c

Sequence 39, Application PC/TUS9311153

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald

Gray, Patrick W.

TITLE OF INVENTION: Novel Seven Transmembrane Receptors

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

Bicknell

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/11153

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/977.452

FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

INFORMATION FOR SEQ ID NO: 39:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: King, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: GH50020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5515
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1342 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-832-399-1

Query Match 2.7%; Score 43; DB 3; Length 1342;
Best Local Similarity 50.2%; Pred. No. 0.017;
Matches 106; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 1136 CTTGCACGAAACCCGCCGAATGCTGCGAGAGACCGCTGTACAGAGCGGGTTGATGA 1195
DB 893 CTTCCAGGAGAGATTTCTGAGAGAGAGACGCGCTTTGTAGAGAGAGAGTGTACAG 834
QY 1196 CCGAGCTGAGTGAAGAAACGCTCCGAGAGAGGAGAGATCATGTACGCCCGGAAGT 1255
DB 833 CTGAGCTGAGTGAAGAAAGTGTGTGTCACCATGTAGAGTGTAGAAATGTACA 774
QY 1256 AGGACCTGCTCAGTGTGCTTGGGTTTGGCCGACCATGATCCCTCGAATCTGGTGG 1315
DB 773 GTGGGTGAGTCCAGCGCTCATCAGTACGATGAGCCTGCGGCGATGTACG 714
QY 1316 GCATCCAGCATACGGCCATGTCTCAACAAT 1346
DB 713 GCAGCCAGCATGACATGATGACCATG 683

RESULT 11
US-09-372-498-1/c
Sequence 1, Application US/09372498
Patent No. 6166182
GENERAL INFORMATION:
APPLICANT: Derek J. Bergsma
APPLICANT: Usman Shabon
TITLE OF INVENTION: NOVEL HUMAN NEUTROPHIL RECEPTOR TYPE 2
TITLE OF INVENTION: AND SPICE VARIANTS THEREOF
FILE REFERENCE: GH-50020-1
CURRENT APPLICATION NUMBER: US/09/372,498
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: 08/832,399
PRIOR FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1342
TYPE: DNA
ORGANISM: HOMO SAPIENS
US-09-372-498-1

Query Match 2.7%; Score 43; DB 4; Length 1342;
Best Local Similarity 50.2%; Pred. No. 0.017;
Matches 106; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 1136 CTTGCACGAAACCCGCCGAATGCTGCGAGAGACCGCTGTACAGAGCGGGTTGATGA 1195
DB 893 CTTCCAGGAGAGATTTCTGAGAGAGAGACGCGCTTTGTAGAGAGAGAGTGTACAG 834
QY 1196 CCGAGCTGAGTGAAGAAACGCTCCGAGAGAGGAGAGATCATGTACGCCCGGAAGT 1255
DB 833 CTGAGCTGAGTGAAGAAAGTGTGTGTCACCATGTAGAGTGTAGAAATGTACA 774

QY 1256 AGGACCTGCTCAGTGTGCTTGGGTTTGGCCGACCATGATCCCTCGAATCTGGTGG 1315
DB 773 GTGGGTGAGTCCAGCGCTCATCAGTACGATGAGTGTAGAGAGAGTGTACAG 714
QY 1316 GCATCCAGCATACGGCCATGTCTCAACAAT 1346
DB 713 GCAGCCAGCATGACATGATGACCATG 683

RESULT 12
US-08-858-876A-1/c
Sequence 1, Application US/08858876A
Patent No. 6022856
GENERAL INFORMATION:
APPLICANT: Daniel CAPUT
APPLICANT: Pascale CHALON
APPLICANT: Pascual FERRARA
APPLICANT: VITA NATALIO
TITLE OF INVENTION: TYPE 2 Neurotensin Receptor
TITLE OF INVENTION: (hMT-R2)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
STREET: 400 Seventh Street
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,876A
FILING DATE: 19-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 9723204
FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,049
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1575 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 37..1266
US-08-858-876A-1

Query Match 2.7%; Score 43; DB 3; Length 1575;
Best Local Similarity 50.2%; Pred. No. 0.018;
Matches 106; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 1136 CTTGCACGAAACCCGCCGAATGCTGCGAGAGACCGCTGTACAGAGCGGGTTGATGA 1195
DB 1150 CTTCCAGGAGAGATTTCTGAGAGAGAGACGCGCTTTGTAGAGAGAGAGTGTACAG 1091
QY 1196 CCGAGCTGAGTGAAGAAACGCTCCGAGAGAGGAGAGATCATGTACGCCCGGAAGT 1255
DB 1090 CTGAGCTGAGTGAAGAAAGTGTGTGTCACCATGTAGAGTGTAGAAATGTACA 1031
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ok

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 6379 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
;   STRAIN: No. 561204ardla corallina B-276 (FERM P-4094; FERM
;   STRAIN: BP-5124; ATCC 31338)
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 910..1935
;   OTHER INFORMATION: /product= "amoA"
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1935..2285
;   OTHER INFORMATION: /product= "amoB"
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 2300..3802
;   OTHER INFORMATION: /product= "amoc"
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 3805..4830
;   OTHER INFORMATION: /product= "amod"
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US-08-499-215-1
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Query Match      2.48; Score 39; DB 1; Length 6379;
Best Local Similarity 49.88; Pred. No. 0.59;
Matches 125; Conservative 0; Mismatches 125; Indels 1; Gaps 1;
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DB 1354 CGGACATGCGCTGCGCAGCGCGCTAGGCCAGGCTCAGGAAGAGCCGTAATCAGACGATG 1295
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DB 1294 GCGAGCGCGGTAGACCTGCGAGAGATCTTCTGCGACCAAGATGGCGGTGATGCCGCCG 1235
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QY 1289 CAGCCATGATC 1299
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DB 1234 ACCECATGGTC 1224
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Search completed: November 7, 2002, 15:58:56
Job time : 97.6676 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 13:45:13 : Search time 70.3601 Seconds
(without alignments)
8163.686 Million cell updates/sec

Title: US-09-970-966-211

Perfect score: 1619
Sequence: 1 ggcacatttgcggtatgtt.....aaaaaaaaaaaaaaaaaaaaa 1619

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published.Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1619	100.0	1619	US-09-825-294-205	Sequence 205, App
2	1619	100.0	1619	US-09-825-294-211	Sequence 211, App
3	1606.2	99.2	1897	US-09-825-294-214	Sequence 210, App
4	613	37.9	625	US-09-825-294-210	Sequence 210, App
5	613	37.9	625	US-09-867-701-10876	Sequence 10876, App
6	497.6	30.7	1362	US-09-825-294-208	Sequence 208, App
7	424.2	26.2	558	US-09-867-701-2375	Sequence 2375, App
8	396.4	24.5	409	US-09-867-701-1240	Sequence 1240, App
9	388.4	24.0	1010	US-09-825-294-212	Sequence 212, App
10	377.4	23.3	430	US-09-867-701-4251	Sequence 4251, App
11	365.4	22.6	369	US-09-825-294-199	Sequence 199, App
12	362	22.4	373	US-09-867-701-1516	Sequence 1516, App
13	362	22.4	396	US-09-825-294-9	Sequence 9, App11
14	354	21.9	390	US-09-867-701-1532	Sequence 1532, App
15	330.8	20.4	381	US-09-867-701-7826	Sequence 7826, App
16	310.2	19.2	349	US-09-867-701-2409	Sequence 2409, App
17	197.8	12.2	480	US-09-825-294-213	Sequence 213, App
18	171.2	10.6	201	US-09-867-701-8894	Sequence 8894, App
19	50	3.1	1464	US-09-149-045-1	Sequence 1, App11

C 20	40	2.5	2036	10	US-09-866-582-17	Sequence 17, App1
C 21	40	2.5	32177	10	US-09-764-877-3251	Sequence 3251, App
C 22	40	2.5	32207	10	US-09-764-877-3250	Sequence 3250, App
C 23	39.6	2.4	332	10	US-09-867-701-9973	Sequence 9973, App
C 24	37.2	2.3	1743	10	US-09-925-301-541	Sequence 541, App
C 25	36.8	2.3	488	10	US-09-924-035A-347	Sequence 347, App
C 26	36.8	2.3	628	10	US-09-770-149-714	Sequence 714, App
C 27	36	2.2	371	10	US-09-969-347-117	Sequence 117, App
C 28	36	2.2	3977	10	US-09-764-869-1999	Sequence 1999, App
C 29	36	2.2	3977	10	US-09-764-869-2001	Sequence 2001, App
C 30	35.8	2.2	21860	10	US-09-764-877-3803	Sequence 3803, App
C 31	35.4	2.2	3007	10	US-09-795-006A-148	Sequence 148, App
C 32	35	2.2	1137	12	US-10-037-616-3	Sequence 3, App11
C 33	34.8	2.1	466	10	US-09-920-300A-1456	Sequence 1456, App
C 34	34.8	2.1	466	12	US-10-033-5528-1084	Sequence 1084, App
C 35	34.8	2.1	495	10	US-09-998-598-1084	Sequence 1084, App
C 36	34.8	2.1	503	10	US-09-998-598-1030	Sequence 1030, App
C 37	34.8	2.1	582	10	US-09-998-598-309	Sequence 309, App
C 38	34.8	2.1	597	10	US-09-777-564-589	Sequence 589, App
C 39	34.8	2.1	624	10	US-09-804-551B-41	Sequence 41, App1
C 40	34.8	2.1	1619	10	US-09-925-300-746	Sequence 746, App
C 41	34.8	2.1	30352	10	US-09-764-869-1768	Sequence 1768, App
C 42	34.6	2.1	227	10	US-09-880-107-2970	Sequence 2970, App
C 43	34.6	2.1	396	10	US-09-825-294-25	Sequence 25, App1
C 44	34.6	2.1	425	10	US-09-960-352-1711	Sequence 1711, App
C 45	34.6	2.1	1368	10	US-09-834-975-825	Sequence 825, App

ALIGNMENTS

RESULT 1
US-09-825-294-205
Sequence 205, Application US/09825294
Patent No. US20020004491A1
GENERAL INFORMATION:
APPLICANT: Xu, Jlangchun
APPLICANT: Stolck, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OR INVENTION: COMPOSITIONS AND METHODS FOR THE
THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C5
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 205
LENGTH: 1619
TYPE: DNA
ORGANISM: Homo sapiens
US-09-825-294-205

Query Match	100.0%	Score 1619:	DB 10:	Length 1619:
Best Local Similarity	100.0%	Pred. No. 0:		
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Db 1	GGCACTTTTGGGATGTTCTTCAGGCTTGGCGTGCAGATTCAGTTCAC	60		
Qy 61	GTGTGAAGATTCAGTGAACAAGATTCAGTTCAGTTCAGTTCAGTTCAC	120		
Db 61	GTGTGAAGATTCAGTGAACAAGATTCAGTTCAGTTCAGTTCAGTTCAC	120		
Qy 121	GGTGAAGCTTAAGACATGTCTCAAGAAAGATGAGAGCAAGTCCGGATCATGTA	180		
Db 121	GGTGAAGCTTAAGACATGTCTCAAGAAAGATGAGAGCAAGTCCGGATCATGTA	180		
Qy 181	CCGCAAGCTTGTGATCATGAGCGCTGTCTCATGCGCTTCGCGGTACCGATCTT	240		
Db 181	CCGCAAGCTTGTGATCATGAGCGCTGTCTCATGCGCTTCGCGGTACCGATCTT	240		

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Oy 361 CACCATCCCTGTTCTCAATTTAGCCCTCTCTCGGACACAGTGTGAAGCTGAAGAGATG 420
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Db 361 CACCATCCCTGTTCTCAATTTAGCCCTCTCTCGGACACAGTGTGAAGCTGAAGAGATG 420
Oy 421 CCACCCCTCTCTGATGTTCTTCCAGCCCTCGCCCCACCCCTCCCTCTGATGTA 480
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Db 421 CCACCCCTCTCTGATGTTCTTCCAGCCCTCGCCCCACCCCTCCCTCTGATGTA 480
Oy 481 GTTCTCTGGGTGTCCTTTTATTTCTGGGTGAGGAGCGGGAGTCCGTCTCTTTTGT 540
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Db 481 GTTCTCTGGGTGTCCTTTTATTTCTGGGTGAGGAGCGGGAGTCCGTCTCTTTTGT 540
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Oy 841 ACATTCAAATCTCATGCTCTGTAAGAACATCTCTGACAGAGAGATTTGGTGTGCGC 900
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Oy 901 CTGAGTTGGCTCTAGTACTGAGACTCAATGACTGGGATTTAGCTGGGCTCGGCT 960
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RESULT 2

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US-09-825-294-211
; Sequence 211, Application US/09825294
; Patent No. US2002004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FASTSeq for Windows Version 3.0
; SEQ ID NO 211
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-211

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Query Match      100.0%; Score 1619; DB 10; Length 1619;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||
Db 541 CCTGTCAATATATGAAGAGCTCGGTAAAGCATTCGTAATTAATTCACCCGACTGAT 600
QY 601 TTTCACTATGACTTGAAGAGAGAGTGAAGTTCAACCCCACTGCTGTGTAAAC 660
    |||
    |||
    |||
Db 601 TTTCACTATGACTTGAAGAGAGAGTGAAGTTCAACCCCACTGCTGTGTAAAC 660
QY 661 CGAGAGCAAGGCGGCTGGCAGAGTCACTCTTGAAGTCACTGAAGTGGGCACTGCC 720
    |||
    |||
    |||
Db 661 CGAGAGCAAGGCGGCTGGCAGAGTCACTCTTGAAGTCACTGAAGTGGGCACTGCC 720
QY 721 TTTTGAAGCCTCAAGTCCATTCATCCCTGATGGGGGATAGTTGAGACTGACGA 780
    |||
    |||
    |||
Db 721 TTTTGAAGCCTCAAGTCCATTCATCCCTGATGGGGGATAGTTGAGACTGACGA 780
QY 781 GTGAGAGTACCTTTTCTTGAAGGCTGAGGCGCAGTCCCACTCAAGGCTCCCTGCTTG 840
    |||
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    |||
Db 781 GTGAGAGTACCTTTTCTTGAAGGCTGAGGCGCAGTCCCACTCAAGGCTCCCTGCTTG 840
QY 841 ACATTCAAACTTCATGCTCCGTAAGAAACCTTCTGACAGAGATTTGGCTGGTTCCGCC 900
    |||
    |||
    |||
Db 841 ACATTCAAACTTCATGCTCCGTAAGAAACCTTCTGACAGAGATTTGGCTGGTTCCGCC 900
QY 901 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTAGACTGGGCTGGGCT 960
    |||
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    |||
Db 901 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTAGACTGGGCTGGGCT 960
QY 961 CGCTCTGAAAAGTCTTAAGAAAATCTTCTCAGTTCTCTTGCAGAGAGACTGGCCGGG 1020
    |||
    |||
    |||
Db 961 CGCTCTGAAAAGTCTTAAGAAAATCTTCTCAGTTCTCTTGCAGAGAGACTGGCCGGG 1020
QY 1021 ACGCAAGAGCAAGCGGCGCTGACAAAGCGGCGCTGCTGGTGGAGAGCCGATGTA 1080
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    |||
    |||
Db 1021 ACGCAAGAGCAAGCGGCGCTGACAAAGCGGCGCTGCTGGTGGAGAGCCGATGTA 1080
QY 1081 CGCGAGAGGCGTCTCTGTTGGTGGCTGCTGAGCGAGCAGCGGCGAGCAGACACTTGC 1140
    |||
    |||
    |||
Db 1081 CGCGAGAGGCGTCTCTGTTGGTGGCTGCTGAGCGAGCAGCGGCGAGCAGACACTTGC 1140
QY 1141 ACGAAGACCCCGGCAAACTGCTGCGAGAGACACCGTGTACAGAGCGGCTGATGACCGAG 1200
    |||
    |||
    |||
Db 1141 ACGAAGACCCCGGCAAACTGCTGCGAGAGACACCGTGTACAGAGCGGCTGATGACCGAG 1200
QY 1201 CTGAGGTAGAAAAGTCTGCGAGAAAGGAGAGATCATGTCGCCGGAAGTAGAGAC 1260
    |||
    |||
    |||
Db 1201 CTGAGGTAGAAAAGTCTGCGAGAAAGGAGAGATCATGTCGCCGGAAGTAGAGAC 1260
QY 1261 CTGCTGTCAGTGTCTGTTGGTGGCGCGACCATGATCTCCGANTCTGGTTGGGCACTC 1320
    |||
    |||
    |||
Db 1261 CTGCTGTCAGTGTCTGTTGGTGGCGCGACCATGATCTCCGANTCTGGTTGGGCACTC 1320
QY 1321 CAGCATAGGCGCAATGTACAAATCAATGACCTGGGAGACACGAGCGAGGAGAGAC 1380
    |||
    |||
    |||
Db 1321 CAGCATAGGCGCAATGTACAAATCAATGACCTGGGAGACACGAGCGAGGAGAGAC 1380
QY 1381 AGAGAAAAGAAAACACAGCATGAGAAACACAGTAATTAATTAATTAATTAATTAATTA 1440
    |||
    |||
    |||
Db 1381 AGAGAAAAGAAAACACAGCATGAGAAACACAGTAATTAATTAATTAATTAATTAATTA 1440
QY 1441 CCCCCTCTCTCTGCTGCTTACTGAGGAGAAATGTAATTTTCACTGTTGAGACTTGA 1500
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    |||
Db 1441 CCCCCTCTCTCTGCTGCTTACTGAGGAGAAATGTAATTTTCACTGTTGAGACTTGA 1500

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QY 1501 CAGCTTCTTTGCCACAGAGAGAGATTTAAGCTTTCAACCCGGGGAGTTGG 1560
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Db 1501 CAGCTTCTTTGCCACAGAGAGAGATTTAAGCTTTCAACCCGGGGAGTTGG 1560
QY 1561 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAGAAAAA 1619
    |||
    |||
    |||
Db 1561 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAGAAAAA 1619

RESULT 3
US-09-825-294-214
: Sequence 214, Application US/09825294
: Patent No. US20020004491A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: TITILE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.48A5
: CURRENT APPLICATION NUMBER: US/09/825,294
: NUMBER OF FILING DATE: 2001-04-03
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 214
: LENGTH: 1897
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(1897)
: OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214

Query Match 99.2%; Score 1606.2; DB 10; Length 1897;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1616; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGCACATTTTGGCGGATTTGTTGCTTCCAGGCTTGGCCTGCAATCCAGTCAACA 60
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    |||
Db 280 GGCACATTTTGGCGGATTTGTTGCTTCCAGGCTTGGCCTGCAATCCAGTCAACA 339
QY 61 GTGTGAAGAAATTCAGCTGAAGAACGACTGCTCCCGGAGTCAATGTAATGCAC 120
    |||
    |||
    |||
Db 340 GTGTGAAGAAATTCAGCTGAAGAACGACTGCTCCCGGAGTCAATGTAATGCAC 399
QY 121 GTGAACGTTCAAGACATGTGTGCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 180
    |||
    |||
    |||
Db 400 GTGAACGTTCAAGACATGTGTGCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 459
QY 181 CCGGAATCCCTGTCATCATCAGAGGCGCTGCTCATGAGCTGTGCGGGAGTCAATCTT 240
    |||
    |||
    |||
Db 460 CCGGAATCCCTGTCATCATCAGAGGCGCTGCTCATGAGCTGTGCGGGAGTCAATCTT 519
QY 241 CTGCTCCCGAGGGAATGTAAGTTCAGTCAAGTGTGCTGCAACACCCCTTTGTAA 300
    |||
    |||
    |||
Db 520 CTGCTCCCGAGGGAATGTAAGTTCAGTCAAGTGTGCTGCAACACCCCTTTGTAA 579
QY 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTGCTGCGGCGCTGAGGCCAGGCTCCGAC 360
    |||
    |||
    |||
Db 580 CGGGCCAAAGGCCCAAGAAAGGGAAGTTGCTGCGGCGCTGAGGCCAGGCTCCGAC 639
QY 361 CACCATCTGCTGCTCAATTAAGCCCTCTGCGGCACTGCTGGAAGCTGAAGAGAGATG 420
    |||
    |||
    |||
Db 640 CACCATCTGCTGCTCAATTAAGCCCTCTGCGGCACTGCTGGAAGCTGAAGAGAGATG 699
QY 421 CACACCCCTCTCCTGATGTTCTTCCAGCCCTGCCCCCAACCCCACTCCCTGAGTGA 480
    |||
    |||
    |||
Db 700 CACACCCCTCTCCTGATGTTCTTCCAGCCCTGCCCCCAACCCCACTCCCTGAGTGA 759
QY 481 GTTCTCTGCGGTGTCCTTTTATCTGGGTAGGAGCGGGAGTCCGTCTCTTTGTT 540
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Db 760 GTTCTCTGGGTCCTTTTATTCGAGGAGGAGCGGAGCTCCCTCTCTTTGTT 819
Qy 541 CCTGTGCAAAATATGAAGAGCTGGTAAAGCATTCGAAATAAATCAGCCTGAT 600
Db 820 CCTGTGCAAAATATGAAGAGCTGGTAAAGCATTCGAAATAAATCAGCCTGAT 879
Qy 601 TTTTCACTATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 880 TTTTCACTATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 939
Qy 661 CGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 940 CGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 999
Qy 721 TTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 1000 TTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1059
Qy 781 GTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 1060 GTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1119
Qy 841 ACATTCAAACTTCATGCTCTGAAAAACCATTCCTGACAGAGAAATGGCTGG 900
Db 1120 ACATTCAAACTTCATGCTCTGAAAAACCATTCCTGACAGAGAAATGGCTGG 1179
Qy 901 CTGAGTTGGGCTCTAGTACTGAGACTCATGACTGGAGACTTGAAGCTGGGCT 960
Db 1180 CTGAGTTGGGCTCTAGTACTGAGACTCATGACTGGAGACTTGAAGCTGGGCT 1239
Qy 961 GCCTCGAAAAAGCTGCTTAAAGAAATCTCTGCTCTGACAGAGAGAGAGAG 1020
Db 1240 GCCTCGAAAAAGCTGCTTAAAGAAATCTCTGCTCTGACAGAGAGAGAGAG 1299
Qy 1021 ACGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1300 ACGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1359
Qy 1081 CGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1360 CGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1418
Qy 1141 ACGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db 1419 ACGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1478
Qy 1201 CTGAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Db 1479 CTGAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1538
Qy 1261 CTGAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Db 1539 CTGAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1598
Qy 1321 CAGCATACGCGCAATGTCAACAATCAAGCCTGGGAGAGAGAGAGAGAGAGAG 1380
Db 1599 CAGCATACGCGCAATGTCAACAATCAAGCCTGGGAGAGAGAGAGAGAGAGAG 1658
Qy 1381 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1659 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1718
Qy 1441 CCCCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1500
Db 1719 CCCCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1778
Qy 1501 CAGCTCTCTTTGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1779 CAGCTCTCTTTGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1838
Qy 1561 CTGTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1619
Db 1839 CTGTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1897

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RESULT 4
US-09-825-294-210
; Sequence 210, Application US/09825294
; Patent No. US2002004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 210
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(625)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-210

Query Match 37.9%; Score 613; DB 10; Length 625;
Best Local Similarity 99.7%; Pred. No. 2,2e-164;
Matches 624; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 992 AGTCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1051
Db 1 AGTCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Qy 1052 GGCCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1111
Db 61 GGCCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Qy 1112 CAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1171
Db 121 CAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 179
Qy 1172 CCGGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1231
Db 180 CCGGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 239
Qy 1232 GGAGAGATCATGTACGCCCGAAGTAGAGACTGCTCAGTCGTCTGTGGTTGGCCGAG 1291
Db 240 GGAGAGATCATGTACGCCCGAAGTAGAGACTGCTCAGTCGTCTGTGGTTGGCCGAG 299
Qy 1292 CCATGATCTCCGAAATCTGTGTGGGATCCAGCATACGGCATATGTCACAAATCAGCC 1351
Db 300 CCATGATCTCCGAAATCTGTGTGGGATCCAGCATATGTCACAAATCAGCC 359
Qy 1352 CTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1411
Db 360 CTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
Qy 1412 GTAATGATTAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1471
Db 420 GTAATGATTAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 479
Qy 1472 TGTATCAATTTTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1531
Db 480 TGTATCAATTTTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 539
Qy 1532 TAAACATGTTTCAAAACCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1591
Db 540 TAAACATGTTTCAAAACCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 599
Qy 1592 GACAGTGTAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1617

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; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT FILING DATE: 2001-05-29
; SOFTWARE: FASTSEQ for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 10912
; SEQUENCE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2375
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc_feature
; LOCATION: (1)...(358)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-2375

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Query Match          26.2% Score 424.2; DB 10; Length 558;
Best Local Similarity 94.5%; Pred. No. 9.1e-111;
Matches 534; Conservative 0; Mismatches 19; Indels 12; Gaps 9;

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Qy 992 AGTTCTCTTCAGAGAGACTGCGCCGCGGAGCGGAGAGCAACGGCGCTGCACAAAGCG 1051
Db 1 AGTTCTCTTCAGAGAGACTGCGCCGCGGAGCGGAGAGCAACGGCGCTGCACAAAGCG 60
Qy 1052 GGGCGCTGCGTGGTGGATGCGCATGTACGGGCGCTTCTGCTGGTGGCGCTG 1111
Db 61 GGGCGCTGCGTGGTGGATGCGCATGTACGGG--AGGCGCTTCTGCTGGTGGCGCTG 118
Qy 1112 CACGAGAGGCGGCGAGCAGCAGCACTTTCAGCAACACCCCGGAAACCTCTCGAGGACA 1171
Db 119 CACGAGAGGCGGCGAGCA--GCACCTGCAACAGACCCCGGAAACCTCTCGAGGACA 175
Qy 1172 CCGGTACAGAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAAGTCTCCGAGAGGGGA 1231
Db 176 CCGGTACAGAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAAGTCTCCGAGAGGGGA 235
Qy 1232 GAGAGATCATGTACG--CCGGGAAGTAGACCTGCTCACTGCTTGGGTTGGCCGCA 1290
Db 236 GAGAGATCATGTACGCGCCGGGAAGTAGACCTGCTCACTGCTTGGGTTGGCCGCA 295
Qy 1291 GCCATGA--TCCTCGGAATCGGTGGGCAATCCAGCATAGGGCAATGTACAACATCAG 1349
Db 296 GCCATGA--TCCTCGGAATCGGTGGGCAATCCAGCATAGGGCAATGTACAACATCAG 355
Qy 1350 CCCTGGGCGAGACAGAGCAGG--AGGGAGAGAGAGAGAAAAAGAAACACAGCATGAGAAC 1408
Db 356 CCCTGGGCGAGACAGAGCAGGAGGAAGAGAGAGAAAAAGAAACACAGCATGAGAAC 415
Qy 1409 ACAGTAATGAATAAACCATAAATATTTAGCCCTCTGCTGTGCTTACTGCCAGG 1468
Db 416 ACAGTAATGAATAA--AAACCATAAATAATTTAG--CCCTCTGCTGTGCTTACTGCCAGG 473
Qy 1469 AATGATACCAATTTTTCAGTGTGACCTTCTTTTGGCACAAGAGAGAGA 1528
Db 474 AATGATAC--ATTTTTCAGTGTGTTACTTTCAGCTTTTGGCACAAGAGAGAG-- 531
Qy 1529 ATTTAACACTGTTTCAACCCGGGG 1553
Db 532 ATTTAACACTGTTTCAACCCGGGG 556

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RESULT 8
US-09-867-701-4240/c
; Sequence 4240, Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.

```

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT FILING DATE: 2001-05-29
; SOFTWARE: FASTSEQ for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 10912
; SEQUENCE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4240
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-4240

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Query Match          24.5% Score 396.4; DB 10; Length 409;
Best Local Similarity 99.5%; Pred. No. 5.9e-103;
Matches 408; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy 1190 TGATGACCGAGCTGAGTAGAAAAAGTCTCCGAGAGGAGAGAGATCATGACGCC 1249
Db 409 TGATGACCGAGCTGAGTAGAAAAAGTCTCCGAGAGGAGAGAGATCATGACGCC 350
Qy 1250 GGAAGTAGACCTGCTCCAGTGTGCTTGGGTTGGCCGAGCCATGATCTCCGAATCT 1309
Db 349 GGAAGTAGACCTGCTCCAGTGTGCTTGGGTT--GCCGAGCCATGATCTCCGAATCT 291
Qy 1310 GATTGGCATCCAGCATGCGCCCAATGTCACAAATACAGCCCTGGGCGAGACAGCAG 1369
Db 290 GATTGGCATCCAGCATGCGCCCAATGTCACAAATACAGCCCTGGGCGAGACAGCAG 231
Qy 1370 GAGGAGAGACAGAAAAAAGAACACAGCATAGAGACACAGTAATTAATTAACCAT 1429
Db 230 GAGGAGAGACAGAAAAAAGAACACAGCATAGAGACACAGTAATTAATTAACCAT 171
Qy 1430 AAAATATTACCCCTCTGCTGTCTGTACTGCTGCGCCAGGAATGTCACATTTTCACT 1489
Db 170 AAAATATTACCCCTCTGCTGTCTGTACTGCTGCGCCAGGAATGTCACATTTTCACT 111
Qy 1490 GTTGACTTGAACAGCTTCTTGGCACAAGCAAGAGAAATTTACACTGTTCAACCC 1549
Db 110 GTTGACTTGAACAGCTTCTTGGCACAAGCAAGAGAAATTTACACTGTTCAACCC 51
Qy 1550 GGGGAGTTGGCTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGT 1599
Db 50 GGGGAGTTGGCTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGT 1

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RESULT 9
US-09-825-294-212
; Sequence 212, Application US/09825294
; Patent No. US2002004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Stolk, John A.
; APPLICANT: Aglate, Paul A.
; APPLICANT: Filing, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.4845
; CURRENT FILING DATE: 2001-04-03
; SOFTWARE: FASTSEQ for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 215
; SEQUENCE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 212
; LENGTH: 1010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-212

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Query Match          24.0% Score 388.4; DB 10; Length 1010;
Best Local Similarity 92.3%; Pred. No. 2e-100; Indels 8; Gaps 5;
Matches 465; Conservative 0; Mismatches 31;
Qy 1 GGCACATTTTGGGAGATTGTTCTGTTC--AGGCTTGGGCTCAATCCAGTGTACC 59

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Db 227 GGAACATTTTGGGAGTGTCTTCTGCTCCAGAGCTTTGCGGTGCAAAATCCAGTGTACC 286
OY 60 AGGTGAAGAAATTCAGTGAACAAACGACGTGCTCCCGCCAGTCAATGTGAATGGA 119
Db 287 AGGTGAAGAAATTCAGTGAACAAACGACGTGCTCCCGCCAGTCAATGTGAATGGA 346
OY 120 CGGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGGATCATGT 179
Db 347 CGGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGGATCATGT 406
OY 180 ACCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCTCTGCGGGATACAGTCT 239
Db 407 ACCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCTCTGCGGGATACAGTCT 466
OY 240 TCTGCTCCCGAGGAAAGTGAAGTCAATGATGATGATGATGATGATGATGATGATGATGAT 299
Db 467 TCTGCTCCCGAGGAAAGTGAAGTCAATGATGATGATGATGATGATGATGATGATGATGAT 526
OY 300 A-CGGGCAAGGCGCAAGAAAGGGAAGTTCGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG 358
Db 527 ACCGCGCAAGGCGCAAGAAAGGGAAGTTCGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG 586
OY 359 ACCACATCTCTGTCTCAATTA--GCCCTCTCTCGGCACTGCTGA--GCTGA 413
Db 587 ACCACATCTCTGTCTCAATTAAGCCCTCTCTCGGCACTGCTGAAGCTTGAAG 646
OY 414 GGAGATGCCACCCCTCGCATTTCTTCCAGCCCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG 473
Db 647 GGAGAGGACACCCACTCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705
OY 474 TGAGTGAATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 497
Db 706 TGAGAGAGCAGCCGCGGAGGAGACC 729
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RESULT 10
US-09-867-701-4251
; Sequence 4251, Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Agate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4251
; LENGTH: 430
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-701-4251
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Query Match 23.3%; Score 377.4; DB 10; Length 430;
Best Local Similarity 96.3%; Pred. No. 1.5e-97;
Matches 419; Conservative 0; Mismatches 11; Indels 5; Gaps 3;
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OY 425 CCCCTCTGCATTTGCTTCTCCAGCCCTGCGCCCAACCCCGCCACCTGCTGAGTGT 484
Db 177 CCGGT-CTGCATTTGCTTCTCCAGCCCTGCGCCCAACCCCGCCACCTGCTGAGTGT 235
OY 485 CTTTGGGTGTCTTTTATTTCTGAGGAGCGGAGTCCGTTCTTTTGTCTG 544
Db 236 CTTTGGGTGTCTTTTATTTCTGAGGAGCGGAGTCCGTTCTTTTGTCTG 295
OY 545 TGCAATATATGAAGAGCTCCGTTAAGCATTTCTGATTAATTCAGCTGACTGAATTTTC 604
Db 236 TGCAAGCATATAAGAGCTCCGTTAAGCATTTCTGATTAATTAATTCAGCTGACTGAATTTTC 355
OY 605 AGTATGACTTGAAGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 664
Db 356 AGTATGACTTGAAGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 415
OY 665 GTCAAGGCCAGGCTG 679
Db 416 GTCAAGGCCAGGCTG 430
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RESULT 11
US-09-825-294-199
; Sequence 199, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Flind, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.4845
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 199
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(369)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-199
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Query Match 22.6%; Score 365.4; DB 10; Length 369;
Best Local Similarity 99.2%; Pred. No. 3.6e-94;
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 1 GGCAACTTTTGGCGATTTGCTTCTTCCAGGCTTTGCGCTGCAAAATCCAGTGTACCA 60
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OY 121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGAGATCATGTA 180
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Db 301 CGGCGCAAGGCGCAAGAAAGGGAAGTTCGCTGCGGCTGAGGCGGAGGCTCCGAC 360
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Db 301 CGGGCCAGGCCCCAAGAAAGGGAAGTTCTGCTCGGCCCTCANGCCATGGCTCCGAC 360
 QY 361 CACCATCT 369
 Db 361 CACCATCT 369

RESULT 12
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; Sequence 1516, Application US/09867701
 ; Patent No. US20020132237A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agilate, Paul A.
 ; APPLICANT: Jones, Robert
 ; APPLICANT: Harlocker, Susan L.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.497
 ; CURRENT APPLICATION NUMBER: US/09/867,701
 ; CURRENT FILING DATE: 2001-05-29
 ; NUMBER OF SEQ ID NOS: 10912
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1516
 ; LENGTH: 373
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-867-701-1516

Query Match 22.4%; Score 362; DB 10; Length 373;
 Best Local Similarity 99.7%; Pred. No. 3.3e-93;
 Matches 373; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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 Db 314 CGGACGATGATCTCTCCGAATCTGTTGGGATCCAGCATAGGCGCAATGTACACAA 255
 QY 1346 TCAGCCCTGGGACACGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1405
 Db 254 TCAGCCCTGGGACACGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 195
 QY 1406 AACACAGTAATGAATAAACCAATATTTAGCCCTCTGTCTGTCTGTCTGTCTGTCT 1465
 Db 194 AACACAGTAATGAATAAACCAATATTTAGCCCTCTGTCTGTCTGTCTGTCTGTCT 135
 QY 1466 AGGAATGTACCAATTTTTCAGTGTGACCTTGACAGCTTTTGGCACAAGCAGAG 1525
 Db 134 AGGAATGTACCAATTTTTCAGTGTGACCTTGACAGCTTTTGGCACAAGCAGAG 75
 QY 1526 AGAATTACACGTTTCAACCCGGGGAGTTGGCTGTGTAAAGAAAGACATTAAAT 1585
 Db 74 AGAATTACACGTTTCAACCCGGGGAGTTGGCTGTGTAAAGAAAGACATTAAAT 15
 QY 1586 GCTTTAGACAGTGT 1599
 Db 14 GCTTTAGACAGTGT 1

RESULT 13
 US-09-825-294-9
 ; Sequence 9, Application US/09825294
 ; Patent No. US20020004491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Fling, Steven P.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; FILE REFERENCE: 210121.484C5

; CURRENT APPLICATION NUMBER: US/09/825,294
 ; CURRENT FILING DATE: 2001-04-03
 ; NUMBER OF SEQ ID NOS: 215
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 396
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(396)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-825-294-9

Query Match 22.4%; Score 362; DB 10; Length 396;
 Best Local Similarity 97.7%; Pred. No. 3.5e-93;
 Matches 377; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

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 QY 181 CCGAGATCTCTGTCATCATCAGCGGCTGTCTCATGCTCTGCGGGTACAGTCTT 240
 Db 191 CCGAGATCTCTGTCATCATCAGCGGCTGTCTCATGCTCTGCGGGTACAGTCTT 250
 QY 241 CTGCTCCCGAGGAATGAACACTGATTGTGATCAGTCTGTGCAACCCCTTTGTA 300
 Db 251 CTGCTCCCGAGGAATGAACACTGATTGTGATCAGTCTGTGCAACCCCTTTGTA 310
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 QY 359 ACCACATCTCTGTTCTCAATTAGC 384
 Db 371 ACCACATCTCTGTTCTCAATTAGC 396

RESULT 14
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 ; Sequence 1532, Application US/09867701
 ; Patent No. US20020132237A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agilate, Paul A.
 ; APPLICANT: Jones, Robert
 ; APPLICANT: Harlocker, Susan L.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.497
 ; CURRENT APPLICATION NUMBER: US/09/867,701
 ; CURRENT FILING DATE: 2001-05-29
 ; NUMBER OF SEQ ID NOS: 10912
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1532
 ; LENGTH: 390
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(390)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-867-701-1532

Query Match 21.9%; Score 354; DB 10; Length 390;

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:55:08 ; Search time 3627.85 Seconds
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Searched: 24791104 seqs, 12571243825 residues

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Listing first 45 summaries

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2	1619	100.0	1619	PCT-US01-45395-211	Sequence 211, App
3	1619	100.0	1619	US-09-713-550-205	Sequence 205, App
4	1619	100.0	1619	US-09-825-294-205	Sequence 205, App
5	1619	100.0	1619	US-09-825-294-211	Sequence 211, App
6	1619	100.0	1619	US-09-825-294-205	Sequence 205, App
7	1619	100.0	1619	US-09-970-966-211	Sequence 211, App
8	1619	100.0	1619	US-09-970-966-205	Sequence 205, App
9	1619	100.0	1619	US-10-212-677-211	Sequence 211, App
10	1606.2	99.2	1897	PCT-US01-45395-214	Sequence 214, App
11	1606.2	99.2	1897	US-09-825-294-214	Sequence 214, App
12	1606.2	99.2	1897	US-09-970-966-214	Sequence 214, App
13	1606.2	99.2	1897	US-10-212-677-214	Sequence 214, App
14	1595.8	98.6	1967	PCT-US02-29864-16	Sequence 16, App
15	1592.2	98.3	1918	US-09-387-822-4454	Sequence 4454, App
16	1592.2	98.3	1918	US-09-808-383-4454	Sequence 4454, App
17	1586	98.0	1925	US-09-652-121-7293	Sequence 7293, App
18	1586	98.0	1925	US-09-652-128-9375	Sequence 9375, App
19	1586	98.0	1925	US-09-652-917-3346	Sequence 3346, App
20	1586	98.0	1925	US-09-699-997-11085	Sequence 11085, App
21	1586	98.0	1925	US-09-710-281-4458	Sequence 4458, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 23 1585.4 97.9 1832 40 US-10-108-2604-197 Sequence 197, App
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c 39 1548.8 95.7 1890 23 US-09-801-833-203 Sequence 203, App
c 40 1418.2 87.6 43729 70 US-60-261-974-9 Sequence 9, App1
c 41 1416.6 87.5 1866 42 US-10-208-408-26 Sequence 26, App1
c 42 1416.6 87.5 1866 74 US-60-295-262-26 Sequence 26, App1
c 43 1416.6 87.5 1866 74 US-60-308-868-26 Sequence 26, App1
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ALIGNMENTS

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RESULT 1
PCT-US01-45395-205
Sequence 205, Application PC/TUS0145395
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Molesh, David Alan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.48401PC
CURRENT APPLICATION NUMBER: PCT/US01/45395
CURRENT FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 205
LENGTH: 1619
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US01-45395-205
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Query Match 100.0%; Score 1619; DB 1; Length 1619;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GCGAATTTTGGCGATTTGTTCTGTCACAGCTTTGGCTGCAATTCAGTCTACCA 60
QY 61 GTGGAAGAAATTCAGCTGGAACAAGAGCTGCTCCCGGAGTCTATTTGTAATTCAC 120
DB 61 GTGGAAGAAATTCAGCTGGAACAAGAGCTGCTCCCGGAGTCTATTTGTAATTCAC 120
QY 121 GGTGAAGCTTCAGACATGTGTGAGAAAGAGTGTGAGACAAAGTCCGGATCATGTA 180
DB 121 GGTGAAGCTTCAGACATGTGTGAGAAAGAGTGTGAGACAAAGTCCGGATCATGTA 180
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DB 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCGCTCGGCCCTCAGGCGCAGGCTCCGAC 360
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DB 781 GTGAGAGTCAAGTTCCTTAAAGGCTGAGGCGCAGTTCCTCACTCAAGCTCCCTGCTG 840
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DB 841 ACATTCATTAATGATCTCTGTAAGCAATTCCTGACACAGATTTGCTGCTGCTGCTG 900
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DB 901 CTGAGTTGGGCTCTAGTACTGACAGTCAATGACTGAGTCTAGTCTGAGTCTGAGCT 960
QY 961 CGCTTGAAAGTGTGTAAGAAATCTTCTCAAGTCTCTGCTGCAAGAGTCTGCGCGG 1020
DB 961 CGCTTGAAAGTGTGTAAGAAATCTTCTCAAGTCTCTGCTGCAAGAGTCTGCGCGG 1020
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DB 1021 ACGGGAAGGCAACGGGCGCTGACAAAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTG 1080
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DB 1321 CAGCATAGGCGCAATGTCAACAATCAAGCCCTGGGAGAGAGAGAGAGAGAGAGAGAG 1380
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Qy	1441	CCCCCTGTTCTGTGCTTACTGATGSCCAGGAATGGTATTCACATTTTCAGATGTTGACCTGA	1500
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Qy	1501	CAGCTTCTTTGGCCACAGCAGCAGAGAGAAATTTAACACTGTTTCAAAACCCGGGGAGTTGG	1560
Db	1501	CAGCTTCTTTGGCCACAGCAGCAGAGAGAAATTTAACACTGTTTCAAAACCCGGGGAGTTGG	1560
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PCT-US01-45395-211
: Sequence 211, Application PC/TUS0145395
: GENERAL INFORMATION:
: APPLICANT: Corixa Corporation
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: APPLICANT: Molesh, David Alan
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.48401PC
: CURRENT APPLICATION NUMBER: PCT/US01/45395
: CURRENT FILING DATE: 2001-11-13
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 211
: LENGTH: 1619
: TYPE: DNA
: ORGANISM: Homo sapiens
PCT-US01-45395-211

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Db	61	GTTGTAAAGAAATTCAGCGTGAACCAACGACTGCTCTCCCCGAGTTCAATTGTGSAATTGCAC	120
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OY	601	TTTTCAGTACTACTTGAAGAGAGAGGTGAGTAAGTCAACCCCAATGTCGTGTAC	660
Db	601	TTTTCAGTACTACTTGAAGAGAGAGGTGAGTAAGTCAACCCCAATGTCGTGTAC	660
OY	661	CGAGTCAGAGCCAGGCTGGCAGAGTCAGTCTTAGAGTCACTAGAGGTGGGACTGACC	720
Db	661	CGAGTCAGAGCCAGGCTGGCAGAGTCAGTCTTAGAGTCACTAGAGGTGGGACTGACC	720
OY	721	TTTTGTAAAGCCTCCACTGTGCATTTCCATTCCTGATGGGGGATAGTTTGAGACTGCAGA	780
Db	721	TTTTGTAAAGCCTCCACTGTGCATTTCCATTCCTGATGGGGGATAGTTTGAGACTGCAGA	780
OY	781	GTGAGAGTACGATTTGCTTAGGGCTGGAGGGGACAGTCCCACTCAAGGCTCCCTGCTTG	840
Db	781	GTGAGAGTACGATTTGCTTAGGGCTGGAGGGGACAGTCCCACTCAAGGCTCCCTGCTTG	840
OY	841	ACATTTCAAACTTCATGCTCCTGAAACCATTCTCTGCAGCAGAAATTTGGCTGTTCCGCC	900
Db	841	ACATTTCAAACTTCATGCTCCTGAAACCATTCTCTGCAGCAGAAATTTGGCTGTTCCGCC	900
OY	901	CTGAGTTGGGCTTAGAGACTCGAGACTCAATACAGTGGGACTTAGACTGGGGCTCGGGCT	960
Db	901	CTGAGTTGGGCTTAGAGACTCGAGACTCAATACAGTGGGACTTAGACTGGGGCTCGGGCT	960
OY	961	CGCTCTGAAAAGTCTTAGAAAATCTTCTCAATTCTCCTGCAGAGCACTGGCCGCCGG	1020
Db	961	CGCTCTGAAAAGTCTTAGAAAATCTTCTCAATTCTCCTGCAGAGCACTGGCCGCCGG	1020
OY	1021	ACGGGAAAGCAACAGGGGCGCTGCACAAAGCGGGCGCTCGGTGGTGGAGTCCGATGTA	1080
Db	1021	ACGGGAAAGCAACAGGGGCGCTGCACAAAGCGGGCGCTCGGTGGTGGAGTCCGATGTA	1080
OY	1081	CGCGCAGGCGCTTCTCGTGTGGCGCTGCAGCAGACAGCGGCGACACAGCACTCTGC	1140
Db	1081	CGCGCAGGCGCTTCTCGTGTGGCGCTGCAGCAGCAGCGGCGGCGACACAGCACTCTGC	1140
OY	1141	ACGAACACCCCGCAAACTGCTGCGAGAGACCTGTACAGAGCGGGGTTGATGACCGAG	1200
Db	1141	ACGAACACCCCGCAAACTGCTGCGAGAGACCTGTACAGAGCGGGGTTGATGACCGAG	1200
OY	1201	CTGAGGTGAAAACGTCCTCGAAGAGGGGAGAGGATCATGTACGCCCGGAAGTAGAGAC	1260
Db	1201	CTGAGGTGAAAACGTCCTCGAAGAGGGGAGAGGATCATGTACGCCCGGAAGTAGAGAC	1260
OY	1261	CTGCTGCAGTGTGCTTGGGTTTTGGCCGACGCCATGATCCTCCGATCTGTGTTGGGCAATC	1320
Db	1261	CTGCTGCAGTGTGCTTGGGTTTTGGCCGACGCCATGATCCTCCGATCTGTGTTGGGCAATC	1320
OY	1321	CAGCATACGGGCATGTGCACAACATTCAGCCCTGGGCAACACGAGCAGAGAGGAGAGAC	1380
Db	1321	CAGCATACGGGCATGTGCACAACATTCAGCCCTGGGCAACACGAGCAGAGAGGAGAGAC	1380
OY	1381	AGAGAAAAGAAAACACAGCATGAGAACAGTAAATGATATAAACCATATAATTTTATG	1440
Db	1381	AGAGAAAAGAAAACACAGCATGAGAACAGTAAATGATATAAACCATATAATTTTATG	1440
OY	1441	CCCCCTCTGTTGTGCTTACTGGCCAGAGAAATGTATCCAAATTTTTTCAGTGTGGACTTGA	1500
Db	1441	CCCCCTCTGTTGTGCTTACTGGCCAGAGAAATGTATCCAAATTTTTTCAGTGTGGACTTGA	1500


```

; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.48A5
; CURRENT APPLICATION NUMBER: US/09/825,294
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO: 205
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-825-294-205

Query Match      100.0%; Score 1619; DB 31; Length 1619;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACATTTTGGCGATTTCTTCTGCTCCAGGCTTGGCGTGCACAAATCCAGTGTACCA 60
DB 1 GGCACATTTTGGCGATTTCTTCTGCTCCAGGCTTGGCGTGCACAAATCCAGTGTACCA 60
QY 61 GTGTGAAGATTCACAGTGTGTCAGAAAGAGTATGAGCAAAAGTCCGGATCATGTAATGAC 120
DB 61 GTGTGAAGATTCACAGTGTGTCAGAAAGAGTATGAGCAAAAGTCCGGATCATGTAATGAC 120
QY 121 GGTGAAGATTCAGATGTGTCAGAAAGAGTATGAGCAAAAGTCCGGATCATGTAATGAC 180
DB 121 GGTGAAGATTCAGATGTGTCAGAAAGAGTATGAGCAAAAGTCCGGATCATGTAATGAC 180
QY 181 CCGCAGCTCTGTGTCATGTCAGAGGCTGTCTCATGCTGCGCGGGGTACACAGCTT 240
DB 181 CCGCAGCTCTGTGTCATGTCAGAGGCTGTCTCATGCTGCGCGGGGTACACAGCTT 240
QY 241 CTCTCTCCCGAGGAACTGAACTGATTTGTCATGCTGTCGACACCCCTTTTGTAA 300
DB 241 CTCTCTCCCGAGGAACTGAACTGATTTGTCATGCTGTCGACACCCCTTTTGTAA 300
QY 301 CGGCGCCAGGCGCCAGAAAGGGGAAAGTTCGCTCGGCGCTTGAAGCCAGGCTCCGAC 360
DB 301 CGGCGCCAGGCGCCAGAAAGGGGAAAGTTCGCTCGGCGCTTGAAGCCAGGCTCCGAC 360
QY 361 CACCATCTCTCTCAATTAAGCCCTCTTCTGCGACACTGCTGAAGCTGAAGAGATG 420
DB 361 CACCATCTCTCTCAATTAAGCCCTCTTCTGCGACACTGCTGAAGCTGAAGAGATG 420
QY 421 CCAACCCCTCTCATGTTCTTCAAGCCCTGCCCCCAACCCCACTCCCTGAGTGA 480
DB 421 CCAACCCCTCTCATGTTCTTCAAGCCCTGCCCCCAACCCCACTCCCTGAGTGA 480
QY 481 GTTCTCTCTGCGGTCTCTTTTATTTCTGGGTAGGAGCGGAGTCCGTTCTTTTGT 540
DB 481 GTTCTCTCTGCGGTCTCTTTTATTTCTGGGTAGGAGCGGAGTCCGTTCTTTTGT 540
QY 541 CCTGTCAAAATTAAGAGAGCTCGTAAGCATTTGTAATTAATTCAGCCTGACTGAAT 600
DB 541 CCTGTCAAAATTAAGAGAGCTCGTAAGCATTTGTAATTAATTCAGCCTGACTGAAT 600
QY 601 TTTTCAGTATCTTGAAGAGAGAGTGAAGTGAAGTTCACCCCATCTGTGTGAAC 660
DB 601 TTTTCAGTATCTTGAAGAGAGAGTGAAGTGAAGTTCACCCCATCTGTGTGAAC 660
QY 661 CGGAGTCAAGGCGAGGCTGGAGAGTCAATCTTGAAGTCACTGAGAGTGGCATTCGCC 720
DB 661 CGGAGTCAAGGCGAGGCTGGAGAGTCAATCTTGAAGTCACTGAGAGTGGCATTCGCC 720
QY 721 TTTTGTAAAGCTTCAGTGTTCATTCATCCCTGATGAGGAGCATATGTTGAGACTGACA 780
DB 721 TTTTGTAAAGCTTCAGTGTTCATTCATCCCTGATGAGGAGCATATGTTGAGACTGACA 780
QY 781 GTGAGAGTACGCTTTCTTGAAGGCTGGAGGCGCATTCCTCCACTCAAGGCTCCCTGCTG 840

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DB 781 GTGAGAGTACGCTTTCTTGAAGGCTGGAGGCGCATTCCTCCACTCAAGGCTCCCTGCTG 840
QY 841 ACATTTCAACTTCTGCTCTGAAAAACCATTTCTGTGAGAGAAATGGCTGTGGCGC 900
DB 841 ACATTTCAACTTCTGCTCTGAAAAACCATTTCTGTGAGAGAAATGGCTGTGGCGC 900
QY 901 CTGAGTGGGCTCTGAGTCTGAGACTCAATGACTGGAGCTTGAAGTGGGCTGGCCT 960
DB 901 CTGAGTGGGCTCTGAGTCTGAGACTCAATGACTGGAGCTTGAAGTGGGCTGGCCT 960
QY 961 CGCTCTGAAAAAGTCTTGAAGAAATCTTCTGATTTCTCTTGCAGAGAGTGGCGCGG 1020
DB 961 CGCTCTGAAAAAGTCTTGAAGAAATCTTCTGATTTCTCTTGCAGAGAGTGGCGCGG 1020
QY 1021 ACAGGAGAGCAAGGCGCTGCAAAAGCGGCGTGGTGGTGGAGTGGGCTGATGTA 1080
DB 1021 ACAGGAGAGCAAGGCGCTGCAAAAGCGGCGTGGTGGTGGAGTGGGCTGATGTA 1080
QY 1081 CGCGAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 CGCGAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 ACGAACACCGCGGAACTGCTGAGAGACACCGTGTACAGAGCGGCTGTATACCGAG 1200
DB 1141 ACGAACACCGCGGAACTGCTGAGAGACACCGTGTACAGAGCGGCTGTATACCGAG 1200
QY 1201 CTGAGTGAAGAAACGCTCCGAGAGAGGAGAGATCATGTCAGGCGGAGTATAGAC 1260
DB 1201 CTGAGTGAAGAAACGCTCCGAGAGAGGAGAGATCATGTCAGGCGGAGTATAGAC 1260
QY 1261 CTCTCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 CTCTCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 CAGCATACGCGCAATGTACAAATACAGCTGAGCTGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 CAGCATACGCGCAATGTACAAATACAGCTGAGCTGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 AGAGAAAGAAACACAGCATGAGAAACAGTAATTAATTAATTAATTAATTAATTAAT 1440
DB 1381 AGAGAAAGAAACACAGCATGAGAAACAGTAATTAATTAATTAATTAATTAATTAAT 1440
QY 1441 CCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1441 CCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1501 CAGCTTCTTTGCGCAAGAGAGAGATTAACACTGTTCAAAACCGGGGAGGTGG 1560
DB 1501 CAGCTTCTTTGCGCAAGAGAGAGATTAACACTGTTCAAAACCGGGGAGGTGG 1560
QY 1561 CTGTGTTAAAGAACATTAATGCTTTAGACAGTGTAAAAAATTAATTAATTAATTAAT 1619
DB 1561 CTGTGTTAAAGAACATTAATGCTTTAGACAGTGTAAAAAATTAATTAATTAATTAAT 1619

RESULT 5
US-09-825-294-211
; Sequence 211, Application us/09825294
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiahong
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.48A5
; CURRENT APPLICATION NUMBER: US/09/825,294
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO: 211
; LENGTH: 1619

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-211

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Query Match	100.0%;	Score 1619;	DB 31;	Length 1619;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1619; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

Qy	1	GGAACTTTTTCGGGAAATGTCTTTCGCTTCAGAGGCTTTCGCTGCAGAAATCCAGTGTACCA	60
Db	1	GGCAACTTTTTCGGGAAATGTCTTTCGCTTCAGAGGCTTTCGCTGCAGAAATCCAGTGTACCA	60
Qy	61	GTTGTAGAAATTCAGTCTCAACAGAGGACGCTCCGCCGAGTTCGAAATGGAAATTCGAC	120
Db	61	GTTGTAGAAATTCAGTCTCAACAGAGGACGCTCCGCCGAGTTCGAAATGGAAATTCGAC	120
Qy	121	GGTGAACGTTCAAGACATGTGTCAAGAAAGATGTAGAGCAAAAGTCCGGGATCATGTA	180
Db	121	GGTGAACGTTCAAGACATGTGTCAAGAAAGATGTAGAGCAAAAGTCCGGGATCATGTA	180
Qy	181	CCGCAAGTCCCTGGATATATACGGGCGCTGTCTCATGCGCTCTCTCCGGATACAGTCTTT	240
Db	181	CCGCAAGTCCCTGGATATATACGGGCGCTGTCTCATGCGCTCTCTCCGGATACAGTCTTT	240
Qy	241	CTGCTCCCGAGGAAATCAACTCAGTTTGGATCAGCTGCTGCAACACCCCTCTTTTAA	300
Db	241	CTGCTCCCGAGGAAATCAACTCAGTTTGGATCAGCTGCTGCAACACCCCTCTTTTAA	300
Qy	301	CGGGCCAGAGCCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCAGGCCAGGCTCCGAC	360
Db	301	CGGGCCAGAGCCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCAGGCCAGGCTCCGAC	360
Qy	361	CACCATCTGTCTCCCAAAATAGCCCTCTTTCGCGCACATCGCTGGAAGCTGAAGAGATG	420
Db	361	CACCATCTGTCTCCCAAAATAGCCCTCTTTCGCGCACATCGCTGGAAGCTGAAGAGATG	420
Qy	421	CCACCCCTCTCGCATTTTCTTCCAGGCCCTCGCCCCAACCCGCCACCTCCCTGAGTGA	480
Db	421	CCACCCCTCTCGCATTTTCTTCCAGGCCCTCGCCCCAACCCGCCACCTCCCTGAGTGA	480
Qy	481	GTTTCTTCCGGGTGCCCTTTATCTCGGGTAGAGGAGGGSAGTCCGTCTCTTTGTT	540
Db	481	GTTTCTTCCGGGTGCCCTTTATCTCGGGTAGAGGAGGGSAGTCCGTCTCTTTGTT	540
Qy	541	CCTGTCAAAATATGAAAGAGCCTCGGTAAAGCATTTGAAATTAATTCAAGCTCAGCAGAT	600
Db	541	CCTGTCAAAATATGAAAGAGCCTCGGTAAAGCATTTGAAATTAATTCAAGCTCAGCAGAT	600
Qy	601	TTTTCAGTATGTACTTGAAGGAAGAGGTGAGTGAAGATTCAACCCCATGTCTGTGTAC	660
Db	601	TTTTCAGTATGTACTTGAAGGAAGAGGTGAGTGAAGATTCAACCCCATGTCTGTGTAC	660
Qy	661	CGGAGTCAAGGCCAGGCTGGGAGAGGTAGTCCCTTAGAAGTCACTGAGGTGGGATCTGCC	720
Db	661	CGGAGTCAAGGCCAGGCTGGGAGAGGTAGTCCCTTAGAAGTCACTGAGGTGGGATCTGCC	720
Qy	721	TTTTGTAAAGCTCAGTGTCCATTCCTCATCCGTATGGGGGCAATATTGAGACGTGACAA	780
Db	721	TTTTGTAAAGCTCAGTGTCCATTCCTCATCCGTATGGGGGCAATATTGAGACGTGACAA	780
Qy	781	GTTGAGAGTGAAGCTTTTTCAGGGCTGGAGGGCCAGTTCCCACTCAAGGCTCCCTGCTTG	840
Db	781	GTTGAGAGTGAAGCTTTTTCAGGGCTGGAGGGCCAGTTCCCACTCAAGGCTCCCTGCTTG	840
Qy	841	ACATTTCAAACTTCATGTCTCTGAAAACATTTCTCTCAGACAGAAATTTGCTGTTTCGGC	900
Db	841	ACATTTCAAACTTCATGTCTCTGAAAACATTTCTCTCAGACAGAAATTTGCTGTTTCGGC	900
Qy	901	CTGAGTTGGGCTCTAGTACTCAGAGCTCAATGACTAGTGGAGCTTTAGACTGGGCTCGGCT	960
Db	901	CTGAGTTGGGCTCTAGTACTCAGAGCTCAATGACTAGTGGAGCTTTAGACTGGGCTCGGCT	960
Qy	961	CGCTCTGAAAAGTGTCTTAAAGAAATCTTCTCAAGTTCCTTCCAGAGAGCAGTGGCGCGG	1020

Db	961	CCCTCTGAAAGAGTGTTAAGAAATCTTTCAGTTCCTTCGAGAGGACCTGGCCGGG	10220
Qy	1021	ACGCCAAGAGCAAGGGGCGCTGCACAAAGGGGGCGCTGCTGGTGGAGTCCGATGTA	1080
Db	1021	ACGCCAAGAGCAAGGGGCGCTGCACAAAGGGGGCGCTGCTGGTGGAGTCCGATGTA	1080
Qy	1081	CGCGAGGCGGCTTCGCGGTGGTGGCGTGTGACGACGAGGGCGGACACACCTTCG	1140
Db	1081	CGCGAGGCGGCTTCGCGGTGGTGGCGTGTGACGACGAGGGCGGACACACCTTCG	1140
Qy	1141	ACGAACACCCGCCGAACCTGCTGCGAGACCCGTGTACAGGAGCGGGTGTGATGACGAG	1200
Db	1141	ACGAACACCCGCCGAACCTGCTGCGAGACCCGTGTACAGGAGCGGGTGTGATGACGAG	1200
Qy	1201	CTGAGGTGTAAGAAAACGTCCTCCGAAAGGAGGAGGATCATGTACGCCCGGAAGTAGAC	1260
Db	1201	CTGAGGTGTAAGAAAACGTCCTCCGAAAGGAGGAGGATCATGTACGCCCGGAAGTAGAC	1260
Qy	1261	CTCGTCAGTCGTGCTTGGGTTTGGCCGACGACCATGTCTCCGAATCTGTTTGGGCAATC	1320
Db	1261	CTCGTCAGTCGTGCTTGGGTTTGGCCGACGACCATGTCTCCGAATCTGTTTGGGCAATC	1320
Qy	1321	CAGCATAGGCGCATGTGCACAACAATACGCCCGGGCGACACGACGAGGAGGAGAC	1380
Db	1321	CAGCATAGGCGCATGTGCACAACAATAGCCCTGGCGACACGACGAGGAGGAGAC	1380
Qy	1381	AGAGAAAAAAGAAAACACAGCATGAGAACACAGTAATGATTAATCACTAAATATTAG	1440
Db	1381	AGAGAAAAAAGAAAACACAGCATGAGAACACAGTAATGATTAATCACTAAATATTAG	1440
Qy	1441	CCCCCTGTTCTGTGCTTACTGGCCAGGAAATGTAACCAATTTTCACTGTTGGACTTGA	1500
Db	1441	CCCCCTGTTCTGTGCTTACTGGCCAGGAAATGTAACCAATTTTCACTGTTGGACTTGA	1500
Qy	1501	CAGCTTCTTTTGCACAAAGCAGAGAGAAATTTACACTGTTTCAAAACCCGGGGAGTTGG	1560
Db	1501	CAGCTTCTTTTGCACAAAGCAGAGAGAAATTTACACTGTTTCAAAACCCGGGGAGTTGG	1560
Qy	1561	CTGTGTTTAAAGAAAGACCATTAATCTCTTTACACAGGTGTAAAAAATTTTTAAAAA	1619
Db	1561	CTGTGTTTAAAGAAAGACCATTAATCTCTTTACACAGGTGTAAAAAATTTTTAAAAA	1619

```

RESULT 6
US-09-970-966-205
: Sequence 205, Application US/09970966
: GENERAL INFORMATION:
: APPLICANT: Stolk, John A.
: APPLICANT: Molesh, David Alan
: APPLICANT: Fling, Steven P.
: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF OVARIAN CANCER
: FILE REFERENCE: 210121.48466
: CURRENT APPLICATION NUMBER: US/09/970,966
: CURRENT FILING DATE: 2001-10-02
: NUMBER OF SEQ. ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO 205
: LENGTH: 1619
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-970-966-205

```

Query Match	Score 1619;	DB 36;	Length 1619;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 1619;	Conservative 0;	Mismatches 0;	Gaps 0;
QY	1	GGCAACTTTTGGGAGTGTCTTCCTCCACAGGCTTTCGGCTGCAGAAATCCAGTACCA	60
Db	1	GGCAACTTTTGGGAGTGTCTTCCTCCACAGGCTTTCGGCTGCAGAAATCCAGTACCA	60

Qy 1 GGCACCTTTTGGCGATGTCTTCCTCCAGGCTTGGCGTGCACATCCAGTCTACCA 606
|||||
Dp 1 GGCACCTTTTGGCGATGTCTTCCTCCAGGCTTGGCGTGCACATCCAGTCTACCA 606

```

QY 61 GTGTGAAGAAATTCAGCTGAAACAAAGACTGCTCTCCCGAGTTGTAATGTAATGCAC 120
    |||
DB 61 GTGTGAAGAAATTCAGCTGAAACAAAGACTGCTCTCCCGAGTTGTAATGTAATGCAC 120
QY 121 GGTGAACGTTCAAGCATGTGTGCAAGAAAGAAAGTGTGAGCAAGATGCCGGGATCATGTA 180
    |||
DB 121 GGTGAACGTTCAAGCATGTGTGCAAGAAAGAAAGTGTGAGCAAGATGCCGGGATCATGTA 180
QY 181 CCGCAAGTCTCTGATCATCAGCGGCTGTCTCATCGCTCTGCGGGGTACAGATCTT 240
    |||
DB 181 CCGCAAGTCTCTGATCATCAGCGGCTGTCTCATCGCTCTGCGGGGTACAGATCTT 240
QY 241 CTGTCTCCCGAGGAAATGAACTCAATGTTGCAATCAGCTGCTGCAACACCCCTTTGTA 300
    |||
DB 241 CTGTCTCCCGAGGAAATGAACTCAATGTTGCAATCAGCTGCTGCAACACCCCTTTGTA 300
QY 301 CCGGCGCAAGGCCCAAGAAAGGGAAGTTCTGCTGCGGCTCTCAGGCGCAAGGCTCCGAC 360
    |||
DB 301 CCGGCGCAAGGCCCAAGAAAGGGAAGTTCTGCTGCGGCTCTCAGGCGCAAGGCTCCGAC 360
QY 361 CAGCATCTGTTCTCAATTAATGAGCTCTCTCGGCAACAGCTGTAAGCTGAAGAGATG 420
    |||
DB 361 CAGCATCTGTTCTCAATTAATGAGCTCTCTCGGCAACAGCTGTAAGCTGAAGAGATG 420
QY 421 CCACCCCTCTCTGATGTTCTTTCAGCCCTGCCCCAACCCCTCCCTGCTGAGTGA 480
    |||
DB 421 CCACCCCTCTCTGATGTTCTTTCAGCCCTGCCCCAACCCCTCCCTGCTGAGTGA 480
QY 481 GTTCTCTGCGGTGTCTTTTATCTGCGGTAGGAGCGGGAATCCGTGTCTCTTTGTT 540
    |||
DB 481 GTTCTCTGCGGTGTCTTTTATCTGCGGTAGGAGCGGGAATCCGTGTCTCTTTGTT 540
QY 541 CCTGTGCAATATATGAAAGAGCTCGTAAAGCAATCTGTAATTAATTCAGCTGATGAT 600
    |||
DB 541 CCTGTGCAATATATGAAAGAGCTCGTAAAGCAATCTGTAATTAATTCAGCTGATGAT 600
QY 601 TTTTCAATATGATGTAAGGAAGAGGTGAGTGAAGTTCAACCCCTGCTGTGTAAAC 660
    |||
DB 601 TTTTCAATATGATGTAAGGAAGAGGTGAGTGAAGTTCAACCCCTGCTGTGTAAAC 660
QY 661 CCGAGTCAAGGGCAGGCTGCGCAGAGTCACTCTTGAAGTCACTGAGGTGGGCAATCTGCC 720
    |||
DB 661 CCGAGTCAAGGGCAGGCTGCGCAGAGTCACTCTTGAAGTCACTGAGGTGGGCAATCTGCC 720
QY 721 TTTTGAAGAGCTCTCAGTGTCTCATTCATCCCTGATGGGGGATGTTGAGATGACAGA 780
    |||
DB 721 TTTTGAAGAGCTCTCAGTGTCTCATTCATCCCTGATGGGGGATGTTGAGATGACAGA 780
QY 781 GTGAGAGTACGTTTTCTTAGGGCTGAGGGCCAGTTCCCACTCAAGGCTCCCTGCTTG 840
    |||
DB 781 GTGAGAGTACGTTTTCTTAGGGCTGAGGGCCAGTTCCCACTCAAGGCTCCCTGCTTG 840
QY 841 ACATTCAAATCTCATGCTCTCTGAAAACCATTTCTCTGACACAAATTTGGTGTTCGCGC 900
    |||
DB 841 ACATTCAAATCTCATGCTCTCTGAAAACCATTTCTCTGACACAAATTTGGTGTTCGCGC 900
QY 901 CTGAGTGTGGCTCTAGTCACTGAGACATCAATGACTGGGACTTAAGCTGGGCTGGGCT 960
    |||
DB 901 CTGAGTGTGGCTCTAGTCACTGAGACATCAATGACTGGGACTTAAGCTGGGCTGGGCT 960
QY 961 CGCTCTGAAAAGTGTAAAGAAAATTTCTCAATCTCTCTGACAGAGCATGGCGCGGG 1020
    |||
DB 961 CGCTCTGAAAAGTGTAAAGAAAATTTCTCAATCTCTCTGACAGAGCATGGCGCGGG 1020
QY 1021 AGCGCAAGAGCAAGGGCGCTGACAAAGCGGGCGTGTGCGGTGTGAGATGCGCATGTA 1080
    |||
DB 1021 AGCGCAAGAGCAAGGGCGCTGACAAAGCGGGCGTGTGCGGTGTGAGATGCGCATGTA 1080
QY 1081 CCGGCAAGGCGCTCTCTGCTGTGCGTGTGCTGACAGACAGGCGGCGACACAGACCTTTC 1140
    |||
DB 1081 CCGGCAAGGCGCTCTCTGCTGTGCGTGTGCTGACAGACAGGCGGCGACACAGACCTTTC 1140
QY 1141 ACGAACACCCCGCAAGTGTCTGCGAGGACACCGTGTACAGAGCGGCTTGTGATGACCGAG 1200

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DB 1141 ACGAACACCCCGCAAGTGTCTGCGAGGACACCGTGTACAGGAGCGGTTGATGACCGAG 1200
QY 1201 CTGAGTAGAAGAAACGCTCCGAGAAAGGGAGAGATGATGACCGCGGAGTATGAGAC 1260
    |||
DB 1201 CTGAGTAGAAGAAACGCTCCGAGAAAGGGAGAGATGATGACCGCGGAGTATGAGAC 1260
QY 1261 CTGCTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
    |||
DB 1261 CTGCTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 CAGCATACGGCAATGTACACAAATATAGCCCTGTGGCAGACAGAGCAGAGGAGAGAC 1380
    |||
DB 1321 CAGCATACGGCAATGTACACAAATATAGCCCTGTGGCAGACAGAGCAGAGGAGAGAC 1380
QY 1381 AGAGAAAAGAAAACACAGATGAGAACAGATGATGATGATGATGATGATGATGATGATG 1440
    |||
DB 1381 AGAGAAAAGAAAACACAGATGAGAACAGATGATGATGATGATGATGATGATGATGATG 1440
QY 1441 CCCCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1500
    |||
DB 1441 CCCCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1500
QY 1501 CAGCTTCTTTTCCACAGACAGAGAGATTTAACTGTTTCAACCCCGGGAGTTGG 1560
    |||
DB 1501 CAGCTTCTTTTCCACAGAGAGAGATTTAACTGTTTCAACCCCGGGAGTTGG 1560
QY 1561 CTGTGTTAAAGAAACCATTAATGCTTTAGACAGTGTAAAGAAAAA 1619
    |||
DB 1561 CTGTGTTAAAGAAACCATTAATGCTTTAGACAGTGTAAAGAAAAA 1619

```

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RESULT 7
US-09-970-966-211
; Sequence 211, Application US/09970966
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Molesh, David Alan
; APPLICANT: Filling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-966-211

```

```

Query Match 100.0%; Score 1619; DB 36; Length 1619;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGCACCTTTTGGGATGTTCTGCTCCAGGCTTGGCGTGAATTCAGTCTACCA 60
    |||
DB 1 GGCACCTTTTGGGATGTTCTGCTCCAGGCTTGGCGTGAATTCAGTCTACCA 60
QY 61 GTGTGAAGAAATTCAGCTGAAACAAAGACTGCTCTCCCGAGTTGTAATGTAATGCAC 120
    |||
DB 61 GTGTGAAGAAATTCAGCTGAAACAAAGACTGCTCTCCCGAGTTGTAATGTAATGCAC 120
QY 121 GGTGAACGTTCAAGCATGTGTGCAAGAAAGAAAGTGTGAGCAAGATGCCGGGATCATGTA 180
    |||
DB 121 GGTGAACGTTCAAGCATGTGTGCAAGAAAGAAAGTGTGAGCAAGATGCCGGGATCATGTA 180
QY 181 CCGCAAGTCTGTGATCATCAGGCGCTGTCTCATCGCTCTCCCGGATCAGATCTT 240
    |||
DB 181 CCGCAAGTCTGTGATCATCAGGCGCTGTCTCATCGCTCTCCCGGATCAGATCTT 240

```

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OY 241 CTGCTCCAGGAACTGAACTAGTTTGATCAGCTGCTGCAACACCCCTCTTTGTA 300
    |||
Db 241 CTGCTCCAGGAACTGAACTAGTTTGATCAGCTGCTGCAACACCCCTCTTTGTA 300
OY 301 CGGGCCAGGCCCCAAGAAAGGGAAGTTCTGCTGGCCCTCAGGCCAGGGCTCCGCAC 360
    |||
Db 301 CGGGCCAGGCCCCAAGAAAGGGAAGTTCTGCTGGCCCTCAGGCCAGGGCTCCGCAC 360
OY 361 CACCATCTCTGCTCAAAATTAAGCCCTTCTGCGACACCTGTGAAGGTGAAGAGAG 420
    |||
Db 361 CACCATCTCTGCTCAAAATTAAGCCCTTCTGCGACACCTGTGAAGGTGAAGAGAG 420
OY 421 CCAACCCCTCTCTCATTTGTTCTTCCAGCCCTGCCCCCAACCCCTCCTGAGTA 480
    |||
Db 421 CCAACCCCTCTCTCATTTGTTCTTCCAGCCCTGCCCCCAACCCCTCCTGAGTA 480
OY 481 GTTCTCTGCGGTGCTCTTTATTTCTGGGTAGGAGAGGGAGTCCGTCTTCTTTGTT 540
    |||
Db 481 GTTCTCTGCGGTGCTCTTTATTTCTGGGTAGGAGAGGGAGTCCGTCTTCTTTGTT 540
OY 541 CCTGTGCAATTAATGAAGAGCTCGGTAAAGCATTTCTGAATAATTCAGCTGAGTA 600
    |||
Db 541 CCTGTGCAATTAATGAAGAGCTCGGTAAAGCATTTCTGAATAATTCAGCTGAGTA 600
OY 601 TTTTCACTATGTAAGAGAGAGAGTGAAGTGAATGTAACCCCATGCTGTGTAA 660
    |||
Db 601 TTTTCACTATGTAAGAGAGAGAGTGAAGTGAATGTAACCCCATGCTGTGTAA 660
OY 661 CGAGTCAAGGCGGAGAGTGAAGTGAATGTAACCCCATGCTGTGTAA 660
    |||
Db 661 CGAGTCAAGGCGGAGAGTGAAGTGAATGTAACCCCATGCTGTGTAA 660
OY 721 TTTTGAAGCCCTCAGTGTCAATTCATCCCTGATGGGGATGATTGAAGTGA 780
    |||
Db 721 TTTTGAAGCCCTCAGTGTCAATTCATCCCTGATGGGGATGATTGAAGTGA 780
OY 781 GTGAGAGTACGTTTCTTAAGGAGTGAAGGAGTGAAGTGAAGTGAAGTGAAG 840
    |||
Db 781 GTGAGAGTACGTTTCTTAAGGAGTGAAGGAGTGAAGTGAAGTGAAGTGAAG 840
OY 841 ACATTAACATTCATGCTCTGCTGCAAAACATCTCTGCAAGCAAAATTTGGTTCG 900
    |||
Db 841 ACATTAACATTCATGCTCTGCTGCAAAACATCTCTGCAAGCAAAATTTGGTTCG 900
OY 901 CTGAGTTGGGCTCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 960
    |||
Db 901 CTGAGTTGGGCTCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 960
OY 961 CGCTCTGAAGAGTCTTAAGAAATCTTCTCACTTCTCTGCAAGAGTGAAGTGA 1020
    |||
Db 961 CGCTCTGAAGAGTCTTAAGAAATCTTCTCACTTCTCTGCAAGAGTGAAGTGA 1020
OY 1021 ACGGCAAGAGCAAGGAGGCTGCAACAAAGCGGCGCTGCTGGTGGAGTGGATGA 1080
    |||
Db 1021 ACGGCAAGAGCAAGGAGGCTGCAACAAAGCGGCGCTGCTGGTGGAGTGGATGA 1080
OY 1081 CGCGAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
    |||
Db 1081 CGCGAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
OY 1141 ACGAACAACCGCGCAAACTGCTGCGAGAGACACCGTGTACAGAGAGGGGTGAC 1200
    |||
Db 1141 ACGAACAACCGCGCAAACTGCTGCGAGAGACACCGTGTACAGAGAGGGGTGAC 1200
OY 1201 CTGAGGTAGAAAAGTCTCCGAGAGAGGAGAGATCATGTAGCCCGGAGTAGAG 1260
    |||
Db 1201 CTGAGGTAGAAAAGTCTCCGAGAGAGGAGAGATCATGTAGCCCGGAGTAGAG 1260
OY 1261 CTGCTCCAGGAGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
    |||
Db 1261 CTGCTCCAGGAGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
OY 1321 CAGCATACGCGCAATGTCAACAATCAAGCCCTGGGCGAGACACGAGAGGAGAG 1380
    |||

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Db 1321 CAGCATACGCGCAATGTCAACAATCAAGCCCTGGGCGAGACACGAGAGGAGAG 1380
    |||
OY 1381 AGAGAAAAGAAAACACAGCATGAGACAGTAATGAATGAATGAATGAATGAAT 1440
    |||
Db 1381 AGAGAAAAGAAAACACAGCATGAGACAGTAATGAATGAATGAATGAATGAAT 1440
OY 1441 CCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
    |||
Db 1441 CCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
OY 1501 CAGCTCTTTTGGCACAAGAGAGAGATTTAAGTGAAGTGAAGTGAAGTGAAGTGA 1560
    |||
Db 1501 CAGCTCTTTTGGCACAAGAGAGAGATTTAAGTGAAGTGAAGTGAAGTGAAGTGA 1560
OY 1561 CTGCTTTAAGAAAGACATTAATGCTTTGACAGTGTAAAAAAGAAAAAAG 1619
    |||
Db 1561 CTGCTTTAAGAAAGACATTAATGCTTTGACAGTGTAAAAAAGAAAAAAG 1619

```

RESULT 8

```

US-10-212-677-205
; Sequence 205, Application US/10212677
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jianshun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212.677
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-677-205

```

```

Query Match      100.0%; Score 1619; DB 42; Length 1619;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GGCACATTTTGGCGGATTTCTTCTGCTTCAAGGCTTTGGCTGCAATTCAGTGTACCA 60
    |||
Db 1 GGCACATTTTGGCGGATTTCTTCTGCTTCAAGGCTTTGGCTGCAATTCAGTGTACCA 60
OY 61 GTGGAAGAAATTCAGCTGAAGCAAGCACTGCTCCCGAGTCAATTTGGAATGGAC 120
    |||
Db 61 GTGGAAGAAATTCAGCTGAAGCAAGCACTGCTCCCGAGTCAATTTGGAATGGAC 120
OY 121 GGTGAAGCTTCAAGACATGCTGCAAGAAAGTGAATGAGACAAAGTCCCGATCATGTA 180
    |||
Db 121 GGTGAAGCTTCAAGACATGCTGCAAGAAAGTGAATGAGACAAAGTCCCGATCATGTA 180
OY 181 GGTGAAGCTTCAAGACATGCTGCAAGAAAGTGAATGAGACAAAGTCCCGATCATGTA 180
    |||
Db 181 GGTGAAGCTTCAAGACATGCTGCAAGAAAGTGAATGAGACAAAGTCCCGATCATGTA 180
OY 181 CCGCAATCTCTGCTCAATCAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
    |||
Db 181 CCGCAATCTCTGCTCAATCAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
OY 241 CTGCTCCCGAGGAAATGAACTAGTTGCAATCAGTGTGCTGCAACACCCCTTTGTA 300
    |||
Db 241 CTGCTCCCGAGGAAATGAACTAGTTGCAATCAGTGTGCTGCAACACCCCTTTGTA 300
OY 301 CGGGCCAGGCCCCAAGAAAGGGAAGTTCGCTGCGCCCTCAGGCCAGAGGCTCCGCAC 360
    |||
Db 301 CGGGCCAGGCCCCAAGAAAGGGAAGTTCGCTGCGCCCTCAGGCCAGAGGCTCCGCAC 360
OY 361 CACCATCTCTGCTCAAAATTAAGCCCTTCTGCGACACCTGTGAAGGTGAAGAGAG 420
    |||
Db 361 CACCATCTCTGCTCAAAATTAAGCCCTTCTGCGACACCTGTGAAGGTGAAGAGAG 420

```


QY	421	CCACGCCCTCCCGGATGTTGTTTCCACACCCCTCGGCCCAACCCCCCAACCTCCTTAGTGA	480
Db	421	CCACCCCTCCTCGATGTTGTTTCCACCCCTCGGCCCAACCCCCCAACCTCCTTAGTGA	480
QY	481	GTTTCTTCGGGTGCTCTTATTTCTGGTAGGGAGCGGGAGTCCGTGTTCTTATGTT	540
Db	481	GTTTCTTCGGGTGCTCTTATTTCTGGTAGGGAGCGGGAGTCCGTGTTCTTATGTT	540
QY	541	CCTGTGCAATTAATGAAGAAGCTCGTAAAGCATTTCTGAATTAATTCAGCTGACTGAAT	600
Db	541	CCTGTGCAAAATAATGAAGAAGCTCGTAAAGCATTTCTGAATTAATTCAGCTGACTGAAT	600
QY	601	TTTTCAGTATGTAATGAAGAAGGTTGGAGTGAAGAAATTACACCCCATGTCTGTATAC	660
Db	601	TTTTCAGTATGTAATGAAGAAGGTTGGAGTGAAGAAATTACACCCCATGTCTGTATAC	660
QY	661	CGGAGTCAAGGCCCAAGGCTGGCAGATGACTTCTAGAAAGTCACTGAGTGGGCATCTGCC	720
Db	661	CGGAGTCAAGGCCCAAGGCTGGCAGATGACTTCTAGAAAGTCACTGAGTGGGCATCTGCC	720
QY	721	TTTTGTAAAGCTCCAGTGTCCATTCATCCCTGATAGGGGGCATAGTTTGAGACTGACGA	780
Db	721	TTTTGTAAAGCTCCAGTGTCCATTCATCCCTGATAGGGGGCATAGTTTGAGACTGACGA	780
QY	781	GTGAGAGTGAAGCTTTTCTTAGGGCTGAGGGCCAGTTCCCACTACAGAGCTCCCTGCTTG	840
Db	781	GTGAGAGTGAAGCTTTTCTTAGGGCTGAGGGCCAGTTCCCACTACAGAGCTCCCTGCTTG	840
QY	841	ACATTCAAACTTCATGCTCCTCGAAACCATTTCTGTGACAGCAANTTGCTGTGTTTCGCG	900
Db	841	ACATTCAAACTTCATGCTCCTCGAAACCATTTCTGTGACAGCAANTTGCTGTGTTTCGCG	900
QY	901	CTGAGTTGGGCTCTAGTAGACATCGAGATCAATATAGGGAGCTAGAGCTGGGGCTGGGCT	960
Db	901	CTGAGTTGGGCTCTAGTAGACATCGAGATCAATATAGGGAGCTAGAGCTGGGGCTGGGCT	960
QY	961	CGCTCTGAAAAGTCTTAAAGAAATCTTCTCAATTCTCCTTGACAGAGACTGGCCCGGG	1020
Db	961	CGCTCTGAAAAGTCTTAAAGAAATCTTCTCAATTCTCCTTGACAGAGACTGGCCCGGG	1020
QY	1021	ACGGGAAGAGCAAGGGGCGCTGCGCAAAAGGGGGGCTGTGCGGTGGGTGGAGTCCGATGA	1080
Db	1021	ACGGGAAGAGCAAGGGGCGCTGCGCAAAAGGGGGGCTGTGCGGTGGGTGGAGTCCGATGA	1080
QY	1081	CGCGCAGGCGTTCCTGTGTTGGGCTGTGACGACAGGCGGCGACAGCACACTCTTGC	1140
Db	1081	CGCGCAGGCGTTCCTGTGTTGGGCTGTGACGACAGGCGGCGACAGCACACTCTTGC	1140
QY	1141	ACGAACACCCGCGCAAACTCTGCGGAGAGACACCGTGTACAGAGCGGGTTGATGACCGAG	1200
Db	1141	ACGAACACCCGCGCAAACTCTGCGGAGAGACACCGTGTACAGAGCGGGTTGATGACCGAG	1200
QY	1201	CTGAGGTAGAAAACCTCTCGAAGAGGGGAGGAGATCATGTACCCCGCGAAGTAGAGAC	1260
Db	1201	CTGAGGTAGAAAACCTCTCGAAGAGGGGAGGAGATCATGTACCCCGCGAAGTAGAGAC	1260
QY	1261	CTGCGCAAGTCTGCTGTGGGTTTGGCGCGACGCATATCTCCGATCTGTGTTGGGCAATC	1320
Db	1261	CTGCGCAAGTCTGCTGTGGGTTTGGCGCGACGCATATCTCCGATCTGTGTTGGGCAATC	1320
QY	1321	CAGCATACGGGCATGTCAACAAATCAAGCCCTGGGCAACACGACGACGAGGAGGAGAAC	1380
Db	1321	CAGCATACGGGCATGTCAACAAATCAAGCCCTGGGCAACACGACGACGAGGAGGAGAAC	1380
QY	1381	AGAGAAAAAGAAAACACAGCATGAGAACACAGTAAATGAATAAACCATTAATATTTAG	1440
Db	1381	AGAGAAAAAGAAAACACAGCATGAGAACACAGTAAATGAATAAACCATTAATATTTAG	1440
QY	1441	CCCCCTGTTCTGAGCTTATCTGGCCAGGAAATGGTCCAAATTTTCAAGTGTGGACTGGA	1500
Db	1441	CCCCCTGTTCTGAGCTTATCTGGCCAGGAAATGGTCCAAATTTTCAAGTGTGGACTGGA	1500

```

Oy 1501 CAGGTTCTTTTGGCACACAGCAGAGATTTTACACAGTGTTCAAACCCGGGAGTTGG 1560
      |||||||
Db 1501 CAGGTTCTTTTGGCACACAGCAGAGAGATTTTAAACAGTGTTCAAACCCGGGAGTTGG 1560
Oy 1561 CTGTGTTAAAGAAAGACCATTAATCTTTAGACAGTGTAAAAAAAAAAAAAAAAAAAAAA 1619
      |||||||
Db 1561 CTGTGTTAAAGAAAGACCATTAATCTTTAGACAGTGTAAAAAAAAAAAAAAAAAAAAAA 1619

RESULT 9
US-10-212-677-211
; Sequence 211, Application US/10212677
; GENERAL INFORMATION:
; APPLICANT: Chenaault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-212-677-211

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Query Match	100.0%	Score 1619	DB 42	Length 1619
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1619	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY 1	GGCACTTTTGGCGATGTGTCTTCAGGCTTTGCGCTGCAGAAATCCAGTGTACCA	60		
Db 1	GGCAACTTTTGGCGATGTGTCTTCAGGCTTTGCGCTGCAGAAATCCAGTGTACCA	60		
QY 61	GTGGAAGAAATTCACACTGACAGACGTCCTCCCGGAGTTCATTTGAAATTCAC	120		
Db 61	GTGGAAGAAATTCACACTGACAGACGTCCTCCCGGAGTTCATTTGAAATTCAC	120		
QY 121	GGTGAAGTTCAGACATGTGTACAGAAAGATGTGAGGCAAAATGTCGCGGATCATGT	180		
Db 121	GGTGAAGTTCAGACATGTGTACAGAAAGATGTGAGGCAAAATGTCGCGGATCATGT	180		
QY 181	CCGGAAGTCTGTGCATCATCAGCGGCTGTGTCTATGCTCTTCGCGGTACAGTCTT	240		
Db 181	CCGGAAGTCTGTGTGCATCATCAGCGGCTGTGTCTATGCTCTTCGCGGTACAGTCTT	240		
QY 241	CTGTCTCCCGAGGAAACTGAACTAGTTTGGATCAGCTGCTGCACACACCTCTTTGTAA	300		
Db 241	CTGTCTCCCGAGGAAACTGAACTAGTTTGGATCAGCTGCTGCACACACCTCTTTGTAA	300		
QY 301	CGGGCCAAAGGCCCAAGAAAGGGGAAGTTTGTCTCTCGGCTCTAGGCTACAGGCTCCGAC	360		
Db 301	CGGGCCAAAGGCCCAAGAAAGGGGAAGTTTGTCTCTCGGCTCTAGGCTACAGGCTCCGAC	360		
QY 361	CACCATCTGTCTCTCAAAATAGCCCTTTTCGGACACACTGTGAAGCTGAAGGAGATG	420		
Db 361	CACCATCTGTCTCTCAAAATAGCCCTTTTCGGACACACTGTGAAGCTGAAGGAGATG	420		
QY 421	CCACCCCTTCGATATGTTCTTCACAGCCCTCGCCCCCAACCCCCACCTCCCTGAAGTA	480		
Db 421	CCACCCCTTCGATATGTTCTTCACAGCCCTCGCCCCCAACCCCCACCTCCCTGAAGTA	480		
QY 481	GTTCCTTCGGGATCTTTATTTCTGGGTGAGGAGCGGAGTCCGGTCTTTTGT	540		
Db 481	GTTCCTTCGGGATCTTTATTTCTGGGTGAGGAGCGGAGTCCGGTCTTTTGT	540		
QY 541	CTGTGCAAAATATGAAAGAGCTGGGTAAAGCATTTGAAATTAATTCAGCTACTGAA	600		
Db 541	CTGTGCAAAATATGAAAGAGCTGGGTAAAGCATTTGAAATTAATTCAGCTACTGAA	600		

Dp	541	CCCTGCGAAATTAATGAAGAGCTCGTAAAGCATTCGTGAATTAATTACAGCTCACTGAAT	600
Qy	601	TTTTCAGTATGTACTTTGAAGGAGGAGGTGGAGTGAAGATTACCCCCATGTCTGTATAC	660
Dp	601	TTTTAGATGTACTTTGAAGGAGGAGGTGGAGTGAAGATTACCCCCATGTCTGTATAC	660
Qy	661	CGGAGTCAAGGCCAGGCGTGGCAGAGTATAGTCTTAGAAGTCACTGAGAGTGGCATGTGCC	720
Dp	661	CGGAGTCAAGGCCAGGCGTGGCAGAGTATAGTCTTAGAAGTCACTGAGAGTGGCATGTGCC	720
Qy	721	TTTTGTAAAGCTTCACAGTGTCCATTCATCCCTGATGAGGGGCATTAGTTTGACCTCAAA	780
Dp	721	TTTTGTAAAGCTTCACAGTGTCCATTCATCCCTGATGAGGGGCATTAGTTTGACCTCAAA	780
Qy	781	GTGAGAGTGAAGCTTTCTCTTAAAGGCTGAGAGGCCAGTATCCACATCAAGGGCTCCCTGCCTTG	840
Dp	781	GTGAGAGTGAAGCTTTCTCTTAAAGGCTGAGAGGCCAGTATCCACATCAAGGGCTCCCTGCCTTG	840
Qy	841	ACATTCAAACTTTCATGCTCTCGAAAACCATTTCTCGCAGCAGAAATTGGCTGTTTGGCGC	900
Dp	841	ACATTCAAACTTTCATGCTCTCGAAAACCATTTCTCGCAGCAGAAATTGGCTGTTTGGCGC	900
Qy	901	CTGAGTTGGGCTCTTAAGTACTTCGAGACTCAATATGATCGGACCTTAAGACTGGGCGCTCGGCCCT	960
Dp	901	CTGAGTTGGGCTCTTAAGTACTTCGAGACTCAATATGATCGGACCTTAAGACTGGGCGCTCGGCCCT	960
Qy	961	CGCTCTGAAAAGTGCTTAAAGAAAATCTTCTCAGTTTCTCTTGGCAGAGAGCATGGCGCGCGG	1020
Dp	961	CGCTCTGAAAAGTGCTTAAAGAAAATCTTCTCAGTTTCTCTTGGCAGAGAGCATGGCGCGCGG	1020
Qy	1021	ACGCGAAGAGCAACAGGGCGCTGACCAAAAGGGGCGCTGTGGTGTGTGAATGGCGCATGTA	1080
Dp	1021	ACGCGAAGAGCAACAGGGCGCTGACCAAAAGGGGCGCTGTGGTGTGTGAATGGCGCATGTA	1080
Qy	1081	CGCGCAGGCGCTTCTCGTGGTGTGGCGTGTGACGACGACGAGCGGACACAGCACTTTCG	1140
Dp	1081	CGCGCAGGCGCTTCTCGTGGTGTGGCGTGTGACGACGAGCGGACACAGCACTTTCG	1140
Qy	1141	ACGAACACCCCCGCAAACTGCTCGAGAGACACCGTGTACAGAGACGGGTTGATGACCGAG	1200
Dp	1141	ACGAACACCCCCGCAAACTGCTCGAGAGACACCGTGTACAGAGACGGGTTGATGACCGAG	1200
Qy	1201	CTGAGGTGAAGAAAACGTCTCCGAGAAGGGGAGAGATCATGTACGCGCCGGAAGTGAAGAC	1260
Dp	1201	CTGAGGTGAAGAAAACGTCTCCGAGAAGGGGAGAGATCATGTACGCGCCGGAAGTGAAGAC	1260
Qy	1261	CTCGTCAAGTGTGTGGGTTTGGCGGACCAATGATCTCCGAAATCTGTGTTGGGCATC	1320
Dp	1261	CTCGTCAAGTGTGTGGGTTTGGCGGACCAATGATCTCCGAAATCTGTGTTGGGCATC	1320
Qy	1321	CAGCATACGGGCANTGTACAAACAAATACGCCCTGGGACACAGAGCAGGAGGAGGAGAC	1380
Dp	1321	CAGCATACGGGCANTGTACAAACAAATACGCCCTGGGACACAGAGCAGGAGGAGGAGAC	1380
Qy	1381	AGAGAAAAGAAAACACACAGATGAGAACACAGTAAATGAATTAACCATTAATATTATAG	1440
Dp	1381	AGAGAAAAGAAAACACACAGATGAGAACACAGTAAATGAATTAACCATTAATATTATAG	1440
Qy	1441	CCCCTCTGTCTGTGTCTTACTGTGCCAGGAAATGTTACCAATTTTTCAGTGTGGACTTGA	1500
Dp	1441	CCCCTCTGTCTGTGTCTTACTGTGCCAGGAAATGTTACCAATTTTTCAGTGTGGACTTGA	1500
Qy	1501	CAGCTTCTTTTGGCAACAGCAAGAGAGAAATTAACTGTGTTCAAAACCGGGGGAGTTGG	1560
Dp	1501	CAGCTTCTTTTGGCAACAGCAAGAGAGAAATTAACTGTGTTCAAAACCGGGGGAGTTGG	1560
Qy	1561	CTGTGTTTAAAGAAAGCATTAAATGCTTTAGACAGTGTAAAAAATTTTTTTTTTTTTTTT	16195
Dp	1561	CTGTGTTTAAAGAAAGCATTAAATGCTTTAGACAGTGTAAAAAATTTTTTTTTTTTTTTT	16195

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Qy 721 TTTTGTAAAGCCTCCAGTGTCCATTCATCCCTGATGAGGGGAGCATGTTGAGACTGCAGA 780
    |||
Db 1000 TTTTGTAAAGCCTCCAGTGTCCATTCATCCCTGATGAGGGGAGCATGTTGAGACTGCAGA 1059
Qy 781 GTGAGAGTGCATGTTTCTTAGGGCTGGAGGGCCAGTTCCCACTAAGGCTCCCTGCTG 840
    |||
Db 1060 GTGAGAGTGCATGTTTCTTAGGGCTGGAGGGCCAGTTCCCACTAAGGCTCCCTGCTG 1119
Qy 841 ACATTCAAACCTTCATGCTCCGTAAGAACCATTCCTGACGAGCAATTTGGCTTGGCCG 900
    |||
Db 1120 ACATTCAAACCTTCATGCTCCGTAAGAACCATTCCTGACGAGCAATTTGGCTTGGCCG 1179
Qy 901 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGAGTACTGAGTGGGCTCGGGCT 960
    |||
Db 1180 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGAGTACTGAGTGGGCTCGGGCT 1239
Qy 961 CGCTCTGAAAGTGTCTTAAAGAAATCTTCTCAGTTCTCTTGCAGAGAGACTGGGGCCGG 1020
    |||
Db 1240 CGCTCTGAAAGTGTCTTAAAGAAATCTTCTCAGTTCTCTTGCAGAGAGACTGGGGCCGG 1299
Qy 1021 ACGGGAAGAGCAAGGGGGGCGACAAAGGGGGGCTGCTGGTGGTGGAGTGGCGATGTA 1080
    |||
Db 1300 ACGGGAAGAGCAAGGGGGGCGACAAAGGGGGGCTGCTGGTGGTGGAGTGGCGATGTA 1359
Qy 1081 CGCGAGAGCGCTTCTCTGTTGGCGCTGACAGCGAGCGGCGAGCAGCAGCACTTGC 1140
    |||
Db 1360 CGCGAGAGCGCTTCTCTGTTGGCGCTGACAGCGAGCGGCGAGCAGCAGCACTTGC 1418
Qy 1141 ACGAAGACCCCGGAACTGCTGCGAGAGACACCGTGTACAGAGGCGGTTGATGACGAG 1200
    |||
Db 1419 ACGAAGACCCCGGAACTGCTGCGAGAGACACCGTGTACAGAGGCGGTTGATGACGAG 1478
Qy 1201 CTGAGTGAAGAAAGCTCCGAGAAAGGGAGAGAGATCATGTACGCCCGAAGTAGAGAC 1260
    |||
Db 1479 CTGAGTGAAGAAAGCTCCGAGAAAGGGAGAGAGATCATGTACGCCCGAAGTAGAGAC 1538
Qy 1261 CTGCTCCAGTGTCTGTTGGGTTGGCGCGAGCATGATCTCTCCGAACTGTTGGGCGATC 1320
    |||
Db 1539 CTGCTCCAGTGTCTGTTGGGTTGGCGCGAGCATGATCTCTCCGAACTGTTGGGCGATC 1598
Qy 1321 CAGCATAGCGGCAATGTCAACAACATCAGCCCTGGGAGACACGAGAGGAGGAGAAC 1380
    |||
Db 1599 CAGCATAGCGGCAATGTCAACAACATCAGCCCTGGGAGACACGAGAGGAGGAGAAC 1658
Qy 1381 AAGAGAAAGAAAGACAGCATGAGAACACAGTAATGATTAATTAATTAATTAATTA 1440
    |||
Db 1659 AAGAGAAAGAAAGACAGCATGAGAACACAGTAATGATTAATTAATTAATTAATTA 1718
Qy 1441 CCCCTCTGTTGCTGCTTACTGGCCAGAGAAATGTAACCAATTTTTCAGTGTGACCTTGA 1500
    |||
Db 1719 CCCCTCTGTTGCTGCTTACTGGCCAGAGAAATGTAACCAATTTTTCAGTGTGACCTTGA 1778
Qy 1501 CAGCTCTTTCGCAAGCAGAGAGAAATTAACACCTTCAACCCGGGGGAGCTGG 1560
    |||
Db 1779 CAGCTCTTTCGCAAGCAGAGAGAAATTAACACCTTCAACCCGGGGGAGCTGG 1838
Qy 1561 CTGTGTAAAGAAAGCACTTAATGCTTAAAGAGTGAAGTGAAGTGAAGTGAAGTGA 1619
    |||
Db 1839 CTGTGTAAAGAAAGCACTTAATGCTTAAAGAGTGAAGTGAAGTGAAGTGAAGTGA 1897

```

```

RESULT 11
: US-09-825-294-214
: Sequence 214, Application US/09825294
: GENERAL INFORMATION:
: APPLICANT: Xu, JIANGCHUN
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: FILE REFERENCE: 210121.484C5
: CURRENT APPLICATION NUMBER: US/09/825.294

```

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: CURRENT FILING DATE: 2001-04-03
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 214
: LENGTH: 1897
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(1897)
: OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214

```

```

Query Match          99.2%; Score 1606.2; DB 31; Length 1897;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1616; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GGCACATTTTGGCGGATGTTCTTCTTCCAGGCTTGGCGTCAAAATCCAGTGTACCA 60
    |||
Db 280 GGCACATTTTGGCGGATGTTCTTCTTCCAGGCTTGGCGTCAAAATCCAGTGTACCA 339
Qy 61 GTGTGAAGATTCAGCTGAACAACGACTGCTCCCGGAGTTCATGTGAATGGAC 120
    |||
Db 340 GTGTGAAGATTCAGCTGAACAACGACTGCTCCCGGAGTTCATGTGAATGGAC 399
Qy 121 GGTGAAGCTTCAAGACATGTGTGAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 180
    |||
Db 400 GGTGAAGCTTCAAGACATGTGTGAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 459
Qy 181 CCGCAAGTCTGTGATCATATACGCGCTGTCTCATCTGCTCGCGGGTACCAATGCTT 240
    |||
Db 460 CCGCAAGTCTGTGATCATATACGCGCTGTCTCATCTGCTCGCGGGTACCAATGCTT 519
Qy 241 CTGCTCCCGAGGGAAGTCAATCAGTTTGATCATGCTGTGCAACCCCTCTTGTGA 300
    |||
Db 520 CTGCTCCCGAGGGAAGTCAATCAGTTTGATCATGCTGTGCAACCCCTCTTGTGA 579
Qy 301 CGGCGCAAGGCGCCAAAGAAAGGGGAGTTGCTGCTCGCCCTCAGGCGAGGCTCCGAC 360
    |||
Db 580 CGGCGCAAGGCGCCAAAGAAAGGGGAGTTGCTGCTCGCCCTCAGGCGAGGCTCCGAC 639
Qy 361 CACCATCTGTCTCTCAAAATTAAGCCCTTCTGCGGACACTGCTGAAGCTGAAGAGATG 420
    |||
Db 640 CACCATCTGTCTCTCAAAATTAAGCCCTTCTGCGGACACTGCTGAAGCTGAAGAGATG 699
Qy 421 CCACCCCTCTGATGTTCTTCCAGCCCGGCGCCCAACCCCGCACCTCCCTGAGTGA 480
    |||
Db 700 CCACCCCTCTGATGTTCTTCCAGCCCGGCGCCCAACCCCGCACCTCCCTGAGTGA 759
Qy 481 GTTCTCTTGGGTTGCTCTTATTTCTGGGTAAGGAGCGGGAGTCCGTTCTCTTGTGT 540
    |||
Db 760 GTTCTCTTGGGTTGCTCTTATTTCTGGGTAAGGAGCGGGAGTCCGTTCTCTTGTGT 819
Qy 541 CCTGTGCAATTAATGAAGAGCTCGGTAAGACATTCGATTAATTAATTAAGCTGACTAAT 600
    |||
Db 820 CCTGTGCAATTAATGAAGAGCTCGGTAAGACATTCGATTAATTAATTAAGCTGACTAAT 879
Qy 601 TTTGAGTATGACTTGAAGGAAGAGGAGGAGTAAGTACACCCCATGCTGTGTAAAC 660
    |||
Db 880 TTTGAGTATGACTTGAAGGAAGAGGAGGAGTAAGTACACCCCATGCTGTGTAAAC 939
Qy 661 CGGAGTCAAGGCGCAGGCTGCGAGAGTCACTTGAAGTCACTGAGTGGGCAATCGCC 720
    |||
Db 940 CGGAGTCAAGGCGCAGGCTGCGAGAGTCACTTGAAGTCACTGAGTGGGCAATCGCC 999
Qy 721 TTTTGTAAAGCCTCCAGTGTCCATTCATCCCTGATGAGGGGCAATGTTGAGACTGAGA 780
    |||
Db 1000 TTTTGTAAAGCCTCCAGTGTCCATTCATCCCTGATGAGGGGCAATGTTGAGACTGAGA 1059
Qy 781 GTGAGAGTGCATGTTTCTTAGGGCTGGAGGGCCAGTTCCCACTAAGGCTCCCTGCTG 840
    |||
Db 1060 GTGAGAGTGCATGTTTCTTAGGGCTGGAGGGCCAGTTCCCACTAAGGCTCCCTGCTG 1119

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QY	841	ACATTCGAAACTTCATGAGCCGCGGAAACCACTTCCTGAGCAGAAATGGGCTGGTTCCGGCC	900
Db	1120	ACATTCGAAACTTCATGAGCCGCGGAAACCACTTCCTGAGCAGAAATGGGCTGGTTCCGGCC	1179
QY	901	CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACTGGAGCTAGACTGGGGCTGGGCT	960
Db	1180	CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACTGGAGCTAGACTGGGGCTGGGCT	1239
QY	961	CGCTCTGAAAAGTGCTTTAAGAAAATCTTTCACAGTTCTCTTGACAGAGACTGGCGCGGG	1020
Db	1240	CGCTCTGAAAAGTGCTTTAAGAAAATCTTTCACAGTTCTCTTGAGAGAGACTGGCGCGGG	1299
QY	1021	ACGCGAAGAGCAACGGGGGCGTCGACAAAGGGGGCGCGTCCGGGGGGTGGAGTGGCATGTA	1080
Db	1300	ACGCGAAGAGCAAGGGGGCGTCGACAAAGGGGGCGCTGTCGGTGGTGGAGTGGCATGTA	1359
QY	1081	CGCGCAGGCGCTTCTCGTGTTGGCGTGCTGACGACAGAGGGGGGACAGCACACTTTC	1140
Db	1360	CGCGCAGGCGCTTCTCGTGTTGGCGTGCTGACGACAGAGGGGGGACAGCACACTTTC	1418
QY	1141	ACGAAACACCCGCCCAAACTGCTGGGAGACACCGCTGTACAGAGCGGGTGTATGACCGAG	1200
Db	1419	ACGAAACACCCGCCCAAACTGCTGGGAGACACCGGTGTACAGAGCGGGTGTATGACCGAG	1478
QY	1201	CTGAGGTGAGAAAACGATCTCCGAGAAAGGAGAGAGATCATGTAGCGCCCGGAAGTAGAGAC	1260
Db	1479	CTGAGGTGAGAAAACGATCTCCGAGAAAGGAGAGAGATCATGTAGCGCCCGGAAGTAGAGAC	1538
QY	1261	CTCGTCAGTGCTGCTTGGGTTTGGCCGACGACCATGATCCTCCGATCTGGTTGGGCAATC	1320
Db	1539	CTCGTCAGTGCTGCTTGGGTTTGGCCGACGACCATGATCCTCCGATCTGGTTGGGCAATC	1598
QY	1321	CAGCATTCGGCCCAATGTGCACAACTATAGCCCTGGGCAACACGAGCAGAGAGGAGAGAC	1380
Db	1599	CAGCATTCGGCCCAATGTGCACAACTATAGCCCTGGGCAACACGAGCAGAGAGGAGAGAC	1658
QY	1381	AGAGAAAAGAAAACACAGCATGAGAACACAGTAATGTAATTAACCATTAATTAATTTTATG	1440
Db	1659	AGAGAAAAGAAAACACAGCATGAGAACACAGTAATGTAATTAACCATTAATTAATTTTATG	1718
QY	1441	CCCTCTGTGTTCTGTGCTTACTGGCCAGGAATGTACCAATTTTTCAGTGTGAGCTTGA	1500
Db	1719	CCCTCTGTGTTCTGTGCTTACTGGCCAGGAATGTACCAATTTTTCAGTGTGAGCTTGA	1778
QY	1501	CAGCTTCTTTTGGCCACAAGCAAGAGAGATTTTACACTGTTTCAAAACCCGGGGGAGTTGG	1560
Db	1779	CAGCTTCTTTTGGCCACAAGCAAGAGAGATTTTACACTGTTTCAAAACCCGGGGGAGTTGG	1838
QY	1561	CTGTGTTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAATTTTTTTTTTTTTTTT	1619
Db	1839	CTGTGTTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAATTTTTTTTTTTTTTTT	1897

```

US-09-970-966-214
RESULT 12
US-09-970-966-214
: Sequence 214, Application US/09970966
: GENERAL INFORMATION:
: APPLICANT: Stolk, John A.
: APPLICANT: Molesh, David Alan
: APPLICANT: Fling, Steven P.
: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF OVARIAN CANCER
: FILE REFERENCE: 210121.4846
: CURRENT APPLICATION NUMBER: US/09/970,966
: CURRENT FILING DATE: 2001-10-02
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 214
: LENGTH: 1897
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-970-966-214

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Query Match	99.2%	Score 1606.2	DB 36	Length 1897
Best Local Similarity	99.8%	Pred. No. 0		
Matches 1616	Conservative	2	Mismatches 0	Indels 1
				Gaps 1
QY	1	GGCAACTTTTGGGATGTGTTCTGCTTCCAGGCTTTGGCTGCAAAATCCAGTGTACCA	60	
Db	280	GGCAACTTTTGGGATGTGTTCTGCTTCCAGGCTTTGGCTGCAAAATCCAGTGTACCA	339	
QY	61	GGTGGAAGAAATTCACCTGAACAAGACAGCTGCTCTCCCGAGTTCAATTGTGCAC	120	
Db	340	GTTGTGAAGAAATTCACCTGAACAAGACAGCTGCTCTCCCGAGTTCAATTGTGCAC	399	
QY	121	GGTGAAGCTTCAAGACATGTGTGAGAAAGATGTGAGCAAAATGCCGGATCATGTA	180	
Db	400	GGTGAAGCTTCAAGACATGTGTGAGAAAGATGTGAGCAAAATGCCGGATCATGTA	459	
QY	181	CCGCAAGTCTCTGTCATCTACAGGGCTGTCTCATCCCTTCCGGGTACCACTCTT	240	
Db	460	CCGCAAGTCTCTGTCATCTACAGGGCTGTCTCATCCCTTCCGGGTACCACTCTT	519	
QY	241	CTGCTCCCGAGGAAACTGAACCTAGTTTGATCAAGCTCTGCAACACCCCTCTTTGTA	300	
Db	520	CTGCTCCCGAGGAAACTGAACCTAGTTTGATCAAGCTCTGCAACACCCCTCTTTGTA	579	
QY	301	CGGGCCAGGCCCAAGAAAAGGGAAGTCTGCTCGGCGCTCAGGCCAGGGCTCCGAC	360	
Db	580	CGGGCCAGGCCCAAGAAAAGGGAAGTCTGCTCGGCGCTCAGGCCAGGGCTCCGAC	639	
QY	361	CACCATCTGTTCTCCAAATTTAGCCCTCTTCGGGACACCTGTAAGTGAAGAGATG	420	
Db	640	CACCATCTGTTCTCCAAATTTAGCCCTCTTCGGGACACCTGTAAGTGAAGAGATG	699	
QY	421	CGACCCCTCTCTGCATTTGTTCTCCAGGCTTCGCCCAACCCCGACCTCCCTAGTA	480	
Db	700	CGACCCCTCTCTGCATTTGTTCTCCAGGCTTCGCCCAACCCCGACCTCCCTAGTA	759	
QY	481	GTTTCTCTGGGTGTCTTTTATTTGGGTAGGAGCGGGAATCCGTCTCTTTGTT	540	
Db	760	GTTTCTCTGGGTGTCTTTTATTTGGGTAGGAGCGGGAATCCGTCTCTTTGTT	819	
QY	541	CGTGTGCAAAATATATAAAGAGCTCGTAAAGCATTTCTGAATTAATTCAGCGTGAAT	600	
Db	820	CGTGTGCAAAATATATAAAGAGCTCGTAAAGCATTTCTGAATTAATTCAGCTGAAT	879	
QY	601	TTTTAGATGTACTTGAAGAGAAGGTGTGAGTGAAGTTCAACCCCATGTCTGTAAAC	660	
Db	880	TTTTAGATGTACTTGAAGAGAAGGTGTGAGTGAAGTTCAACCCCATGTCTGTAAAC	939	
QY	661	CGGAGTCAAGGCGAGGCTGGCGAGTCAAGTCTTGAAGTCACTGAGGTGGGCAATGCC	720	
Db	940	CGGAGTCAAGGCGAGGCTGGCGAGTCAAGTCTTGAAGTCACTGAGGTGGGCAATGCC	999	
QY	721	TTTTTAAAGCTCCAGTGTCCATTCCTCGATGTGGGGCATAGTTTGAAGTGCAGA	780	
Db	1000	TTTTTAAAGCTCCAGTGTCCATTCCTCGATGTGGGGCATAGTTTGAAGTGCAGA	1059	
QY	781	GTTGAAGTGTACTTTTCTTAAGGCTGTGAAGGGCCACTTCCCACTCAAGGCTCCCTGCTG	840	
Db	1060	GTTGAAGTGTACTTTTCTTAAGGCTGTGAAGGGCCACTTCCCACTCAAGGCTCCCTGCTG	1119	
QY	841	ACATTCAAACTCATGCTCTGTAAGAACCATTTCTGCGAGCAAAATTTGGCTGTGGGC	900	
Db	1120	ACATTCAAACTCATGCTCTGTAAGAACCATTTCTGCGAGCAAAATTTGGCTGTGGGC	1179	
QY	901	CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACTGGGACTTGAAGTGGGCTCGGCT	960	
Db	1180	CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACTGGGACTTGAAGTGGGCTCGGCT	1239	
QY	961	CGCTGTGAAGATGTGTGAAGAAATCTTCTGAGTTCTCTTGACAGAGACTGCGCGGG	1020	
Db	1240	CGCTGTGAAGATGTGTGAAGAAATCTTCTGAGTTCTCTTGACAGAGACTGCGCGGG	1299	

QY 1021 ACCGAAAGACAGCGGCGCTGCACAAAGCGGCCCTGTGGGTGGAGTGCATGTA 1080
 DB 1300 AGCGAAAGACAGCGGCGCTGCACAAAGCGGCCCTGTGGGTGGAGTGCATGTA 1359
 QY 1081 CGCGAGGCGCTTCTGTGGGTGGAGTGCACAGGCGGCGGAGACAGCAGCTTGC 1140
 DB 1360 CGCGAGGCGCTTCTGTGGGTGGAGTGCACAGGCGGCGGAGACAGCAGCTTGC 1418
 QY 1141 AGCAACACCGCGGAGAACTGTGCGAGGACACCTGTACAGAGCGGGTGTGATCCAG 1200
 DB 1419 AGCAACACCGCGGAGAACTGTGCGAGGACACCTGTACAGAGCGGGTGTGATCCAG 1478
 QY 1201 CTGAGTAGAAAAACGCTCCGAGAGGAGAGAGATCATGTACGCCCGGAATGAGAC 1260
 DB 1479 CTGAGTAGAAAAACGCTCCGAGAGGAGAGAGATCATGTACGCCCGGAATGAGAC 1538
 QY 1261 CTGTCACAGTGTGGGTGGAGGCGGAGGAGATCATGTACGCCCGGAATGAGAC 1320
 DB 1539 CTGTCACAGTGTGGGTGGAGGCGGAGGAGATCATGTACGCCCGGAATGAGAC 1598
 QY 1321 CAGCATACGCGCAATGTACACAAATCAGCCCTGGGACAGACAGAGAGAGAGAC 1380
 DB 1599 CAGCATACGCGCAATGTACACAAATCAGCCCTGGGACAGACAGAGAGAGAGAC 1658
 QY 1381 AGAGAAAAAGAAACACAGCATGAGACACAGTAATGATTAATTAATTTAG 1440
 DB 1659 AGAGAAAAAGAAACACAGCATGAGACACAGTAATGATTAATTAATTTAG 1718
 QY 1441 CCCCTGT 1500
 DB 1719 CCCCTGT 1778
 QY 1501 CAGCTTCTTTTCCACAGCAAGAGAGATTTACACTGTTTCAACCCGGGAGTTGG 1560
 DB 1779 CAGCTTCTTTTCCACAGCAAGAGAGATTTACACTGTTTCAACCCGGGAGTTGG 1838
 QY 1561 CTGTGTAAAGAAACCATTAATGCTTTAGACAGTGTAAAAAAGAAAAA 1619
 DB 1839 CTGTGTAAAGAAACCATTAATGCTTTAGACAGTGTAAAAAAGAAAAA 1897

RESULT 13
 US-10-212-677-214
 ; Sequence 214, Application US/10212677
 ; GENERAL INFORMATION:
 ; APPLICANT: Chenuault, Ruth A.
 ; APPLICANT: Xu, Jlangchun
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: McNeill, Patricia D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.484C7
 ; CURRENT APPLICATION NUMBER: US/10/212.677
 ; NUMBER OF SEQ ID NOS: 288
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 214
 ; LENGTH: 1897
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-212-677-214

Query Match 99.2%; Score 1606.2; DB 42; Length 1897;
 Best Local Similarity 99.8%; Pred. No. 0; Mismatches 0; Indels 1; Gaps 1;
 Matches 1616; Conservative 2;

QY 1 GGCACACTTTTGGGATGTTCTTCTCCAGGCTTTGCGCTGCAAAATCCAGTGTACCA 60
 DB 280 GGCACACTTTTGGGATGTTCTTCTCCAGGCTTTGCGCTGCAAAATCCAGTGTACCA 339
 QY 61 GTGTGAAGATTCAGCTGACACAGACTGCTCTCCCGGAGTTCAATGTGAATGCAC 120

DB 340 GTGTGAAGATTCAGCTGACACAGACTGCTCTCCCGGAGTTCAATGTGAATGCAC 399
 QY 121 GGTGAAGATTCAGCTGACATGTTGTGCAAGAAAGATGATGAGCAAAAGTGGGATCATGTA 180
 DB 400 GGTGAAGATTCAGCTGACATGTTGTGCAAGAAAGATGATGAGCAAAAGTGGGATCATGTA 459
 QY 181 CGGCAAGTCTGTGCATCATCAGCGGCGCTGTCTCATGCGCTTGCAGGATACAGTCTT 240
 DB 460 CGGCAAGTCTGTGCATCATCAGCGGCGCTGTCTCATGCGCTTGCAGGATACAGTCTT 519
 QY 241 CTGCTCCCGAGGAGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 300
 DB 520 CTGCTCCCGAGGAGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 579
 QY 301 CGGCGCAAGGCGCCCAAGAAAGGGAAGTTGCTGCTGCGGCTTCAAGGCGGATCCGAC 360
 DB 580 CGGCGCAAGGCGCCCAAGAAAGGGAAGTTGCTGCTGCGGCTTCAAGGCGGATCCGAC 639
 QY 361 CACCATCCTGTCTCTCAAAATTAAGCCCTTCTGCGCACACTGCTGAGAGTGAAGAGATG 420
 DB 640 CACCATCCTGTCTCTCAAAATTAAGCCCTTCTGCGCACACTGCTGAGAGTGAAGAGATG 699
 QY 421 CCACCCCTCTCTGATTTGTTCTTCAACCCCTCGCCCAACCCCTCTCTGATGTA 480
 DB 700 CCACCCCTCTCTGATTTGTTCTTCAACCCCTCGCCCAACCCCTCTCTGATGTA 759
 QY 481 GTTCTCTGCGGTGCTCTTATCTGCGGTGAGAGGAGGAGTCCGTCTCTTGT 540
 DB 760 GTTCTCTGCGGTGCTCTTATCTGCGGTGAGAGGAGGAGTCCGTCTCTTGT 819
 QY 541 CCTGTGCAAAATTAAGAAAGAGTCTGTAAGCAATTCGAATTAATTCAGCTGATGAT 600
 DB 820 CCTGTGCAAAATTAAGAAAGAGTCTGTAAGCAATTCGAATTAATTCAGCTGATGAT 879
 QY 601 TTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 DB 880 TTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 939
 QY 661 CGGAGTCAAGGCGCGGCGGAGAGTGTAGAGTGTAGAGTGTAGAGTGTAGAGTGTAGAG 720
 DB 940 CGGAGTCAAGGCGCGGCGGAGAGTGTAGAGTGTAGAGTGTAGAGTGTAGAGTGTAGAG 999
 QY 721 TTTTGTAAAGCCTCAGTGTCCATTCATCCCTGATGAGGAGGATGATGATGATGATGAT 780
 DB 1000 TTTTGTAAAGCCTCAGTGTCCATTCATCCCTGATGAGGAGGATGATGATGATGATGAT 1059
 QY 781 GTGAGATGAGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 840
 DB 1060 GTGAGATGAGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1119
 QY 841 ACATTTCAACTTCATGCTCTGAAAGAAACATTTCTGAGAGAAATGGCTGTGGCGG 900
 DB 1120 ACATTTCAACTTCATGCTCTGAAAGAAACATTTCTGAGAGAAATGGCTGTGGCGG 1179
 QY 901 CTGAGTGTGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960
 DB 1180 CTGAGTGTGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1239
 QY 961 CGCTCTGAAAAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020
 DB 1240 CGCTCTGAAAAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1299
 QY 1021 ACAGGAGAGAGCAAGGCGGCTGCAAAAGGCGGCGTGTGGGTGATGAGTGCAGTGA 1080
 DB 1300 ACAGGAGAGAGCAAGGCGGCTGCAAAAGGCGGCGTGTGGGTGATGAGTGCAGTGA 1359
 QY 1081 CGCGCAGGCGCTTCTGCTGT 1140
 DB 1360 CGCGCAGGCGCTTCTGCTGT 1418
 QY 1141 ACAGCAACCGCGCAAACTGCTGAGAGACACCGTGTACAGAGAGGAGGATGATGACCGAG 1200
 DB 1419 ACAGCAACCGCGCAAACTGCTGAGAGACACCGTGTACAGAGAGGAGGATGATGACCGAG 1478

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QY 1201 CTGAGGTAGAAAAACGCTCCGAGAGAGAGATCATGTACGCCGGAAGTAGAC 1260
    |||||||
Db 1479 CTGAGGTAGAAAAACGCTCCGAGAGAGAGATCATGTACGCCGGAAGTAGAC 1538
QY 1261 CTGCTCCAGTGTGCTGGGTTGGCCGACGACCATGATCTCCGAATCTGTTGGGCAATC 1320
    |||||||
Db 1539 CTGCTCCAGTGTGCTGGGTTGGCCGACGACCATGATCTCCGAATCTGTTGGGCAATC 1598
QY 1321 CAGCATAGCGCCAAATGTCACAAATCAGCCCTGGGACAGACGAGAGAGAGAGAC 1380
    |||||||
Db 1599 CAGCATAGCGCCAAATGTCACAAATCAGCCCTGGGACAGACGAGAGAGAGAGAC 1658
QY 1381 AGAGAAAAAAGAAAAACACACATGAGACACAGTAATGAATTAACCAATTAATATTAG 1440
    |||||||
Db 1659 AGAGAAAAAAGAAAAACACACATGAGACACAGTAATGAATTAACCAATTAATATTAG 1718
QY 1441 CCCCTCTGTTCTGTGCTTACTGCGCAGAAATGTACCAATTTTCACTGTTGACCTTGA 1500
    |||||||
Db 1719 CCCCTCTGTTCTGTGCTTACTGCGCAGAAATGTACCAATTTTCACTGTTGACCTTGA 1778
QY 1501 CAGCTCTTTTGGCCACACAGAGAGAAATTTAACACTGTTCACAAACCCGGGGAGTTGG 1560
    |||||||
Db 1779 CAGCTCTTTTGGCCACACAGAGAGAAATTTAACACTGTTCACAAACCCGGGGAGTTGG 1838
QY 1561 CTGTGTTAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAATTAATTAATTAATTAAT 1619
    |||||||
Db 1839 CTGTGTTAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAATTAATTAATTAATTAAT 1897

RESULT 14
PCT-US02-29964-16
: Sequence 16, Application PC/TUS0229964
:
: APPLICANT: Tang, Y. Tom
: APPLICANT: Ren, Felyan
: APPLICANT: Zhang, Jie
: APPLICANT: Zhao, Qing A.
: APPLICANT: Wang, Jian-Rui
: APPLICANT: Xue, Aidong J.
: APPLICANT: Wang, Duntui
: APPLICANT: Ghosh, Malabika
: APPLICANT: Asundi, Vinod
: APPLICANT: Wehrman, Tom
: APPLICANT: Zhou, Ping
: APPLICANT: Goodrich, Ryle W.
: APPLICANT: Meng, Gezh
: APPLICANT: Haley-Vicente, Dana
: APPLICANT: Drmanac, Radoje T
: TITLE OF INVENTION: Novel Nucleic Acids and
: FILE REFERENCE: 809ACIP PCT
: CURRENT APPLICATION NUMBER: PCT/US02/29964
: CURRENT FILING DATE: 2002-09-19
: PRIOR APPLICATION NUMBER: US 60/323,739
: PRIOR FILING DATE: 2001-09-19
: PRIOR APPLICATION NUMBER: US 09/488,725
: PRIOR FILING DATE: 2000-01-21
: PRIOR APPLICATION NUMBER: US 09/552,317
: PRIOR FILING DATE: 2000-04-25
: PRIOR APPLICATION NUMBER: PCT/US00/35017
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: US 09/491,404
: PRIOR FILING DATE: 2000-01-25
: PRIOR APPLICATION NUMBER: PCT/US01/02623
: PRIOR FILING DATE: 2001-01-25
: PRIOR APPLICATION NUMBER: US 09/496,914
: PRIOR FILING DATE: 2000-02-03
: PRIOR APPLICATION NUMBER: US 09/560,875
: PRIOR FILING DATE: 2000-04-27
: PRIOR APPLICATION NUMBER: PCT/US01/03800
: PRIOR FILING DATE: 2001-02-05
: PRIOR APPLICATION NUMBER: US 09/515,126

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: PRIOR FILING DATE: 2000-02-28
: Remaining Prior Application data removed - see file Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 992
: SOFTWARE: PL_FL_genes Version 6.0
: SEQ ID NO 16
: LENGTH: 1967
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (338)..(763)
: PCT-US02-29964-16

Query Match          98.6%; Score 1595.8; DB 1; Length 1967;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1608; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GCGAAGCTTTTGGCGAATGTTCTTGTCTCCAGGCTTTCGCTGCAATTCAGTGTACCA 60
    |||||||
Db 358 GCGAAGCTTTTGGCGAATGTTCTTGTCTCCAGGCTTTCGCTGCAATTCAGTGTACCA 417
QY 61 GTTGGAAGATTCAGCTGAACACGACTGCTCTCCCGAGTTTCAATTGTGAC 120
    |||||||
Db 418 GTTGGAAGATTCAGCTGAACACGACTGCTCTCCCGAGTTTCAATTGTGAC 477
QY 121 GGTGAAGCTTCAAGACATGTGTGCAAAAGAGATGAGACAAAGTCCGGATCATGTA 180
    |||||||
Db 478 GGTGAAGCTTCAAGACATGTGTGCAAAAGAGATGAGACAAAGTCCGGATCATGTA 537
QY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCTCTGCGGGATCAGTCTT 240
    |||||||
Db 538 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCTCTGCGGGATCAGTCTT 597
QY 241 CTGTCTCCCGAGGAAGTGAATCAGTTTGCATCAGTGTGCAACACCCCTTTGTA 300
    |||||||
Db 598 CTGTCTCCCGAGGAAGTGAATCAGTTTGCATCAGTGTGCAACACCCCTTTGTA 657
QY 301 CGGGCAAGGCCCAAGAAAAGGGGAAGTTCTGCTCGGCTCAGGCGCAGGCTCGCAC 360
    |||||||
Db 658 CGGGCAAGGCCCAAGAAAAGGGGAAGTTCTGCTCGGCTCAGGCGCAGGCTCGCAC 717
QY 361 CACCATCTGTCTCTCAATTAATGACCTCTCTGCGCACACTGCTGAAGCTGAAGAGATG 420
    |||||||
Db 718 CACCATCTGTCTCTCAATTAATGACCTCTCTGCGCACACTGCTGAAGCTGAAGAGATG 777
QY 421 CCACCCCTCTGATGTTCTTCCAGCCCTCGCCCAACCCCAACCTCCCTGAGTGA 480
    |||||||
Db 778 CCACCCCTCTGATGTTCTTCCAGCCCTCGCCCAACCCCAACCTCCCTGAGTGA 837
QY 481 GTTCTTCTGGGTCTCTTTTATCTGGTAGAGAGCGGAGTCCGTTCTTTTGT 540
    |||||||
Db 838 GTTCTTCTGGGTCTCTTTTATCTGGTAGAGAGCGGAGTCCGTTCTTTTGT 897
QY 541 CTTGTCAATTAATGAAGAAGCTCGTAAGCAATTCGTAATTAATTCAGCTGACGAAT 600
    |||||||
Db 898 CTTGTCAATTAATGAAGAAGCTCGTAAGCAATTCGTAATTAATTCAGCTGACGAAT 957
QY 601 TTTTGTATGATCTTGAAGAAGAGAGTGAAGTGAAGTTCAACCCCATGTCTGTATAC 660
    |||||||
Db 958 TTTTGTATGATCTTGAAGAAGAGAGTGAAGTGAAGTTCAACCCCATGTCTGTATAC 1017
QY 661 CGGAGTCAAGGCCAGGCTGCGACAGTCACTTGAAGTCACTGAGAGTGGCATCTGCC 720
    |||||||
Db 1018 CGGAGTCAAGGCCAGGCTGCGACAGTCACTTGAAGTCACTGAGAGTGGCATCTGCC 1077
QY 721 TTTTGTAAAGCTTCAGTGTCCATTCATCCGATGAGGAGCATATTGAGACTGCAGA 780
    |||||||
Db 1078 TTTTGTAAAGCTTCAGTGTCCATTCATCCGATGAGGAGCATATTGAGACTGCAGA 1137
QY 781 GTGAGATGACGTTTCTTGAAGGCTGAGAGGCCAGTTCCACATCAAGGCTCCTGCTTG 840
    |||||||
Db 1138 GTGAGATGACGTTTCTTGAAGGCTGAGAGGCCAGTTCCACATCAAGGCTCCTGCTTG 1197

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282

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QY 901 CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACTGGACTTAGACTGGGCTCGGCT 960
    |||||||
Db 1196 CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACTGGACTTAGACTGGGCTCGGCT 1255
    |||||||
QY 961 CGCTCTGAAAAAGTCTTAAAGAAATCTTCTCACTTCTCTTGCAGAGACTGGCGCGGG 1020
    |||||||
Db 1256 CGCTCTGAAAAAGTCTTAAAGAAATCTTCTCACTTCTCTTGCAGAGACTGGCGCGGG 1315
    |||||||
QY 1021 ACGGGAAGACACAGGGGCGTGCACAAAGGGGCGCTGTCGGTGGAGTGGCATGTA 1080
    |||||||
Db 1316 ACGGGAAGACACAGGGGCGTGCACAAAGGGGCGCTGTCGGTGGAGTGGCATGTA 1375
    |||||||
QY 1081 CGGCAAGGCGCTTCTCGTGGTGGCTGCTGAGCAGACAGGCGGCGAGACACCTTGC 1140
    |||||||
Db 1376 CGGCAAGGCGCTTCTCGTGGTGGCTGCTGAGCAGACAGGCGGCGAGACACCTTGC 1434
    |||||||
QY 1141 ACGAACAACCGCGGAACTGCTGCGAGACACCGTGTACAGAGCGGGTTGATGACCGAG 1200
    |||||||
Db 1435 ACGAACAACCGCGGAACTGCTGCGAGACACCGTGTACAGAGCGGGTTGATGACCGAG 1494
    |||||||
QY 1201 CTGAGGTAGAAAAACGTCGCCGAGAGGGAGAGATCATGTACGCCCGGAAAGTAGAG 1260
    |||||||
Db 1495 CTGAGGTAGAAAAACGTCGCCGAGAGGGAGAGATCATGTACGCCCGGAAAGTAGAG 1554
    |||||||
QY 1261 CTGTCACAGTCTGCTTGGGTTGGCCGAGCCATGATCTCCGATCTGTTGGGATC 1320
    |||||||
Db 1555 CTGTCACAGTCTGCTTGGGTTGGCCGAGCCATGATCTCCGATCTGTTGGGATC 1614
    |||||||
QY 1321 CAGCATACGGCCAAATGTACACACAATCAGCCCTGGGAGACACGAGAGGAGAGAGAC 1380
    |||||||
Db 1615 CAGCATACGGCCAAATGTACACACAATCAGCCCTGGGAGACACGAGAGGAGAGAGAC 1674
    |||||||
QY 1381 AGAGAAAAAGAAAAACAGATGAGAACACAGTAATGAAATGAAATGAAATATTTAG 1440
    |||||||
Db 1675 AGAGAAAAAGAAAAACAGATGAGAACACAGTAATGAAATGAAATGAAATATTTAG 1734
    |||||||
QY 1441 CCCCTCTGTTCTGCTTACTGCGCAGAAATGTAACAATTTTTCAGTGTGACTTGA 1500
    |||||||
Db 1735 CCCCTCTGTTCTGCTTACTGCGCAGAAATGTAACAATTTTTCAGTGTGACTTGA 1794
    |||||||
QY 1501 CAGCTTCTTTTGGCCACAGCAGAGAGAAATTTTACACTGTTTCAAAACCGGGGAGTTGG 1560
    |||||||
Db 1795 CAGCTTCTTTTGGCCACAGCAGAGAGAAATTTTACACTGTTTCAAAACCGGGGAGTTGG 1854
    |||||||
QY 1561 CTGTTTAAAGAAAGACATTAATGCTTTAGACAGTAAAAAAA 1609
    |||||||
Db 1855 CTGTTTAAAGAAAGACATTAATGCTTTAGACAGTAAAAAAA 1903
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Search completed: November 7, 2002, 17:54:32
 Job time : 3636.85 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 10:10:48 ; Search time 45.2315 Seconds
(without alignments)
3937.596 Million cell updates/sec

Title: US-09-970-966-211

Perfect score: 1619
Sequence: 1 ggcacatttgcgattgt.....aaaaaaaaaaaaaaaaaaaaa 1619

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 193892 seqs, 55004114 residues

Total number of hits satisfying chosen parameters: 387784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1373	84.8	1524	6	US-10-230-437-15
2	40.6	2.5	2196	6	US-10-270-333-38
3	40.6	2.5	6472	6	US-10-270-333-37
4	38.8	2.4	667	7	US-60-416-112-67
5	34.8	2.1	990	6	US-10-270-333-116
6	34.8	2.1	5927	6	US-10-270-333-115
7	34.6	2.1	15825	6	US-10-240-485-111
8	34.6	2.1	135259	6	US-10-240-485-1585
9	34.4	2.1	1024	6	US-10-270-377-1
10	34.4	2.1	1201	6	US-10-240-425-334
11	34	2.1	18331	6	US-10-267-255-96
12	33.2	2.1	53500	6	US-10-267-255-76
13	33.2	2.1	4902	6	US-10-270-333-193
14	33.2	2.1	23683	6	US-10-240-485-176
15	33	2.0	2158	6	US-10-264-237-1277
16	33	2.0	2706	1	PCT-US02-33408-3
17	33	2.0	2845	6	US-10-131-813A-207
18	33	2.0	2845	6	US-10-131-819A-207
19	33	2.0	2845	6	US-10-131-823A-207
20	33	2.0	2845	6	US-10-131-824A-207
21	33	2.0	2845	6	US-10-131-826A-207
22	33	2.0	2845	6	US-10-131-829A-207
23	33	2.0	2845	6	US-10-125-926A-207
24	33	2.0	2845	6	US-10-127-832A-207
25	33	2.0	2845	6	US-10-127-831A-207
26	33	2.0	2845	6	US-10-127-835A-207

27	33	2.0	2845	6	US-10-127-837A-207	Sequence 207, App
28	33	2.0	2845	6	US-10-127-842A-207	Sequence 207, App
29	33	2.0	2845	6	US-10-127-850A-207	Sequence 207, App
30	33	2.0	2845	6	US-10-127-901A-207	Sequence 207, App
31	33	2.0	2845	6	US-10-128-689A-207	Sequence 207, App
32	33	2.0	2845	6	US-10-131-830A-207	Sequence 207, App
33	33	2.0	2845	6	US-10-131-833A-207	Sequence 207, App
34	33	2.0	2845	6	US-10-131-837A-207	Sequence 207, App
35	33	2.0	2845	6	US-10-125-930A-207	Sequence 207, App
36	33	2.0	2845	6	US-10-127-825A-207	Sequence 207, App
37	33	2.0	2845	6	US-10-127-838B-207	Sequence 207, App
38	33	2.0	2845	6	US-10-127-843A-207	Sequence 207, App
39	33	2.0	2845	6	US-10-127-849A-207	Sequence 207, App
40	33	2.0	2845	6	US-10-128-684A-207	Sequence 207, App
41	33	2.0	2845	6	US-10-128-685A-207	Sequence 207, App
42	33	2.0	2845	6	US-10-128-686A-207	Sequence 207, App
43	33	2.0	2845	6	US-10-128-690A-207	Sequence 207, App
44	33	2.0	2845	6	US-10-128-693A-207	Sequence 207, App
45	33	2.0	2845	6	US-10-131-821A-207	Sequence 207, App

ALIGNMENTS

RESULT 1
US-10-230-437-15
Sequence 15, Application US/10230437
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P350P1C94
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: US/10/230,437
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 15
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo Sapien
US-10-230-437-15
Query Match 84.8%; Score 1373; DB 6; Length 1524;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 1 GGCACATTTTTCGCGATTTCTTCCAGGCTTGGGCTGCAATTCAGTCTACCA 60
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Db 141 GGCACATTTTTCGCGATTTCTTCCAGGCTTGGGCTGCAATTCAGTCTACCA 200
QY 61 GTGTGAAGAATTCAGCTAACAAGACTGCTCTCCCGAGTTCATTGTGAATTGAC 120
    |||
Db 201 GTGTGAAGAATTCAGCTAACAAGACTGCTCTCCCGAGTTCATTGTGAATTGAC 260
QY 121 GGTGAAGCTTCAAGACATGTGTGAGAAAGATGATGAGCAAGTGGCGGATCATGTA 180
    |||
Db 261 GGTGAAGCTTCAAGACATGTGTGAGAAAGATGATGAGCAAGTGGCGGATCATGTA 320
QY 181 CGCAGATCTCTGATCATCATCAGCGGCTGTCTCATCGCTCTGCGGGTACAGTCTT 240
    |||
Db 321 CGCAGATCTCTGATCATCATCAGCGGCTGTCTCATCGCTCTGCGGGTACAGTCTT 380
QY 241 CTGCTCCCAAGGAAATCACTCACTGATTTGATCATCAGCTGCTCAACACCCCTTTGTGA 300
    |||
Db 381 CTGCTCCCAAGGAAATCACTCACTGATTTGATCATCAGCTGCTCAACACCCCTTTGTGA 440
QY 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCCCTCAGGCCAGGGCTCCGAC 360
    |||
Db 441 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCCCTCAGGCCAGGGCTCCGAC 500
QY 361 CACCATCTGTTCTCTCAAAATTAAGCCCTCTTCTGCGCACACTGTGAAGTGAAGATG 420
    |||
Db 501 CACCATCTGTTCTCTCAAAATTAAGCCCTCTTCTGCGCACACTGTGAAGTGAAGATG 560
QY 421 CCACCCCTCTGATTTCTTCCAGCCCTGCGCCCAACCCCACTCCCTGCTAGAGA 480
    |||
Db 561 CCACCCCTCTGATTTCTTCCAGCCCTGCGCCCAACCCCACTCCCTGCTAGAGA 620
QY 481 GTTCTCTTGGGCTCTCTTTTATTTCTGAGGAGGAGCGGAGTCCGTCTCTTTTGT 540
    |||
Db 621 GTTCTCTTGGGCTCTCTTTTATTTCTGAGGAGGAGCGGAGTCCGTCTCTTTTGT 680
QY 541 CCTGTCCAAATAATGAAGAGCTCGGTAAAGCAATTCATTAATTCAGCTGACTGAAT 600
    |||
Db 681 CCTGTCCAAATAATGAAGAGCTCGGTAAAGCAATTCATTAATTCAGCTGACTGAAT 740
QY 601 TTTTCAATGATCTTGAAGAGAGGAGTGAAGTCAACCCCATGCTGTGTATAC 660
    |||
Db 741 TTTTCAATGATCTTGAAGAGAGGAGTGAAGTCAACCCCATGCTGTGTATAC 800
QY 661 CGGAGTCAAGGCGGAGCTGAGAGAGTCACTCTTGAAGTCACTGAGTGGGCATCTGCC 720
    |||
Db 801 CGGAGTCAAGGCGGAGCTGAGAGAGTCACTCTTGAAGTCACTGAGTGGGCATCTGCC 860
QY 721 TTTTGTAAAGCTCCAGTGTCCATTCATTCCTGATGGGGGCAATGTTGAACATGACAGA 780
    |||
Db 861 TTTTGTAAAGCTCCAGTGTCCATTCATTCCTGATGGGGGCAATGTTGAACATGACAGA 920
QY 781 GTGAGAGTACGTTTCTTGAAGGCTGAGGCGAGTTCACACTCAAGGCTCCCTGCTTG 840
    |||
Db 921 GTGAGAGTACGTTTCTTGAAGGCTGAGGCGAGTTCACACTCAAGGCTCCCTGCTTG 980
QY 841 ACATTCAAACTCATGCTCTGAAAAACATTCCTGACAGCAGAAATTTGGCTTTCGCGC 900
    |||
Db 981 ACATTCAAACTCATGCTCTGAAAAACATTCCTGACAGCAGAAATTTGGCTTTCGCGC 1040
QY 901 CTGAGTGGGGCTCTAGTACCTGAGACCTAATGACTGGGACTTGAAGTGGGCTGCGCT 960
    |||
Db 1041 CTGAGTGGGGCTCTAGTACCTGAGACCTAATGACTGGGACTTGAAGTGGGCTGCGCT 1100
QY 961 CGCTTGAAAAGTCTTAAGAAAATCTCTCAGTCTCTTGCAGAGGAGCTGGCGCGGG 1020
    |||
Db 1101 CGCTTGAAAAGTCTTAAGAAAATCTCTCAGTCTCTTGCAGAGGAGCTGGCGCGGG 1160
QY 1021 ACAGCAAGAGCAAGGCGGCTGCACAAAGCGGCGCTGCGGTGTGAGTGCAGATGTA 1080
    |||

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Db 1161 ACAGCAAGAGCAAGGCGGCTGCACAAAGCGGCGGCTGTGCGGTGTGAGTGCAGATGTA 1220
QY 1081 CGCGCAGCGCTTCTGTTGGTGGCTGTGTCAGCGACGACGCGGCGACACAGACCTTGC 1140
    |||
Db 1221 CGCGCAGCGCTTCTGTTGGTGGCTGTGTCAGCGACGACGCGGCGACACAGACCTTGC 1279
QY 1141 ACAGCAAGCGGCGGAACTGTGCGAGAGACACCGTGTACAGAGAGCGGCTGTGATGACGAG 1200
    |||
Db 1280 ACAGCAAGCGGCGGAACTGTGCGAGAGACACCGTGTACAGAGAGCGGCTGTGATGACGAG 1339
QY 1201 CTGAGGTAGAAAACGTCCTCGAAGAGGAGAGAGATCATGTACGCCCGGAAGTAGAC 1260
    |||
Db 1340 CTGAGGTAGAAAACGTCCTCGAAGAGGAGAGAGATCATGTACGCCCGGAAGTAGAC 1399
QY 1261 CTGCTCCAGTGTCTTGGGTTTGGCGGACCATGATCTCTCGAATCTGTTGGGCTATC 1320
    |||
Db 1400 CTGCTCCAGTGTCTTGGGTTTGGCGGACCATGATCTCTCGAATCTGTTGGGCTATC 1459
QY 1321 CAGCATACGGCCCAATGTACACAAATCAGCCCTGCGAGACAGAGCAGGAGAGAGAC 1380
    |||
Db 1460 CAGCATACGGCCCAATGTACACAAATCAGCCCTGCGAGACAGAGCAGGAGAGAGAC 1519
QY 1381 AGAGA 1385
    |||
Db 1520 AGAGA 1524

```

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RESULT 2
US-10-270-333-38/c
: Sequence 38, Application US/10270333
: GENERAL INFORMATION:
: APPLICANT: Craychik, Anbal
: TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
: FILE REFERENCE: THEREOF AS INSECTICIDAL TARGETS
: FILE REFERENCE: CL000733CON
: CURRENT FILING DATE: 2002-10-15
: PRIOR FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/168,677
: PRIOR FILING DATE: 1999-12-03
: PRIOR APPLICATION NUMBER: 60/175,691
: PRIOR FILING DATE: 2000-01-12
: PRIOR APPLICATION NUMBER: 60/191,638
: PRIOR FILING DATE: 2000-03-23
: NUMBER OF SEQ ID NOS: 198
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 38
: LENGTH: 2196
: TYPE: DNA
: ORGANISM: Drosophila
US-10-270-333-38

```

Query Match 2.5%; Score 40.6; DB 6; Length 2196;
Best Local Similarity 49.8%; Pred. No. 0.069;
Matches 103; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

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QY 1139 GCAGGAACACCCGCGGAACGTCGCGAGGACACCGTGTACAGAGCGGTTGATGCCG 1198
    |||
Db 799 GCTTGAACACCCCTTGAAGACTGTGTGTCGACATCAGGTTGTAAAGATGCGATTGCGCG 740
QY 1199 AGCTGAGGTAGAAAACGTCCTCGAAGAGGAGAGGATCATGTACGCCCGGAAGTAGG 1258
    |||
Db 739 AGTTGAGGTAGACATGATCTCTACAGAAAGTACACAGCTGTGTAGTACGACCAATCCCA 680
QY 1259 ACTCTGTCAGTCTGCTTGGGTTTGGCGGACGACATGATCTCTCGAATCTGTTGGGCA 1318
    |||
Db 679 GATCTGACAGTGTGTCGCTGCTGAGATGATCACAGGTTGTAGAGACGCGGAAGGGCA 620
QY 1319 TCCAGCATACGCGCAATGTACACAA 1345
    |||
Db 619 GCAGGCAAGCAAGAGAGACGACAA 593

```

RESULT 3
US-10-270-333-37/c
; Sequence 37, Application US/10270333
; GENERAL INFORMATION:
; APPLICANT: Cravchik, Anibal
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
; NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF AS INSECTICIDAL TARGETS
; FILE REFERENCE: CL000733CON
; CURRENT APPLICATION NUMBER: US/10/270,333
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/168,677
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/175,691
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/191,638
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 6472
; TYPE: DNA
; ORGANISM: Drosophila
US-10-270-333-37

Query Match 2.5%; Score 40.6; DB 6; Length 6472;
Best Local Similarity 49.8%; Pred. No. 0.13;
Matches 103; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 1139 GCACGACACCCGCGAATGCTGCTGAGACACCGCTGACAGAGCGGCTGATGACCG 1198
DB 2805 GCTTGAACCCCTTGGAACCTGCTGACATCATGCTGTAAGAATCGGATTACGGCCG 2746
QY 1199 ACCTGAGTAGAAAAACGCTCTCCGAGAGGAGAGAGATCATGTACGCCCGGAGTAGG 1258
DB 2745 ACCTGAGTAGAACATGATGATCTACAGAGTACAGACGCTGATAGCGCACCATGCCA 2686
QY 1259 ACCTGCTCCAGCTGCTGCTGGGTTGGCCGACCATGATCTCCGAATCTGGTTGGCA 1318
DB 2685 GATTCGTGCACTGTTGGTCCGCTGCTGAGAGATGTCACAGGCTGAGGACCGCGAAGGCA 2626
QY 1319 TCCACATGAGCGCAATGTCACACAA 1345
DB 2625 GCAGCGACAGCAAGAAAGACACACAA 2599

RESULT 4
US-60-416-172-67
; Sequence 67, Application US/60416172
; GENERAL INFORMATION:
; APPLICANT: Chang, Hwai Men
; APPLICANT: Feltz, Katherine A.
; APPLICANT: Warren, Amy J.
; APPLICANT: Cooper, Judith R.
; TITLE OF INVENTION: Genes from Human Cancer Cells and Human Tumors
; FILE REFERENCE: 216019-153
; CURRENT APPLICATION NUMBER: US/60/416,172
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Gallus gallus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Human extended sequence for V063_71
US-60-416-172-67

Query Match 2.4%; Score 38.8; DB 7; Length 667;
Best Local Similarity 47.7%; Pred. No. 0.11;
Matches 144; Conservative 0; Mismatches 157; Indels 1; Gaps 1;

QY 1037 GCGCTGCACAAAGCGCGCGCTGCTGCTGAGAGTGGCATGTACGGCAGCGGCTTCTC 1096
DB 187 GCGGAGAGACACAGACGACCGCTTACGGGGTGGCCGGGGCTTGCCACCGCTTGACGGGA 246
QY 1097 GTGTTGGCGCTGCTGACGAGCAGCGCGGACACAGCATTGACGAACACCGCGGA 1156
DB 247 GTGGGTGAGTGGCGGAGCAGCGCTGCGGCGACAGCCCGCGCGGAGTGCAGCC-CG 305
QY 1157 ACTGCTGCGAGACACCGCTGTACAGAGAGCGGTTGATGATCCGAGCTGAGTGAAGAA 1216
DB 306 AGTACGAGGACTTCATGTGATGATGACCCGACCAAGCTGCTGCTGCGGTTGAAAAA 365
QY 1217 TCTCCGAGAGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1276
DB 366 TCTGAGACACAGGAGACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 425
QY 1277 TGGGTTTGGCGGACCATGATCTCCGAATCTGTTGGGATCATCAGCATACGCGCAATG 1336
DB 426 AGGCTGAGAGAGACACCGCGGCTGAGGACAGGAGACCTGCGAGGAGCCGACGCGCTCG 485
QY 1337 TC 1338
DB 486 TC 487

RESULT 5
US-10-270-333-116/c
; Sequence 116, Application US/10270333
; GENERAL INFORMATION:
; APPLICANT: Cravchik, Anibal
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
; NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF AS INSECTICIDAL TARGETS
; FILE REFERENCE: CL000733CON
; CURRENT APPLICATION NUMBER: US/10/270,333
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/168,677
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/175,691
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/191,638
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Drosophila
US-10-270-333-116

Query Match 2.1%; Score 34.8; DB 6; Length 990;
Best Local Similarity 55.9%; Pred. No. 1.9;
Matches 66; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1143 GACACCCCGCGAATGCTGCGAGACACCGCTGTACAGAGCGGCTTGTGACCGAGCT 1202
DB 972 GAAAGCCTTCGGAATTCGCGAGAGAGAGGCTGAGAGCGGATGATGATGATGATGATGAT 913
QY 1203 GAGTAGAAAAACGCTCCGAGAGAGGAGAGAGATCATGTACCGCGGAGTAGAGAC 1260
DB 912 GCTTAGCGCAGAGTCTGGGCGGTGACCTGATGATGATGATGATGATGATGATGATGATGAT 855

RESULT 6
US-10-270-333-115
; Sequence 115, Application US/10270333
; GENERAL INFORMATION:
; APPLICANT: Cravchik, Anibal
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
; NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF AS INSECTICIDAL TARGETS
; FILE REFERENCE: CL000733CON
; CURRENT APPLICATION NUMBER: US/10/270,333


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```

Query Match	2.1%;	Score 34,4;	DB 6;	Length 1024;
Best Local Similarity	48.5%;	Pred. No. 2.5;		
Matches 128; Conservative	0;	Mismatches 131;	Indels 5;	Gaps 1

QY	1031	CAACGGGCGGTGCACAAAGCGGGCGGTGTGCGGTGTGTGAGTGTGGATGTACGCGGACGGCG	1090
Db	591	CAAGGGGCGCGCCGACGACGACGGCGGTCTCGGCGCAAGGGGACCACTGTCCGCTGTGGGCCCGGGGCG	650
QY	1091	CTTCTGCTGTGTGGCTGCTGTCAGCGACAGGGCGGCGAGCAAGCACTTGTGACGAACACCC	1150
Db	651	TTCGTGCGCTGTCTCACACGCGTCCGCGTCCGCTGGAGAACTGTGGCTGGGCGGATTTGGGT	710
QY	1151	GCCCAAACTCTGT-----CGAGACACACCGGTGTACAGAGCGGGTTGTATGACCGAGACTGAG	1205
Db	711	GCTTGTCCGACAGGGAGGTGCAATGTGACATGTGTGATCGGCGGGGTGCGGACCAATTTCCG	770
QY	1206	GTACAAAAACGTCTCGAGAGAGGGGAGAGGATCATGTACGCCCGGAAGTAGACTTCTGT	1265
Db	771	GCGCGCAAAACATCATACGCGGAGATCAAGACAGAGACCTGCACCGCCTGTGAAGCCCGACACGTT	830
QY	1266	CCAGTGTGCTTGGGCTTTGGCCCC	1289
Db	831	GCCAGCGCCCTGCTGCGTGTGCCCG	854

```

RESULT 10
US-10-240-425-334
; Sequence 334, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Metzzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 334
; LENGTH: 1201
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AB000584
US-10-240-425-334

```

Query Match	2.1%	Score 34.4	DB 6	Length 1201
Best Local Similarity	48.5%	Pred. No. 2.7		
Matches 128	Conservative	0	Mismatches 131	Indels 5
Gaps				1

0y	1031	CACGGGCGCTGCACAAACGGGGCGCTGTGGTGTGAGTGGCCCATGTACGGCGCAGCGG	1090									

Accession	Sequence	Position
Db	CAGGGGGGGCGCCGACGAGCGGGTGGCGGCCAACGGGACACCACTGTCCGTGGGGCCGGGGC	658
Qy	CTTCTCGTGGTGGCGCTGCTGCACGACGACGGCGGACACGACCACTTGCACGACACCC	115
Db	TTGTGTCGCGTCTGCACACGGGTCCCGCGTGGTGGAAAGCACTGGGGCTGGGCGATTGGGT	718
Qy	GCCAAACACTGCTG-----CGAGGACACCGCTGTACAGGAGCGGGTGTGATGACGAGCTGAG	120
Db	GCTGTCCGCGACGGGAGGTCGAAGTGAACCATGTGCATGTGGCGGCTGCCCGACGATTCCG	778
Qy	GTGAAAAACGTCCTTCGAGAAAGGGAGGAGATCATGTACGCCCGGAAGTAGGACCTCGT	126
Db	GCGCGCAACACATGCACCGCGGACGATCAAGACAGACCTTCACCGCTTAAGGCCGACACGGT	838
Qy	CCAGTCGTCGTTGGGTTTGGCGC	1289
Db	GCCACGCGCCCTGCTGCTGCTGCCCGC	862

```

RESULT 11
US-10-267-255-96/C
Sequence 96, Application US/10267255
GENERAL INFORMATION:
APPLICANT: Sherman, D
APPLICANT: Mao, Y
APPLICANT: Vargolu, M
APPLICANT: He, M
APPLICANT: Sheldon, P
TITLE OF INVENTION: Micromycin biosynthetic gene cluster
FILE REFERENCE: 600,456US1
CURRENT APPLICATION NUMBER: US/10/267,255
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US 09/266,965
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: US 08/624,447
PRIOR FILING DATE: 1996-08-19
PRIOR APPLICATION NUMBER: PCT/US94/11279
PRIOR FILING DATE: 1994-10-06
PRIOR APPLICATION NUMBER: US 08/133,963
PRIOR FILING DATE: 1993-10-07
NUMBER OF SEQ ID NOS: 145
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 96
LENGTH: 18331
TYPE: DNA
ORGANISM: Streptomyces lavendulae
US-10-267-255-96

```

	Query Match	Similarity	2.1%	Score 34;	DB 6;	Length 18331;
	Best Local	Similarity	50.6%;	Pred No. 18;	Mismatches	Gaps
	Matches	82;	Conservative	0;	Mismatches	80; Indels 0; Gaps 0;
QY	309	GGCCCAAGAAAGGGGAMATTCTGCCTCGGCCCTCAGGCCGACCCGACACCATTC	368			
Db	16079	GGTCCAGCACGAAGGTGTGCGCTCGGCCCGCGCTCCAGGACACGAGATCGCATGACGGCCC	16020			
QY	369	TGTTCTCCAATTAGCCCTCTTCTGTGGCACACTGCTGAAGTGAAGAGATGCCACCCCC	428			
Db	16019	GGTGGGGCGCCGCTCCCGCTCGGACTCCACCGGGCCAGCGGATCAGCTCCACCCTT	15960			
QY	429	TCTGCATTGTCTTCCAGCCCTGCGCCCGCAACCCCCCACT	470			
Db	15359	CCACCGCTGATGCTCGCAACTGGCGCCCTTCCACGGGAACT	15918			

```

RESULT 12
US-10-267-255-76/c
; Sequence 76, Application US/102672555
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M

```

```

; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/10/267,255
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 09/266,965
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 08/624,447
; PRIOR FILING DATE: 1996-08-19
; PRIOR APPLICATION NUMBER: PCT/US94/11279
; PRIOR FILING DATE: 1994-10-06
; PRIOR APPLICATION NUMBER: US 08/133,963
; PRIOR FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 76
; LENGTH: 53500
; TYPE: DNA
; ORGANISM: Streptomyces lavendulae
US-10-267-255-76

```

```

Query Match
Best Local Similarity 2.1%; Score 34; DB 6; Length 53500;
Matches 82; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

```

```

Qy 309 GGCCCAAGAAAGGGAAGTCTGCTGGCCCTCAGGCGCAGGCGCTCCACACCATCC 368
Db 3930 GGTCCACGACACAGGTCCTGCGCCCGCTCCAGACAGGATCGCATGAGCGCCC 3871
Qy 369 TGTTCCTCAATTAAGCCCTCTTCGCGACACACTGCTGAAGTGAAGAGATGCCACCCC 428
Db 3870 GGTTCGCGGAGCGCTCCGCGCGCTCGAGATCCAGCGGCGAGGATGATGACCTCT 3811
Qy 429 TCTTCGATGTCTCTTCACGCTCCGCCCAACCCCACT 470
Db 3810 CCACGCTGATGCTCGACACTGCGCCCGCTCCAGGCAACT 3769

```

RESULT 13

```

US-10-270-333-193
; Sequence 193, Application US/10270333
; GENERAL INFORMATION:
; APPLICANT: Cravchik, Anibal
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
; FILE REFERENCE: C1000733CON
; CURRENT APPLICATION NUMBER: US/10/270,333
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/168,677
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/175,691
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/191,638
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 193
; LENGTH: 4902
; TYPE: DNA
; ORGANISM: Drosophila
US-10-270-333-193

```

```

Query Match
Best Local Similarity 2.1%; Score 33.2; DB 6; Length 4902;
Matches 114; Conservative 0; Mismatches 113; Indels 3; Gaps 1;

```

```

Qy 1144 AACACCCCGCAAGCTGTCGAGACACCGTGTACAGAGCGGTTGATGACGAGCTG 1203
Db 2139 AAGGCTCAGAACTTGCTCTATGATGTGTAGACAGCGGTTGATGACGAGCTG 2198
Qy 1204 AGGTGAAAGAAAGCTCTCCGAGAGGAGGAGGATGATGATGACCGCCGGAAGTAGACCTC 1263

```

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Db 2199 AGGAAGTAGAAGAACCCGAGCATATAGTCGAGGATGCTGAACAGCTGTGAACCACTGG 2258
Qy 1264 GTC---CAGTCGTCTGGGTTGGCCGACGCATGATCTCCGATTCGTGGGCTATC 1320
Db 2259 GATCAATGCGCCGAGGATGATCATAGACCGCATACGCGCTGGCGGTGAAGGGGCGC 2318
Qy 1321 CAGCATGCGGCCAATGTCACACAAATCAGCCCTGGCGACAGACGAGCAGG 1370
Db 2319 CAGCATGTAAGAAAGGCGCCAGCGCCACCGCATCTGGGAAGTGGATTAAGG 2368

```

RESULT 14

```

US-10-240-485-176/c
; Sequence 176, Application US/10240485
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: Metastasis
; FILE REFERENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240,485
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03970
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 202
; SEQ ID NO: 176
; LENGTH: 23683
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-485-176

```

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Query Match
Best Local Similarity 2.1%; Score 33.2; DB 6; Length 23683;
Matches 121; Conservative 0; Mismatches 123; Indels 4; Gaps 1;

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Qy 1375 AGACACGAGAAAAAGAAAAACACAGCATGAGACACAGTAAATGAATTAACATTAAT 1434
Db 15435 ATATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 15376
Qy 1435 ATTAAAGCCCTCTGTTGCTTACTGCGCAGGAAATGTACCAATTTTTCAGTGTGG 1494
Db 15375 AATTAAACCTTATCTTAGTCTCTCTCTCGAAAAAATTAATTTTACTTACTTAATTC 15316
Qy 1495 A---CTTGACAGCTTCTTTTGCACAGCAAGAGAGATTTAACACTGTTCAACCCG 1550
Db 15315 AATATTTAACAATCTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTA 15256
Qy 1551 GGGAGTTGGCTGTGTTAAAGAAAGAACATTAAATGTTAGACAGTGAATTAATTAAT 1610
Db 15255 AATAATATTAATCTCTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 15196
Qy 1611 AAAAAAAA 1618
Db 15195 AACACAAA 15188

```

RESULT 15

```

US-10-264-237-1277
; Sequence 1277, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

```

FILE REFERENCE: PA131P1
 CURRENT APPLICATION NUMBER: US/10/264,237
 CURRENT FILING DATE: 2002-10-04
 PRIOR APPLICATION NUMBER: PCT/US01/16450
 PRIOR FILING DATE: 2001-05-18
 PRIOR APPLICATION NUMBER: US 60/205,515
 PRIOR FILING DATE: 2000-05-19
 NUMBER OF SEQ ID NOS: 2876
 SOFTWARE: PatentIn Ver. 3.1
 SEQ ID NO: 1277
 LENGTH: 2158
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-264-237-1277

Query Match 2.0%; Score 33; DB 6; Length 2158;
 Best Local Similarity 73.7%; Pred. No. 9.7;
 Matches 42; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 Oy 1563 GTGTTAAGAAAGACCATTAATGCTTTAGACAGTGTAAAGAAAAA 1619
 Db 2085 GTTGTAAAGCCAGCTAATAAATGCTTTAGTTGAGCATAAAAA 2141

Search completed: November 7, 2002, 18:01:51
 Job time : 331.231 secs

482

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 16:56:48 ; Search time 4825.36 Seconds

(without alignments)
11441.218 Million cell updates/sec

Title: US-09-970-966-214

Perfect score: 1897
Sequence: 1 gccacaccgcgagcctcgcg.....aaaaaaaaaaaaaaaaaa 1897Scoring table: OLIGO_NWC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 10
Total number of hits satisfying chosen parameters: 2188596Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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9: gb_pr:*
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37: em_htg_vtl:*
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41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1526	80.4	1832	AK094501	AK094501 Homo sapi
2	1422	75.0	1524	AX358762	AX358762 Sequence
3	1422	75.0	1524	AX362255	AX362255 Sequence
4	1344	70.8	1890	AX136281	AX136281 Sequence
5	1328	70.0	129676	AC079773	AC079773 Homo sapi
6	1218	65.2	2528	AX319944	AX319944 Sequence
7	858	44.2	946	BC017318	BC017318 Homo sapi
8	661	34.8	826	BC011449	BC011449 Homo sapi
9	511	26.9	591	AX136556	AX136556 Sequence
10	506	26.7	1362	AX319942	AX319942 Sequence
11	506	26.7	1362	AF034633	AF034633 Homo sapi
12	366	19.3	587	AX136698	AX136698 Sequence
13	364	19.2	444	AX150120	AX150120 Sequence
14	316	16.7	396	AX093191	AX093191 Sequence
15	315	16.6	369	AX093381	AX093381 Sequence
16	294	15.5	147131	AC010974	AC010974 Homo sapi
17	47	2.5	209885	AC124493	AC124493 Mus muscu
18	38	2.0	1797	AB041649	AB041649 Mus muscu
19	30	1.6	125703	AC123338	AC123338 Rattus no
20	27	1.4	487	AF150733	AF150733 Homo sapi
21	27	1.4	1086	AF082874	AF082874 Medicago
22	27	1.4	1114	AY118558	AY118558 Drosophila
23	27	1.4	1368	AX285020	AX285020 Sequence
24	27	1.4	1614	AK026521	AK026521 Homo sapi
25	27	1.4	2625	BC028978	BC028978 Homo sapi
26	26	1.4	3155	AY094780	AY094780 Drosophila
27	27	1.4	48206	AL645986	AL645986 Mouse dna
28	27	1.4	92874	AC112072	AC112072 Rattus no
29	27	1.4	127524	AL807806	AL807806 Mus muscu
30	27	1.4	138851	AL645938	AL645938 Mouse dna
31	32	27	1.4	151602	AC126321 Polypectu
32	27	1.4	170255	AC027118	AC027118 Homo sapi
33	32	27	1.4	179364	AC074245 Homo sapi
34	34	27	1.4	195782	AC074389 Homo sapi
35	27	1.4	209572	AC099615	AC099615 Mus muscu
36	27	1.4	212690	AC110232	AC110232 Mus muscu
37	37	27	1.4	214411	AC069297 Mus muscu
38	26	1.4	1275	AL133395	AL133395 Human DNA
39	26	1.4	1409	AF297044	AF297044 Zee mayr
40	26	1.4	2481	AF176571	AF176571 Alternari
41	26	1.4	2745	AX056894	AX056894 Sequence
42	26	1.4	3889	AF314845	AF314845 Rana cala
43	26	1.4	3889	BC034500	BC034500 Homo sapi
44	26	1.4	7940	AF044209	AF044209 Homo sapi
45	26	1.4	94336	AC005250	AC005250 Homo sapi

ALIGNMENTS

RESULT 1
AK094501
LOCUS
DEFINITION
AK094501 1832 bp mRNA linear PRI 15-JUL-2002
Homo sapiens CDNA FLJ37182 fls, clone BRAL2001350, weakly similar
to Homo sapiens Gz-selective GTPase-activating protein (RG520)
mRNA.
ACCESSION
AK094501
VERSION
AK094501.1 GI:21753575
KEYWORDS
Oligo capping, fls (full insert sequence).
SOURCE
Homo sapiens alzheimer cortex cDNA to mRNA, clone BRAL22
Clone:BRAL22001350.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1

AUTHORS

Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R.,
Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
Masuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Magetsuna, M., Murekawa, K., Kanemori, K., Takahashi-Fujii, A.,
Oshima, A., Suzuki, Y., Sugano, S., Nagahara, K., Masuko, Y., Nagai, K.,
and Isogai, T.

TITLE

NEDO human cDNA sequencing project

JOURNAL

unpublished

REFERENCE

2 (bases 1 to 1832)

AUTHORS

Isogai, T. and Yamamoto, J.

TITLE

Direct Submission

JOURNAL

Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7

COMMENT

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
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NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan: cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; Clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.

FEATURES

source

1. 1832
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CDS

BASE COUNT 411 a 501 c 513 g 407 t
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Query Match 80.4% Score 1526; DB 9; Length 1832;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1676; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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LOCUS	AX362255	1524 bp	DNA	linear	PAT 15-FEB-2002
DEFINITION	Sequence 15 from Patent WO0208288.				
ACCESSION	AX362255				
VERSION	AX362255.1	GI:18694585			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Baker,K.P., Desnoyers,L., Gerltsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,Y., Stephan,J.P., Watanabe,C.K. and Wood,W.I.				
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same				
JOURNAL	Patent: WO 0208288-A 15 31-JAN-2002;				
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ORIGIN					
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Best Local Similarity	99.9%; Pred. No. 0;				
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Db	121 ATGTGGGTCCTAGGACATCGCGCAACTTTTTCGGATTGTTCTTCCAGAGCTTTGGC	180			
QY	320 CTGCAATTCAGATGCTTACAGAGTGAAGAATCCAGCTGAACAAGACATGCTTCCGCC	379			
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QY	440 CAAAGTGGCGGATCATGTACCGCAAGTCTGTGCATCATACAGGGCTGTCTATCGCC	499			
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QY	500 TCTGGCGGGTACAGAGCTTCTGCTCCCGCAGGAAATCAACTCAAGTTGCATCAGCTGC	559			
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QY	620 CTCAGGCCACGGGCTCGCACACATCTCTGTCTCAAAATTAGCCCTCTTTCGGGACAC	679			
Db	481 CTCAGGCCACGGGCTCGCACACATCTCTGTCTCAAAATTAGCCCTCTTTCGGGACAC	540			
QY	680 TCGTGAAGGTGAAGGAGATGCCACCCCTCTGCAATGTTCTTCCAGCCCTCGCCCCAA	739			
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Qy	860	TAAATTCAGCTGATGAATAATTTTCGTATGTACTGGAAGAGAGGTGAGTGAAGTT	919
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Qy	980	CACGTAGGTGGGCACTCCCTTTTGTAAAGCTCCAGTGCATTCATTCCTCGTAGGG	1039
Db	841	CACGTAGGTGGGCACTCCCTTTTGTAAAGCTCCAGTGCATTCATTCCTCGTAGGG	900
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Best Local Similarity 99.9%; Pred. No. 0;
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LOCUS	AX319944	2528 bp	DNA
DEFINITION	Sequence 3 from Patent WO0181634.		linear
ACCESSION	AX319944		
VERSION	AX319944.1	GI:17901491	
KEYWORDS			
SOURCE	human.		

REFERENCE
AUTHORS
TITLE
JOURNAL

1 Galvin, K.A. and Rudolph-Owen, A.A.
Methods and compositions for the diagnosis and treatment of
cardiovascular and tumorigenic disease using 4941
patent: WO 0181634-A 3 01-NOV-2001;
Millennium Pharmaceuticals, Inc. (US)

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OY	1210	ATGACTGGGACTTGAAGCTGGGGCTCGGGCCCTGCTGAAATAAGCTTTAAGAAATCTTCT	1269
Db	1317	ATGACTGGGACTTGAAGCTGGGGCTCGGGCCCTGCTGAAATAAGCTTTAAGAAATCTTCT	1258
OY	1270	CAGTTCTCCTTGACAGAGACTGGCGCGGAGCCGAAAGACAGAGGCGCTGCACAAAGC	1329
Db	1257	CAGTTCTCCTTGACAGAGACTGGCGCGGAGCCGAAAGACAGAGGCGCTGCACAAAGC	1198
OY	1330	GGGCGCTGCTGGTGTGAGTAGTGCAGATGTAACGGCAGGGCGCTTCTGAGTGTGGGCGCT	1389
Db	1197	GGGCGCTGCTGGTGTGAGTAGTGCAGATGTAACGGCAGGGCGCTTCTGAGTGTGGGCGCT	1138
OY	1390	GCAGGACACGGGGGAGCAGACGACACTGCAGAAACACCCCGGAAACGCTGCGAGNACA	1449
Db	1137	GCAGGACACGGGGGAGCAGACGACACTGCAGAAACACCCCGGAAACGCTGCGAGNACA	1078
OY	1450	CCGTGTACAGAGCGGGTTGATGACGAGGTGAGTAAAAAAGTCTCCGAGAAAGGGA	1509
Db	1077	CCGTGTACAGAGCGGGTTGATGACGAGGTGAGTAAAAAAGTCTCCGAGAAAGGGA	1018
OY	1510	GGAGGATCATGTAGCCCGCGGGAAGTAGAAGCTCGTCAGAGTGTGGGTTTGGCCGAG	1569
Db	1017	GGAGGATCATGTAGCCCGCGGGAAGTAGAAGCTCGTCAGAGTGTGGGTTTGGCCGAG	958
OY	1570	GCATGATCTCCGATCTGGTGGGCACTCCAGATTAAGGGCAATGTCAACAAATCAAGC	1629

DB	957	CCATGATCCTCGGATCTGTGGCATTCGACATACGCGCAATGTCAACAAATCAGCC	898
RESULT 7			
LOCUS	BC017318	946 bp	mRNA
DEFINITION	Homo sapiens, clone MGC:29643 IMAGE:3641660,	linear	PRI 09-NOV-2001
ACCESSION	BC017318		complete cds.
VERSION	BC017318.1	GI:16878239	
KEYWORDS	MGC.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 946)		
TITLE	Strausberg, R.		
JOURNAL	Direct Submission Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.ncl.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapbs-ref@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland: Web site: http://www.nisc.nih.gov/ Contact: nisc_mgc@nhgri.nih.gov Shvachenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brock, R., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, O.L., Mastello, C., Mestrian, S.D., McElroskey, J.C., McQuell, J., Pearson, R., Snyder, B., Stantirip, S., Thomas, P.J., Tlonsong, E.E., Touchman, J.W., Tsurgueon, C., Vogt, J.L., Walker, M.A., Zhang, L., H. and Green, E.D.		
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov Series: IRAL Plate: 39 Row: D Column: 19 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein. Location/Qualifiers 1. 946		
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CDS			
BASE COUNT	197 a 292 c 261 g 196 t		
ORIGIN			
Query Match	45.2%; Score 858; DB 9; Length 946;		
Best Local Similarity	99.9%; Pred. NO. 0;		
Matches 908; Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
19	GGTGTCTGGCCCGGAGCGCGGAGGAGACAGAGACCCGACCGGAGACCCGAGCG	78	

Db	20	66TGTCTCGCCCGGAGGCGGAGCGGAGGAGACAGAGACCCGCGAGCCGGAGCCGAGACGG	79
QY	79	CGGGGATGACAGAGCTCCCGGAGCGGACACTCGGCTCTCTTAAGTACGACACGTCGTCTC	138
Db	80	CGGGGATGACAGAGCTCCCGGAGCGGACACTCGGCTCTCTTAAGTACGACACGTCGTCTC	139
QY	139	CGCGGACAGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG	198
Db	140	CGCGGACAGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG	199
QY	199	CTCCGCTCTGTCTGCGGCTCTGTATGCGCTTGCCTCTCCGCGGCGGAGCGGAGCGGAG	258
Db	200	CTCCGCTCTGTCTGCGGCTCTGTATGCGCTTGCCTCTCCGCGGCGGAGCGGAGCGGAG	259
QY	259	AATGTGGGTCTTACGAGATCGGCGGAACTTTTGGCGATTTGTTCTTCCAGCTTTTGC	318
Db	260	AATGTGGGTCTTACGAGATCGGCGGAACTTTTGGCGATTTGTTCTTCCAGCTTTTGC	319
QY	319	GCTGCAATTCAGTCTCTACAGTGTGAAGAAATTCAGTGTGAACAGATGCTCTCTCC	378
Db	320	GCTGCAATTCAGTCTCTACAGTGTGAAGAAATTCAGTGTGAACAGATGCTCTCTCC	379
QY	379	CGAGTTCAATTGTGAATTCACAGGTTCAAGATGTTCAAGATGTTCAAGATGTTCAAGATG	438
Db	380	CGAGTTCAATTGTGAATTCACAGGTTCAAGATGTTCAAGATGTTCAAGATGTTCAAGATG	439
QY	439	GCAAGATGCGGAGATCATGTATCCGCAAGTCTGTGCATCATATCAGCGGCTGTCTATCGC	498
Db	440	GCAAGATGCGGAGATCATGTATCCGCAAGTCTGTGCATCATATCAGCGGCTGTCTATCGC	499
QY	499	CTCTCCGCGGATACAGTCT	558
Db	500	CTCTCCGCGGATACAGTCT	559
QY	559	CTGCAACACCCCTCTTGTATACGCGGCAAGGCGGCAAGGAGGAGGAGGAGGAGGAGGAG	618
Db	560	CTGCAACACCCCTCTTGTATACGCGGCAAGGCGGCAAGGAGGAGGAGGAGGAGGAGGAG	619
QY	619	CCTCAGGCGGAGGCTCCGCAACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	678
Db	620	CCTCAGGCGGAGGCTCCGCAACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	679
QY	679	CTGCTGAAGCTGAAGAGATGCGACCCCTCTGATGTTCTTCCAGGCTCTGCGGCCCA	738
Db	680	CTGCTGAAGCTGAAGAGATGCGACCCCTCTGATGTTCTTCCAGGCTCTGCGGCCCA	739
QY	739	ACCCGCAACCTCTGAGAGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	798
Db	740	ACCCGCAACCTCTCTGAGAGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	799
QY	799	GAGTCCGTTCTCTTGTCT	858
Db	800	GAGTCCGTTCTCTTGTCT	859
QY	859	ATAAATTACGCTTGAAGATTTTCAATGTTACTTTGAAGAGAGAGGAGGAGGAGGAGGAG	918
Db	860	ATAAATTACGCTTGAAGATTTTCAATGTTACTTTGAAGAGAGAGGAGGAGGAGGAGGAG	919
QY	919	TCACCCCGCA 927	
Db	920	TCACCCCGCA 928	
RESULT 8			
LOCUS	BC011449	826 bp	mRNA
DEFINITION	Homo sapiens, clone IMAGE:4026092, mRNA.	linear	PRI 22-AUG-2001
ACCESSION	BC011449		
VERSION	BC011449.1	GI:15277472	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

REFERENCE 1 (bases 1 to 826)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
 COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC/DCTP/DTP
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
<http://www.systemsbio.org>
 contact: amadansystemsbiology.org
 Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Kettelman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRIL Plate: 25 Row: n Column: 18
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES
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 /db_xref="taxon:9606"
 /clone="IMAGE:4026092"
 /tissue_type="Skin, melanotic melanoma."
 /clone_lib="NIH-MGC-20"
 /lab_host="DH10B-R"
 /note="Vector: pORB7"
 BASE COUNT 237 a 197 c 228 g 164 t
 ORIGIN

Query Match 34.8%; Score 661; DB 9; Length 826;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 711; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1186 TGGGCTCTGTGAGCTGAGACTCAATGACTGGAGCTTAGACTGGGGCTCGGCTGCTCT 1245
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 DB 105 TGGGCTCTGTGAGCTGAGACTCAATGACTGGAGCTTAGACTGGGGCTCGGCTGCTCT 164
 QY 1246 GAAAGTGTCTAAGAAATCTTCAGTCTCTCTTGCAGAGAGACTGGCGCGGAGCGGA 1305
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 DB 165 GAAAGTGTCTAAGAAATCTTCAGTCTCTTGCAGAGAGACTGGCGCGGAGCGGA 224
 QY 1306 AGAGCAAGCGGCGCTGCACAAAGCGGCGCTGCGGTGGTGAAGCGCATGTACGCGCA 1365
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 DB 225 AGAGCAAGCGGCGCTGCACAAAGCGGCGCTGCGGTGGTGAAGCGCATGTACGCGCA 284
 QY 1366 GCGGCTCTCGTGGTGGGCTGCTGACGAGCGGCGGACGACGACACTTGCAGAAACA 1425
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 DB 285 GCGGCTCTCGTGGTGGGCTGCTGACGAGCGGCGGACGACGACACTTGCAGAAACA 344
 QY 1426 CCGGCGGAAGCTGCGGAGGAGACCGGTGACAGAGGGGGTGTGATGACCGAGCTGAGGT 1485
 |||||||
 DB 345 CCGGCGGAAGCTGCGGAGGAGACCGGTGACAGAGGGGGTGTGATGACCGAGCTGAGGT 404
 QY 1486 AGAAAAAGCTCTCGAGAAAGGAGAGAGATCATGTACGCCCGGAAGTAGACCTGCTCC 1545
 |||||||
 DB 405 AGAAAAAGCTCTCGAGAAAGGAGAGAGATCATGTACGCCCGGAAGTAGACCTGCTCC 464
 QY 1546 AGTGTGCTTGGGTTGGCGCAGCATGATCTCGAATCTGTTGGGCAATCCAGATA 1605
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 DB 465 AGTGTGCTTGGGTTGGCGCAGCATGATCTCGAATCTGTTGGGCAATCCAGATA 524
 QY 1606 GGGCCAATGTCAACAAATCAGACCTTGGGCGAGACGAGCAGAGAGAGAGAGAGAGAAA 1665
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 DB 525 GGGCCAATGTCAACAAATCAGACCTTGGGCGAGACGAGCAGAGAGAGAGAGAGAGAAA 584

QY 1666 AGAAAAACAGCATGAGACAGAGTAATGATTAATAAACATTAATATTAGCCCTCT 1725
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 DB 565 AGAAAAACAGCATGAGACAGAGTAATGATTAATAAACATTAATATTAGCCCTCT 644
 QY 1726 GTTGTGCTTACTGAGCGGAGGAAATGTACCAATTTTTCAGTGTGAGCTGACAGCTTC 1785
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 DB 645 GTTGTGCTTACTGAGCGGAGGAAATGTACCAATTTTTCAGTGTGAGCTGACAGCTTC 704
 QY 1786 TTTTGGCCCAAGCAAGAGAGAAATTTAACTGTTTCAACCCGGGGAGTTGGCTGTGT 1845
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 DB 705 TTTTGGCCCAAGCAAGAGAGAAATTTAACTGTTTCAACCCGGGGAGTTGGCTGTGT 764
 QY 1846 AAGAGAAAGCATTAATATGCTTTAGACAGGTAAATTAATTAATTAATTAATTAAT 1897
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 DB 765 AAGAGAAAGCATTAATATGCTTTAGACAGGTAAATTAATTAATTAATTAATTAAT 816

RESULT 9
 AX136556 591 bp DNA linear PAT 30-MAY-2001
 LOCUS AX136556
 DEFINITION Sequence 478 from Patent EP1067182.
 ACCESSION AX136556
 VERSION AX136556.1 GI:14272960
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 591)
 Oca,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
 Hayashi,K.
 TITLE Secretory protein or membrane protein
 JOURNAL Patent: EP 1067182-A 478 10-JAN-2001;
 Helix Research Institute (JP)
 FEATURES
 source 1..591
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 108 a 198 c 173 g 109 t 3 others
 ORIGIN

Query Match 26.9%; Score 511; DB 6; Length 591;
 Best Local Similarity 100.0%; Pred. No. 2,8e+294;
 Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGTGCTGGCCCGGAGCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 78
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 DB 33 GGTGCTGGCCCGGAGCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 92
 QY 79 GGGCGATGAGAGGCTCGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 138
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 DB 93 GGGCGATGAGAGGCTCGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 152
 QY 139 GCGGCGAGAGCGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 198
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 DB 153 GCGGCGAGAGCGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 212
 QY 199 CTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 258
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 DB 213 CTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 272
 QY 259 AATGTGGTCTTAGAGCAATGCGGCAATTTTGGGATTTGCTTGTGCTTCCAGAGCTTTC 318
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 DB 273 AATGTGGTCTTAGAGCAATGCGGCAATTTTGGGATTTGCTTGTGCTTCCAGAGCTTTC 332
 QY 319 GCTGCAATCCAGTGTCAACAGTGTGAAGAAATTCAGCTGAACAGAGCTGCTCTCC 378
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 DB 333 GCTGCAATCCAGTGTCAACAGTGTGAAGAAATTCAGCTGAACAGAGCTGCTCTCC 392
 QY 379 CGAGTTCATTTGTGAATTCAGAGGTAAGAGTTCAGAGCAATGCTGAGAGAGAGTATGA 438
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 DB 393 CGAGTTCATTTGTGAATTCAGAGGTAAGAGTTCAGAGCAATGCTGAGAGAGAGTATGA 452

QY	439	GC	AAAGTCCGGGATCATGTACCGCAATCCGTGCATCATCAGAGGCGCTGCATCGC	498
Db	453	GCAAGTCCGGGATCATGTACCGCAATCCGTGCATCATCAGAGGCGCTGCATCGC	512	
QY	499	CTCTGCCGGGTACCAAGTCTCTCTGCCCA	529	
Db	513	CTCTGCCGGGTACCAAGTCTCTCTGCCCA	543	
RESULT 10				
AX319942/c				
LOCUS	AX319942	1362 bp	DNA	linear
DEFINITION	Sequence 1 from Patent WO0181634.			PAT 14-DEC-2001
ACCESSION	AX319942			
VERSION	AX319942.1	GI:17901489		
KEYWORDS	human.			
ORGANISM	human.			
REFERENCE	Human sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
JOURNAL	Galvin, K.A. and Rudolph-Owen, L.A.			
FEATURES	Methods and compositions for the diagnosis and treatment of cardiovascular and tumorigenic disease using 4941			
source	Patent: WO 0181634-A 1 01-NOV-2001;			
	Millennium Pharmaceuticals, Inc. (US)			
CDS	Location/Qualifiers			
	1..1362			
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	ARQRTIIFLRILIVTLVLCAMPNQIRIRIMAAKCRHDMTRSYFRAYMLLPFSEFPLP			
	LSVINPLLYVSSQOFRRVFOVLCRLSLQHNHNEKRLVHNSITDSARFVORPPI			
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	HEV"			
BASE COUNT	263 a	435 c	362 g	302 t
ORIGIN				
Query Match	26.7%;	Score 506;	DB 6;	Length 1362;
Best Local Similarity	100.0%;	Pred. No. 3e-291;		
Matches	506;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1124	TCGAACCTTCAGTCTCTCGTGAACCAATTCCTCTGCAGACAGCAATTGGCTGTTTGGCGCTGA	1183	
Db	1362	TCGAACCTTCAGTCTCTCGTGAACCAATTCCTCTGCAGACAGCAATTGGCTGTTTGGCGCTGA	1303	
QY	1184	GTTGGGCTCTAGTACTGAGACCTCAATGACTGGGACTAGACTGGGGCTGGCCCTCGCT	1243	
Db	1302	GTTGGGCTCTAGTACTGAGACCTCAATGACTGGGACTAGACTGGGGCTGGCCCTCGCT	1243	
QY	1244	CTGAAAGTGTCTTAAGAAATCTTCTCAGTTCCTCTGTCAGAGAGACTGGCGCGGAGCC	1303	
Db	1242	CTGAAAGTGTCTTAAGAAATCTTCTCAGTTCCTCTGTCAGAGAGACTGGCGCGGAGCC	1183	
QY	1304	GAAAGCAACGGGCGCTGCACAAAGCGGGCGCTGTGCGTGGTGGAGTGGCGCATGTACGGG	1363	
Db	1182	GAAAGCAACGGGCGCTGCACAAAGCGGGCGCTGTGCGTGGTGGAGTGGCGCATGTACGGG	1123	
QY	1364	CAGGCGCTTCTGTGTTGGCTGTGTCAGACAGACAGGCGGACAGACAGCTGCACGAA	1423	
Db	1122	CAGGCGCTTCTGTGTTGGCTGTGTCAGACAGACAGGCGGACAGACAGCTGCACGAA	1063	
QY	1424	CACCCGCGAAACTGCTGCGAGAGACACCGGTGTACAGAGCGGGGTGTATGACCGAGCTGAG	1483	

	Dn	1062	CACCGGCGGAAGTGTCTGGAGCACCCTGTACGAGCGGGTTGATGCACCAACTG	1003
OY	1484	GTAAGAAAAAAGTCITCCAGAAGGGAGAGATCATGTACGCCCGGAAAGTAGAACCTTG	1543	
Dn	1002	GTAGAAAACAAGTCTCCGAGAAGGGAGAGATCATGTACCCCCGGAAGTAGAACCTTG	943	
OY	1544	CCAGTCGCTGTGGATTGGCCGCGCACCATCATCTCCGAAATCTGTTGGGCATCCAGCA	1603	
Dn	942	CCAATCGTCGCTTGGGTGGCCCGCAGCCATCATCTCCGAATCTGTTGGGCATCCAGCA	883	
OY	1604	TACGGCCAATGTACACACATTCAGCC	1629	
Dn	882	TACGGCCAATGTACACACATTCAGCC	857	
RESULT 11 AF034633/c				
LOCUS	AF034633	1362 bp	mRNA	linear PRI 13-JUL-1998
DEFINITION	Homo sapiens orphan G protein-coupled receptor (GPR39) mRNA,			
complete cds.				
ACCESSION	AF034633			
VERSION	AF034633.1	GI:2654160		
KEYWORDS				
SOURCE				
ORGANISM	Homo sapiens. Homo sapiens. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	' 1 (bases 1 to 1362)			
AUTHORS	Mckee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feigheimer,S.D., Hreniak,D.L., Smith,R.G., Howard,A.D. and Van der Plieg,L.H. Cloning and characterization of two human G protein-coupled receptor genes (GPR38 and GPR39) related to the growth hormone secretagogue and neurotensin receptors <i>Genomics</i> 46 (3), 426-434 (1997)			
JOURNAL MEDLINE PUBMED	98110578 9411746			
REFERENCE	2 (bases 1 to 1362)			
AUTHORS	Mckee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D., Hreniak,D.L., Smith,R.G., Van Der Plieg,L.H.T. and Howard,A.D. Direct Submission Submitted (17-NOV-1997) Biochemistry and Physiology, Merck and Co.,, Inc., PO Box 2000, Rahway, NJ 07065, USA			
TITLE JOURNAL	Location/Qualifiers			
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CDS	/gene="GPR39"			
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	/protein_id="AAC26082.1"			
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BASE COUNT	263 a	435 c	362 g	302 t
ORIGIN				

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Db 131 CTTGACAGCTCTTTTCCCAAGCAAGAGAGATTTTCAACTGTTTCAACCCGGGCA 72
QY 1834 GTTGCGTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAA 1888
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Db 71 GTTGCGTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAA 17
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RESULT 14
AX093191 396 bp DNA linear PAT 30-MAR-2001
LOCUS
DEFINITION Sequence 9 from Patent WO0118046.
ACCESSION AX093191 GI:13509640
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 396)
AUTHORS Xu, J. and Stolk, J. A.
TITLE Ovarian tumor sequences and methods of use therefor
JOURNAL Patent: WO 0118046-A 9 15-MAR-2001;
CORIXA CORPORATION (US)
FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 1. .396
/note="n = A,T,C or G"
BASE COUNT 90 a 117 c 95 g 92 t 2 others
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Query Match 16.7%; Score 316; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.9e-177; Mismatches 0; Indels 0; Gaps 0;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 274 CATCGCGGCACTTTTGGGATGTTCTTGGCTTCAGGCTTTGGGCTGCAATCCAGTG 333
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Db 5 CATCGCGGCACTTTTGGGATGTTCTTGGCTTCAGGCTTTGGGCTGCAATCCAGTG 64
|||||
QY 334 CTACCAAGTGTGAAGATTCACAGTGAACAGACAGTCTCTCCCGAGTTATTGTGA 393
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QY 394 TTGCACGGGAGTGTCAAGCATGTGTGAGAAAGAGTGAAGCAAGTCCGGGAT 453
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Db 125 TTGCACGGGAGTGTCAAGCATGTGTGAGAAAGAGTGAAGCAAGTCCGGGAT 184
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QY 454 CATGTACCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTTCCCGGATACA 513
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Db 185 CATGTACCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTTCCCGGATACA 244
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QY 514 GTTCCTTCTGCTCCCGAGGAAACTGAACATGTTGATCAGCTGCTGCAACCCCTCT 573
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Db 245 GTTCCTTCTGCTCCCGAGGAAACTGAACATGTTGATCAGCTGCTGCAACCCCTCT 304
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QY 574 TTGTACGGGCAAGG 589
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Db 305 TTGTACGGGCAAGG 320
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RESULT 15
AX093381 369 bp DNA linear PAT 30-MAR-2001
LOCUS
DEFINITION Sequence 199 from Patent WO0118046.
ACCESSION AX093381 GI:13509829
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 369)
AUTHORS Xu, J. and Stolk, J. A.
TITLE Ovarian tumor sequences and methods of use therefor
JOURNAL Patent: WO 0118046-A 199 15-MAR-2001;
CORIXA CORPORATION (US)
FEATURES
source
1. .369
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 1. .369
/note="n = A,T,C or G"
BASE COUNT 82 a 109 c 90 g 86 t 2 others
ORIGIN
Query Match 16.6%; Score 315; DB 6; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.2e-176; Mismatches 0; Indels 0; Gaps 0;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 309 CAGGCTTGGCGCTGCAATCCAGTGTACAGTGTGAAGATTCACGTGAACAGT 368
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Db 30 CAGGCTTGGCGCTGCAATCCAGTGTACAGTGTGAAGATTCACGTGAACAGT 89
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QY 369 GCTCCTCCCCGAGTTCATTGTGAATTGCAAGGTTGAACGTTCAAGACATGTGAGAAG 428
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Db 90 GCTCCTCCCCGAGTTCATTGTGAATTGCAAGGTTGAACGTTCAAGACATGTGAGAAG 149
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QY 429 AAGTATGAGCAAGATCCGGGATGATGATCCGCAAGTCTGTGATCATCAGCGGCT 488
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Db 150 AAGTATGAGCAAGATCCGGGATGATGATCCGCAAGTCTGTGATCATCAGCGGCT 209
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QY 489 GTCTCATGCGCTTGGCGGATGATGATCCGCAAGTCTGTGATCATCAGCGGCT 548
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Db 210 GTCTCATGCGCTTGGCGGATGATGATCCGCAAGTCTGTGATCATCAGCGGCT 269
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QY 549 GCATCAGTGTGCAACACCCCTCTTTGTAAAGGCGCAAGGCGCAAGAAAGGGAAGTT 608
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Db 270 GCATCAGTGTGCAACACCCCTCTTTGTAAAGGCGCAAGGCGCAAGAAAGGGAAGTT 329
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QY 609 CTGCTCGGCGCTCA 623
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Db 330 CTGCTCGGCGCTCA 344
|||||
RESULT 16
AC010974/c 147131 bp DNA linear PRI 01-MAR-2002
LOCUS
DEFINITION Homo sapiens BAC clone RP11-159N20 from 2, complete sequence.
ACCESSION AC010974
VERSION AC010974.9 GI:19033964
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 147131)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 147131)
AUTHORS VanBrunt, A. and Strommatt, C.
TITLE The sequence of Homo sapiens BAC clone RP11-159N20
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 147131)
AUTHORS Waterston, R. H.
TITLE Direct Submission
JOURNAL Submitted (28-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 147131)
AUTHORS Waterston, R. H.
TITLE Direct Submission

JOURNAL

Submitted (23-MAR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE
5 (bases 1 to 147131)

AUTHORS

Waterston, R.

JOURNAL

Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 1, 2002 this sequence version replaced gi:13435273.

COMMENT

Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: saplens@wustl.wustl.edu
----- Summary Statistics -----
Center project name: H_NH0159N20

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P. Y., Zhao, B., Frengen, E., Tatenno, M., Catanese, J. J. and de Jong, P. J. (1996) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-458A7, 200 bp overlap; the clone sequenced to the right is RP11-258B17. Actual start of this clone is at base position 1 of RP11-159N20; actual end is at base position 147131 of RP11-159N20.

FEATURES

source

There are polymorphic base differences in the overlap between the clone RP11-159N20 and RP11-258B17.

Location/Qualifiers

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1. 147131
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  /db_xref="taxon:9606"
  /chromosome="2"
  /map="2"
  /clone="RP11-159N20"
  /clone_1lb="RPCT-11"
  21. 67
  repeat_region
  /rpt_family="MIR"
  118. 1013
  repeat_region
  /rpt_family="L1"
  984. 1176
  /note="match to EST BG200048 (NID:g13721735)"
  991. 1176
  /note="match to EST BG184021 (NID:g13705708)"
  991. 1176
  /note="match to EST BG187166 (NID:g13708853)"
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  /rpt_family="Alu"
repeat_region 1525. 1552
  /rpt_family="(TTTA)n"
repeat_region 1526. 1814
  /rpt_family="Alu"
repeat_region 2299. 2596
  /rpt_family="Alu"
repeat_region 4880. 5129
  /rpt_family="MaLR"
repeat_region 5738. 5757
  /rpt_family="(TG)n"
repeat_region 6131. 6178
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  7310. 7364
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  7811. 7881
  /rpt_family="MIR"
repeat_region 8227. 8260
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  8373. 8683
  /rpt_family="L1"
  8640. 9120
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  8776. 8838
  /rpt_family="MIR"
  8810. 9257
  /note="match to EST AA434316 (NID:g2139230) zw24e08.r1"
  9348. 9395
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  9731. 9895
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  9743. 9895
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  15767. 15789
  /rpt_family="AT-rich"
  15864. 18081
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  16665. 17055
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  16665. 16984
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  misc_feature
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----- Project Information
Center project name: GUSG
Center clone name: CH230-71J19
Summary Statistics
Sequencing vector: Plasmid:
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 82161 bases at least Q40
Consensus quality: 88014 bases at least Q30
Consensus quality: 92229 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 52 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
1165: contig of 1165 bp in length
1166: gap of unknown length
1266: contig of 1381 bp in length
2647: gap of unknown length
2747: gap of unknown length
4305: contig of 1559 bp in length
4306: gap of unknown length
4405: contig of 1442 bp in length
5847: gap of unknown length
5848: contig of 1648 bp in length
7595: gap of unknown length
7596: contig of 1151 bp in length
8846: gap of unknown length
8847: contig of 1117 bp in length
10063: gap of unknown length
10163: contig of 1318 bp in length
11481: gap of unknown length
11581: contig of 1071 bp in length
12652: gap of unknown length
12752: contig of 1004 bp in length
13755: gap of unknown length
13756: contig of 1043 bp in length
13856: gap of unknown length
14899: contig of 1043 bp in length
14900: gap of unknown length
15000: contig of 1179 bp in length
16179: gap of unknown length
16278: contig of 1436 bp in length
17714: gap of unknown length
17815: contig of 1691 bp in length
19505: gap of unknown length
19605: contig of 2279 bp in length
21884: gap of unknown length
21885: contig of 1585 bp in length
23569: gap of unknown length
23570: contig of 1760 bp in length
25429: gap of unknown length
25530: contig of 1294 bp in length
26823: gap of unknown length
26923: contig of 1578 bp in length
28501: gap of unknown length
28502: contig of 1030 bp in length
28602: gap of unknown length
28631: contig of 1082 bp in length
29731: gap of unknown length
30813: contig of 1716 bp in length
30913: gap of unknown length
32629: gap of unknown length
32729: contig of 1173 bp in length
33902: gap of unknown length
34002: contig of 1364 bp in length
35366: gap of unknown length
35466: contig of 1651 bp in length
37117: gap of unknown length
37217: contig of 1608 bp in length
38825: gap of unknown length
38925: contig of 1608 bp in length

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38926 41573: contig of 2648 bp in length
41574 41673: gap of unknown length
41674 43020: contig of 1347 bp in length
43021 43120: gap of unknown length
43121 44790: contig of 1670 bp in length
44791 44890: gap of unknown length
44891 46626: contig of 1736 bp in length
46627 46726: gap of unknown length
46727 47819: contig of 1093 bp in length
47820 47919: gap of unknown length
47920 49621: contig of 1702 bp in length
49622 49721: gap of unknown length
49722 51446: contig of 1725 bp in length
51447 51546: gap of unknown length
51547 53382: contig of 1836 bp in length
53383 53482: gap of unknown length
53483 55863: contig of 2381 bp in length
55864 55963: gap of unknown length
55964 58398: contig of 2435 bp in length
58399 58498: gap of unknown length
58499 61923: contig of 3425 bp in length
61924 62023: gap of unknown length
62024 65252: contig of 3229 bp in length
65253 65352: gap of unknown length
65353 67262: contig of 1910 bp in length
67263 67362: gap of unknown length
67363 69711: contig of 2348 bp in length
69711 69810: gap of unknown length
69810 73439: contig of 3629 bp in length
73440 73539: gap of unknown length
73540 76475: contig of 2936 bp in length
76476 76575: gap of unknown length
76576 80568: contig of 3993 bp in length
80569 80668: gap of unknown length
80669 84177: contig of 3509 bp in length
84178 84277: gap of unknown length
84278 89159: contig of 4882 bp in length
89160 89259: gap of unknown length
89260 92924: contig of 3665 bp in length
92925 93024: gap of unknown length
93025 96972: contig of 3948 bp in length
96973 97072: gap of unknown length
97073 100972: contig of 3900 bp in length
100973 101072: gap of unknown length
101073 107076: contig of 6004 bp in length
107077 107176: gap of unknown length
107177 113525: contig of 6349 bp in length
113526 113625: gap of unknown length
113626 119430: contig of 5805 bp in length
119431 119530: gap of unknown length
119531 125703: contig of 6173 bp in length.

FEATURES
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1.125703 "Rattus norvegicus"
/db_xref="taxon:10116"

Query Match
Best Local Similarity 100.0% Score 30: DB 2: Length 125703:
Matches 30: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1868 TAGCAGCTGTAAAAAAAAAAAAAAAAAAAAA 1897
Db 37842 TAGCAGCTGTAAAAAAAAAAAAAAAAAAAAA 37813

RESULT 20
AF150733
LOCUS AF150733 487 bp mRNA linear PRI 04-MAY-2000
DEFINITION Homo sapiens AD-014 protein mRNA, complete cds.
ACCESSION AF150733
VERSION AF150733.1 GI:7688664
KEYWORDS Homo sapiens.
SOURCE

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ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 487)
AUTHORS       Fu, S., Gu, Y., Li, Y., Peng, Y., Gu, J., Zhang, L., Jiang, C., Yu, Y.,
              Fu, G., Wang, Y., Chen, Z., and Han, Z.
              A novel gene expressed in human adrenal gland
              Unpublished
TITLE         2 (bases 1 to 487)
JOURNAL       Fu, S., Gu, Y., Li, Y., Peng, Y., Gu, J., Zhang, L., Jiang, C., Yu, Y.,
              Fu, G., Wang, Y., Chen, Z., and Han, Z.
              Direct Submission
              Submitted (12-May-1999) Chinese National Human Genome Center at
              Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
              Shanghai 201203, P. R. China
              Location/Qualifiers
FEATURES      source
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               PEPYVSLIMG"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1871 ACAGCTGTAACAAAAA 1897
|||||
Db 452 ACAGCTGTAACAAAAA 478

RESULT 21
AF082874 1086 bp mRNA linear PLN 20-AUG-1998
LOCUS      Medicago sativa glycolate oxidase mRNA, partial cds.
DEFINITION AF082874
ACCESSION  AF082874
VERSION     AF082874.1 GI:3435305
KEYWORDS
SOURCE      Medicago sativa.
ORGANISM    Medicago sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
REFERENCE   1 (bases 1 to 1086)
AUTHORS     Stout, J.M. and McKersie, B.D.
              Gene expression in alfalfa
              Unpublished
TITLE       2 (bases 1 to 1086)
JOURNAL     Stout, J.M. and McKersie, B.D.
              Direct Submission
              Submitted (07-AUG-1998) Plant Biotechnology Division, Dept of Plant
              Agriculture, University of Guelph, Crop Science Building, Guelph,
              Ont N1G 2W1, Canada
              Location/Qualifiers
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               /db_xref="taxon:3879"
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MDQANDSGLASVAGMNRFLSKVDKQNTSLPFLVKGVLTAEDTLVAQSCAG
IIGPNHGARQLDVYPPNNKGFKEVAAAGRPVFLDGVPRGTNFKALAGASIF
IGRPVYSLEPAEEGAVRKVLQMLRDEFELTMSLSCRSKLEITSDHIVADWDPFVN
PRALPR"
BASE COUNT   332 a      199 c      249 g      306 t
ORIGIN
Query Match  1.4%: Score 27; DB 8; Length 1086;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1871 ACAGCTGTAACAAAAA 1897
|||||
Db 1053 ACAGCTGTAACAAAAA 1079

RESULT 22
AY118558 1114 bp mRNA linear INV 15-JUN-2002
LOCUS      Drosophila melanogaster full insert cDNA.
DEFINITION AY118558
ACCESSION  AY118558
VERSION     AY118558.1 GI:21428533
KEYWORDS   FLY CDNA.
SOURCE      fruit fly
ORGANISM    Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 1114)
AUTHORS     Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
              Champe, M., Chavez, C., Dorsett, V., Dresmek, D., Farfan, D., Frise, E.,
              George, R., Gonzalez, M., Guarin, H., Krommiller, B., Li, P., Liao, G.,
              Miranda, A., Mungall, C.J., Nuno, J., Pacleb, J., Paragas, V., Park, S.,
              Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
              and Ceolnik, S.
              Direct Submission
              Submitted (07-JUN-2002) Berkeley Drosophila Genome Project,
              Lawrence Berkeley National Laboratory, One Cyclotron Road,
              Berkeley, CA 94720, USA
              Sequence submitted by:
              Berkeley Drosophila Genome Project
              Lawrence Berkeley National Laboratory
              Berkeley, CA 94720
              This clone was sequenced as part of a high-throughput process to
              sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
              Science 2000). The sequence has been subjected to integrity checks
              for sequence accuracy, presence of a polyA tail and contiguity
              within 100 kb in the genome. Thus we believe the sequence to
              reflect accurately this particular cDNA clone. However, there are
              artifacts associated with the generation of cDNA clones that may
              have not been detected in our initial analyses such as internal
              priming, priming from contaminating genomic DNA, retained introns
              due to reverse transcription of unspliced precursor RNAs, and
              reverse transcriptase errors that result in single base changes.
              For further information about this sequence, including its location
              and relationship to other sequences, please visit our Web site
              (http://fruitfly.berkeley.edu) or send email to
              cna@fruitfly.berkeley.edu.
              Location/Qualifiers
FEATURES    source
              1..1114
               /organism="Drosophila melanogaster"
               /strain="y; cn bw sp"
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               /gene="CG13601"
               /db_xref="FLYBASE:FBgn0039126"
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PROFMYVYKTRKMAIANGGRVNPPLNEAVALIEGALLGEFIIFSAGLLIFEY
SRITIKENKNEIADSEKMLINMLTENFRLERODAOIREMTYVLADDSNIRFMH
KEPIQEVPEFDPDQASARNPKFDSLDPDQMAFRALHFLDTQIFVGRNRKA
KEALHIDVAVOLEQSLGEAAVAVASLSPKADL"
BASE COUNT      334 a      259 c      278 g      243 t
ORIGIN

Query Match      1.4%; Score 27; DB 3; Length 1114;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1871 ACAGTGTAACAAAAA 1897
|||||
Db 1066 ACAGTGTAACAAAAA 1092

RESULT 23
AX285020      1368 bp      DNA      linear      PAT 20-NOV-2001
LOCATION      Sequence 825 from Patent WO0179556.
DEFINITION   AX285020
ACCESSION    AX285020
VERSION      AX285020.1 GI:17045708
KEYWORDS
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS      Lillie,J., Brown,J.L., Bolt,A. and van Hufel,C.
TITLE        Novel genes, compositions and methods for the identification,
              assessment, prevention, and therapy of human cancers
              Patent: WO 0179556-A 825 25-OCT-2001.
JOURNAL      Millennium Predictive Medicine, Inc. (US)
FEATURES
Source       1..1368
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              /db_xref="taxon:9606"
BASE COUNT   517 a      312 c      321 g      213 t      5 others
ORIGIN

Query Match      1.4%; Score 27; DB 6; Length 1368;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1871 ACAGTGTAACAAAAA 1897
|||||
Db 459 ACAGTGTAACAAAAA 485

RESULT 24
AK026521      1614 bp      mRNA      linear      PRI 29-SEP-2000
LOCUS        Homo sapiens cDNA: FLJ22868 fls, clone KAT02340, highly similar to
DEFINITION   HUMFSLIC Homo sapiens transcription factor S11 mRNA.
ACCESSION    AK026521
VERSION      AK026521.1 GI:10439398
KEYWORDS     oligo capping; fls (full insert sequence).
SOURCE       Homo sapiens signet-ring cell carcinoma cell_line:KATO III cDNA to
              mRNA, clone lib:KAT clone:KAT02340.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (sites)
REFERENCE    1 (sites)
AUTHORS      Watanabe,K., Kunagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,
              Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
              Nakamura,Y., Isogai,T. and Sugano,S.
TITLE        NEDO human cDNA sequencing project
JOURNAL      unpublished

```

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REFERENCE
AUTHORS      2 (bases 1 to 1614)
              Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
              Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE        Direct Submission
JOURNAL      Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
              University of Tokyo, Laboratory of Genome Structure Analysis, Human
              Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
              Japan (E-mail:cdna@leims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
              Fax:81-3-5449-5416)
COMMENT      NEDO human cDNA sequencing project supported by Ministry of
              International Trade and Industry of Japan: cDNA full insert
              sequencing: Research Association for Biotechnology; cDNA library
              construction: 5'-6' 3'-end one pass sequencing: Department of
              Virology and Human Genome Center, Institute of Medical Science,
              University of Tokyo (partly supported by Science and Technology
              Agency).
FEATURES
Source       1..1614
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="KAT02340"
              /cell_line="KATO III"
              /cell_type="signet-ring cell carcinoma"
              /clone_lib="KAT"
              /note="cloning vector pME18SFL3"
              1..1614
              /note="highly similar to HUMFSLIC Homo sapiens
              transcription factor S11 mRNA"
BASE COUNT   557 a      296 c      337 g      424 t
ORIGIN

misc_feature
              1..1614
              /note="highly similar to HUMFSLIC Homo sapiens
              transcription factor S11 mRNA"
BASE COUNT   557 a      296 c      337 g      424 t
ORIGIN

Query Match      1.4%; Score 27; DB 9; Length 1614;
Best Local Similarity 100.0%; Pred. No. 0.00089;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1871 ACAGTGTAACAAAAA 1897
|||||
Db 1581 ACAGTGTAACAAAAA 1607

RESULT 25
BC028978      2625 bp      mRNA      linear      PRI 16-MAY-2002
LOCUS        Homo sapiens, clone IMAGE:3919084, mRNA.
DEFINITION   BC028978
ACCESSION    BC028978
VERSION      BC028978.1 GI:20810049
KEYWORDS
SOURCE       Homo sapiens.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 2625)
REFERENCE    Direct Submission
AUTHORS      Submitted (01-MAY-2002) National Institutes of Health, Mammalian
              Gene Collection (MGC), Cancer Genomics Office, National Cancer
              Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
              USA
REMARK      NIH-MGC Project URL: http://mgc.ncl.nih.gov
              Contact: MGC help desk
              Email: cgaps@ncl.nih.gov
              Tissue Procurement: ATCC/DCFD/PTP
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA Sequencing by: Baylor College of Medicine Human Genome
              Sequencing Center
              Center code: BCM-HGSC
              Web Site: http://www.hgsc.bcm.tmc.edu/cdna/
              Contact: amg@bcm.tmc.edu
              Gunaratne, P.H., Garcia, A.M., Lu, X., Huilyk, S.W., Hale, S.M.,
              Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
              Richards, S., Gibbs, R.A.

```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/URL at: <http://image.llnl.gov>
 Series: IRAX Plate: 42 Row: b Column: 17.
 Location/Qualifiers

FEATURES

1. 2625

source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3919084"
 /tissue="type="Skin, melanotic melanoma."
 /clone_id="NHL_MGC_72"
 /lab_host="DH10B"
 /note="vector: pCMV-SPORT6"
 BASE COUNT 860 a 538 c 502 g 725 t
 ORIGIN

Query Match 1.4%; Score 27; DB 9; Length 2625;
 Best local Similarity 100.0%; Pred. No. 0.00092;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1871 ACAGTGTAAAAA 1897
 Db 2567 ACAGTGTAAAAA 2593

RESULT 26
 AY094780 3155 bp mRNA linear INV 15-APR-2002
 LOCUS Drosophila melanogaster LD11626 full insert cDNA.
 DEFINITION AY094780
 ACCESSION AY094780.1 GI:20151546
 VERSION
 KEYWORDS
 SOURCE Drosophila melanogaster.
 ORGANISM Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 3155)
 AUTHORS Stapleton, M., Brokstein, P., Hong, L., Agdayani, A., Carlson, J., Champe, M., Chavez, C., Dorsett, Y., Dresnek, D., Farfan, D., Frise, E., George, R., Gonzalez, M., Guatin, H., Krommiller, B., Li, P., Liao, G., Miranda, A., Mungall, C. J., Nuno, J., Paclet, J., Paragas, V., Park, S., Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Rubin, G. M. and Celisner, S.
 DIRECT SUBMISSION
 Submitted (03-APR-2002) Berkeley Drosophila Genome Project,
 Lawrence Berkeley National Laboratory, One Cyclotron Road,
 Berkeley, CA 94720, USA

TITLE
 JOURNAL
 COMMENT
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Berkeley, CA 94720

This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcriptase errors of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our web site (<http://fruitfly.berkeley.edu>) or send email to cdna@fruitfly.berkeley.edu.

FEATURES
 source
 Location/Qualifiers

1. 3155
 /organism="Drosophila melanogaster"
 /strain="y: cn bw sp"
 /db_xref="taxon:7227"
 /map="43D3-43D3"
 1. 3155
 gene

CDS

/gene="Orcl"
 /note="alignment with genomic scaffold AE003840 and gene has no introns and polyA tail is encoded in the genomic"
 /db_xref="FlyBase:FBgn0022772"
 112..2886

ORIGIN
 BASE COUNT 847 a 864 c 821 g 623 t
 Query Match 1.4%; Score 27; DB 3; Length 3155;
 Best local Similarity 100.0%; Pred. No. 0.00093;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1871 ACAGTGTAAAAA 1897
 Db 3127 ACAGTGTAAAAA 3153

RESULT 27
 AL645986/c 48206 bp DNA linear ROD 19-JUN-2002
 LOCUS Mouse DNA sequence from clone DN-35368 on chromosome 1, complete
 DEFINITION AL645986
 ACCESSION AL645986
 VERSION AL645986.6 GI:18855238
 KEYWORDS
 SOURCE HTG.
 ORGANISM Mus musculus.
 Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

Submitted (18-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 On Feb 21, 2002 this sequence version replaced gi:117529535.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following


```

* 12015 13145: contig of 1131 bp in length
* 13146 13245: gap of unknown length
* 13246 14584: contig of 1339 bp in length
* 14585 14684: gap of unknown length
* 14685 16404: contig of 1720 bp in length
* 16405 16504: gap of unknown length
* 16505 17655: contig of 1151 bp in length
* 17656 17755: gap of unknown length
* 17756 19240: contig of 1485 bp in length
* 19340 19340: gap of unknown length
* 19341 20647: contig of 1307 bp in length
* 20648 20747: gap of unknown length
* 20748 22171: contig of 1424 bp in length
* 22172 22271: gap of unknown length
* 22272 23762: contig of 1491 bp in length
* 23763 23862: gap of unknown length
* 23863 25556: contig of 1694 bp in length
* 25557 25656: gap of unknown length
* 25657 26711: contig of 1055 bp in length
* 26712 26811: gap of unknown length
* 26812 28747: contig of 1936 bp in length
* 28748 28847: gap of unknown length
* 28848 30564: contig of 1717 bp in length
* 30565 30664: gap of unknown length
* 30665 32046: contig of 1382 bp in length
* 32047 32146: gap of unknown length
* 32147 33729: contig of 1583 bp in length
* 33730 33829: gap of unknown length
* 33830 35524: contig of 1695 bp in length
* 35525 35624: gap of unknown length
* 35625 37292: contig of 1668 bp in length
* 37293 37392: gap of unknown length
* 37393 38486: contig of 1094 bp in length
* 38487 38586: gap of unknown length
* 38587 40145: contig of 1559 bp in length
* 40146 40245: gap of unknown length
* 40246 41925: contig of 1680 bp in length
* 41926 42025: gap of unknown length
* 42026 43669: contig of 1644 bp in length
* 43670 43769: gap of unknown length
* 43770 45713: contig of 1944 bp in length
* 45714 45813: gap of unknown length
* 45814 47315: contig of 1502 bp in length
* 47316 47415: gap of unknown length
* 47416 4852: contig of 1437 bp in length
* 4853 48952: gap of unknown length
* 48953 50511: contig of 1559 bp in length
* 50512 50611: gap of unknown length
* 50612 52672: contig of 2061 bp in length
* 52673 52772: gap of unknown length
* 52773 54274: contig of 1502 bp in length
* 54275 54374: gap of unknown length
* 54375 55993: contig of 2619 bp in length
* 55994 57093: gap of unknown length
* 57094 59151: contig of 2422 bp in length
* 59152 59615: gap of unknown length
* 59616 61878: contig of 2263 bp in length
* 61879 61978: gap of unknown length
* 61979 64520: contig of 2442 bp in length
* 64521 64620: gap of unknown length
* 64621 67430: contig of 2810 bp in length
* 67431 67530: gap of unknown length
* 67531 68852: contig of 1322 bp in length
* 68853 68952: gap of unknown length
* 68953 70700: contig of 1748 bp in length
* 70701 70800: gap of unknown length
* 70801 72350: contig of 1550 bp in length
* 72351 72450: gap of unknown length
* 72451 74628: contig of 2178 bp in length
* 74629 74728: gap of unknown length
* 74729 75922: contig of 2194 bp in length
* 75923 77022: gap of unknown length
* 77023 79345: contig of 2323 bp in length

```

```

* 79346 79445: gap of unknown length
* 79446 82316: contig of 2871 bp in length
* 82317 82417: gap of unknown length
* 82418 84866: contig of 2450 bp in length
* 84867 84966: gap of unknown length
* 84967 87959: contig of 2993 bp in length
* 87960 88060 92874: contig of 4815 bp in length.
* 88060 92874: contig of 4815 bp in length.

FEATURES
  source
    1. 92874
    /organism="Rattus norvegicus"
    /db_xref="taxon:10116"
    /clone="CH230-286021"

BASE COUNT      23927 a 19653 c 20425 g 23828 t 5041 others

ORIGIN
Query Match      1.4%; Score 27; DB 2; Length 92874;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1500 GAGAGGAGGAGGATCATGTACGCC 1526
Db 75643 GAGAGGAGGAGGATCATGTACGCC 75669
|||||

```

```

RESULT 29
AL807806/c
LOCUS
DEFINITION
MUS musculus chromosome X clone RP23-67K19, *** SEQUENCING IN
PROGRESS ***, 2 unordered pieces.
ACCESSION
AL807806
VERSION
AL807806.4 GI:22416117
KEYWORDS
HTG: HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 127524)
Whitehead, S.
Direct Submission
Submitted (16-Aug-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonequest@sanger.ac.uk
On Aug 21, 2002 this sequence version replaced gi:21694507.
Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
Project Information
Center project name: BM67K19
Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 127311 bases at least Q40
Consensus quality: 127389 bases at least Q30
Consensus quality: 127413 bases at least Q20
Insert size: 127424; sum-of-ctrls
Insert size: 142249; 4.2% error; agarose-fp
Quality coverage: 8.1lx in Q20 bases; sum-of-ctrls Quality
coverage: 7.35x in Q20 bases; agarose-fp

```

```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 24018: contig of 24018 bp in length
* 24019 24118: gap of 100 bp
* 24119 127524: contig of 103406 bp in length.

```

```

FEATURES
  source
    Location/Qualifiers
      1..127524
        /organism="Mus musculus"
        /db_xref="taxon:10090"
        /chromosome="X"
        /clone_11b="RPCI-23"
        /clone_11b="RPCI-23"
        /note="assembly_fragment:00530"
      misc_feature
        24119..127524
          /note="assembly_fragment:00777.0"
      misc_feature
        37921 a 23572 c 23574 g 42574 t 100 others
      BASE COUNT
      ORIGIN

Query Match
  Best Local Similarity 100.0%; Pred. No. 0.0012;
  Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1871 ACAGTGTAACAAAAA 1897
|||||
DB 87560 ACAGTGTAACAAAAA 87534

RESULT 30
AL645938 138851 bp DNA linear ROD 11-APR-2002
LOCUS Mouse DNA sequence from clone RP23-15E24 on chromosome 1, complete
DEFINITION
ACCESSION AL645938
VERSION AL645938.9 GI:20145949
KEYWORDS HTG.
SOURCE house mouse.
ORGANISM Mus musculus.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
  1
  Corby, N.
  Direct Submission
  Submitted (11-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
  Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
  humquerry@sanger.ac.uk; clonerequests@sanger.ac.uk
  On Apr 12, 2002 this sequence request replaced gi:20135756.
  During sequence assembly data is compared from overlapping clones.
  Where differences are found these are annotated as variations
  together with a note of the overlapping clone name. Note that the
  variation annotation may not be found in the sequence submission
  corresponding to the overlapping clone, as we submit sequences with
  only a small overlap as described above.
  This sequence was finished as follows unless otherwise noted: all
  regions were either double-stranded or sequenced with an alternate
  chemistry or covered by high quality data (i.e., phred quality >=
  30); an attempt was made to resolve all sequencing problems, such
  as compressions and repeats; all regions were covered by at least
  one plasmid subclone or more than one M13 subclone; and the
  assembly was confirmed by restriction digest. The following
  abbreviations are used to associate primary accession numbers given
  in the feature table with their source databases: Em., EMBL; SW.,
  SWISSPROT; Tr., TrEMBL; Wp., WormPeP; Information on the WormPeP
  database can be found at
  http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-15E24 is
  from the RPCI-23 Mouse PAC Library
  constructed by the group of Pieter de Jong.
  For further details see http://www.chori.org/dacpac/home.htm
  VECTOR: pBAC3.6.

FEATURES
  source
    Location/Qualifiers
      1..138851
        /organism="Mus musculus"
        /db_xref="taxon:10090"
        /chromosome="X"
        /clone="RP23-15E24"
        /clone_11b="RPCI-23"
      BASE COUNT
      ORIGIN
    40695 a 25907 c 27333 g 44916 t

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```

Query Match
  Best Local Similarity 100.0%; Pred. No. 0.0012;
  Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1871 ACAGTGTAACAAAAA 1897
|||||
DB 31571 ACAGTGTAACAAAAA 31545

RESULT 31
AC126321 151602 bp DNA linear HTG 05-JUL-2002
LOCUS Polypertus bichir clone -22F22, *** SEQUENCING IN PROGRESS ***, 1
DEFINITION
ACCESSION AC126321
VERSION AC126321.1 GI:21699164
KEYWORDS HTG; HTGS_PHASE2; HTGS_FULFILL; HTGS_ACTIVEFIN.
SOURCE Polypertus bichir.
ORGANISM Polypertus bichir.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Actinopterygii; Polypteriformes; Polypteridae; Polypterus.

REFERENCE
  1 (bases 1 to 151602)
  Birren, B., Nusbaum, C. and Lander, E.
  Polypertus bichir, clone -22F22
  Unpublished
  2 (bases 1 to 151602)
  Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
  Batta, N., Bastien, V., Bloom, T., Boguslavsky, L., Bokkhalter, B.,
  Camarata, J., Chang, J., Chazaro, T., Choepel, Y., Collymore, A.,
  Cook, A., Cooke, P., DeArrellano, R., Dewar, K., Diaz, J.S., Dodge, S.,
  Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
  Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
  Horton, L., Huine, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
  Karatas, A., Kellis, C., Landers, T., Levine, R., Lindblad-Toh, K.,
  Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
  McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V.,
  Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
  O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
  Plunkhang, P., Plerre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
  Roman, J., Roy, A., Schauer, S., Schupbach, R., Seaman, S., Severy, P.,
  Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
  Testaye, S., Theodores, J., Topham, K., Travers, M., Vassiliev, H.,
  Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zalnoun, J.,
  Zembek, L., Zimmer, A. and Zody, M.
  Direct Submission
  Submitted (05-JUL-2002) Whitehead Institute/MIT Center for Genome
  Research, 320 Charles Street, Cambridge, MA 02141, USA
  All repeats were identified using RepeatMasker:
  Smit, A.F.A. & Green, P. (1996-1997)
  http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L20497
Center clone name: 22_F_22

-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
  1 151602: contig of 151602 bp in length.

FEATURES
  source
    Location/Qualifiers
      1..151602
        /organism="Polypertus bichir"

```

```

/d/_xref="taxon:31136"
/clone_1ib="Bichir"
BASE COUNT      48679 a 27446 c 26903 g 48574 t
ORIGIN

Query Match      1.4%; Score 27; DB 2; Length 151602;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1869 AGCAGCTGTAAAAA1895
Db 80517 AGCAGCTGTAAAAA80491

RESULT 32
AC027118      170255 bp   DNA   linear   PRI 23-APR-2002
LOCUS
DEFINITION      Homo sapiens chromosome 10 clone RP11-573111, complete sequence.
ACCESSION      AC027118
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS      Smith,D.R.
TITLE      Genome Therapeutics Corporation Sequencing Center: Human Genome
Sequence Data
JOURNAL
REFERENCE      2 (bases 1 to 170255)
AUTHORS      Smith,D.R.
TITLE      Direct Submission
JOURNAL
REFERENCE      Submitted (27-MAR-2002) Genome Therapeutics Corporation, 100 Beaver
AUTHORS      Street, Waltham, MA 02453, USA
TITLE      3 (bases 1 to 170255)
JOURNAL
REFERENCE      Submitted (23-JAN-2002) Genome Therapeutics Corporation, 100 Beaver
AUTHORS      Street, Waltham, MA 02453, USA
TITLE      4 (bases 1 to 170255)
JOURNAL
REFERENCE      Smith,D.R.
TITLE      Direct Submission
JOURNAL
REFERENCE      Submitted (28-MAR-2002) Genome Therapeutics Corporation, 100 Beaver
AUTHORS      Street, Waltham, MA 02453, USA
TITLE      5 (bases 1 to 170255)
JOURNAL
REFERENCE      Direct Submission
AUTHORS      Submitted (23-APR-2002) Genome Therapeutics Corporation, 100 Beaver
JOURNAL      Street, Waltham, MA 02453, USA
COMMENT
FEATURES
source
1. 170255
/organism="Homo sapiens"
/d/_xref="taxon:9606"
/chromosome="10"
/clone="RP11-573111"
/clone_1ib="RP11-573111"
BASE COUNT      53463 a 30250 c 31205 g 55337 t
ORIGIN

Query Match      1.4%; Score 27; DB 9; Length 170255;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1871 ACAGTGTAAAAA1897
Db 136987 ACAGTGTAAAAA137013

RESULT 33
AC074245

```

```

LOCUS      AC074245      179364 bp   DNA   linear   HTG 24-AUG-2000
DEFINITION      Homo sapiens chromosome 2 clone RP11-341F8, WORKING DRAFT SEQUENCE,
ACCESSION      AC074245
VERSION      AC074245.3   GI:9887809
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
ORGANISM      Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS      Waterston,R.H.
TITLE      The sequence of Homo sapiens clone
JOURNAL
REFERENCE      2 (bases 1 to 179364)
AUTHORS      Waterston,R.H.
TITLE      Direct Submission
JOURNAL
REFERENCE      Submitted (22-JUL-2000) Genome Sequencing Center, Washington
AUTHORS      University School of Medicine, 444 Forest Park Parkway, St. Louis,
JOURNAL      MO 63108, USA
COMMENT
On Aug 24, 2000 this sequence version replaced gi:965207.

```

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information -----
Center project name: H_NH0341F08
----- Summary Statistics -----
Sequencing vector: MJ3; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 167601 bases at least Q40
Consensus quality: 170488 bases at least Q30
Consensus quality: 171954 bases at least Q20
Insert size: 179000; agarose-fp
Insert size: 17364; sum-of-contigs
Quality coverage: 4.14 in Q20 bases; agarose-fp
Quality coverage: 4.29 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1477: contig of 1477 bp in length
* 1478 1577: gap of unknown length
* 1578 3799: gap of 2222 bp in length
* 3800 3899: gap of unknown length
* 3900 6403: contig of 2504 bp in length
* 6404 6503: gap of unknown length
* 6504 10328: contig of 3825 bp in length
* 10329 10428: gap of unknown length
* 10429 13400: contig of 2972 bp in length
* 13401 13500: gap of unknown length
* 13501 18872: contig of 5372 bp in length
* 18873 18972: gap of unknown length
* 18973 25292: contig of 6320 bp in length
* 25293 25392: gap of unknown length
* 25393 30836: contig of 5444 bp in length
* 30837 30936: gap of unknown length
* 30937 36567: contig of 5631 bp in length
* 36568 36667: gap of unknown length
* 36668 45290: contig of 8623 bp in length
* 45291 45390: gap of unknown length
* 45391 55146: contig of 9756 bp in length
* 55147 55246: gap of unknown length
* 55247 66342: contig of 11096 bp in length

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* 66343 66442: gap of unknown length
* 66443 76462: contig of 10020 bp in length
* 76463 76562: gap of unknown length
* 76563 89099: contig of 12537 bp in length
* 89100 89199: gap of unknown length
* 89200 102001: contig of 12802 bp in length
* 102002 102101: gap of unknown length
* 102102 119488: contig of 17387 bp in length
* 119489 119589: gap of unknown length
* 119589 135844: contig of 16256 bp in length
* 135845 135945: gap of unknown length
* 135945 153641: contig of 17697 bp in length
* 153642 153741: gap of unknown length
* 153742 175739: contig of 21998 bp in length
* 175740 175839: gap of unknown length
* 175840 177387: contig of 1548 bp in length
* 177388 177488: gap of unknown length
* 177488 179364: contig of 1877 bp in length.

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Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-341F8"
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clone_end:r7
vector_side:left"
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3900..6403
misc_feature /note="assembly_name:Contig12"
6504..10328
misc_feature /note="assembly_name:Contig13"
10429..13400
misc_feature /note="assembly_name:Contig14"
13501..18872
misc_feature /note="assembly_name:Contig15"
18973..25292
misc_feature /note="assembly_name:Contig16"
25393..30836
misc_feature /note="assembly_name:Contig17"
30937..36567
misc_feature /note="assembly_name:Contig18"
36668..45290
misc_feature /note="assembly_name:Contig19"
45391..55146
misc_feature /note="assembly_name:Contig20"
55247..66342
misc_feature /note="assembly_name:Contig21"
66443..76462
misc_feature /note="assembly_name:Contig22"
76563..89099
misc_feature /note="assembly_name:Contig23"
89200..102001
misc_feature /note="assembly_name:Contig24"
102102..119488
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119589..135844
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vector_side:left"
135945..153641
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/note="assembly_name:Contig9"

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BASE COUNT 56993 a 32967 c 33013 g 54383 t 2008 others
ORIGIN

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Query Match 1.4%: Score 27: DB 2: Length 179364;
Best Local Similarity 100.0%: Pred. No. 0.0012;
Matches 27: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1871 ACAGTGTAACAAAAA 1897
Db 166939 ACAGTGTAACAAAAA 166965

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RESULT 34
AC074389
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 195782)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
9847074
2 (bases 1 to 195782)
Cordes,M., Doeber,A., Hawkins,M. and Kozlowicz,A.
The sequence of Homo sapiens BAC clone RP11-510K8
Unpublished (2002)
3 (bases 1 to 195782)
Waterston,R.H.
Direct Submission
Submitted (30-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 195782)
Waterston,R.H.
Direct Submission
Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 195782)
Waterston,R.
Direct Submission
Submitted (10-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 3, 2002 this sequence version replaced gi:14209801.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0510K08
-----

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION: The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping

Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.mrgri.nih.gov/DIR/GB/CHR/>, send <mailto:egreen@mrgri.nih.gov>, or see <http://genome.wustl.edu/usc>

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frenken, E., Tatem, M., Catanesse, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-16P10, 2000 bp overlap. Actual start of this clone is at base position 112086 of RP11-16P10; actual end is at base position 195782 of RP11-510K8.

Data from AC093734 was used to finish this clone, AC074389. There is single M13 clone coverage from 64639 to 64773.

FEATURES

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   /db_xref="taxon:9606"
   /chromosome="7"
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   /clone_1lb="RP11-11"
   3. 269
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   304. 372
   /rpt_family="MIR"
   558. 736
   /rpt_family="Alu"
   807. 844
   /rpt_family="(TTCA)n"
   946. 1126
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   3175. 3277
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   3599. 3761
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   4030. 4073
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7375. 7426
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7503. 7784
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7650. 7671
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7816. 8125
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8100. 8151
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(NID:g14340025)"
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/note="similar to Homo sapiens EST B1831665
(NID:g15943215)"
8973. 9366
/note="similar to Homo sapiens EST BM153036
(NID:g1717822)"
8976. 9411
/note="similar to Homo sapiens EST AA449551 (NID:g2163301)
zx08b07.r1"
8982. 9519
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xz20d05.x1"

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Query Match

1.4%; Score 27; DB 9; Length 195782;

Best Local Similarity 100.0%; Pred. No. 0.0012;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1871 ACAGGTGTAACAAAAA 1897
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Db 55644 ACAGGTGTAACAAAAA 55670

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misc_feature 79728..97908 /note="assembly-fragment"
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misc_feature /note="assembly-fragment"
vector_side:right"
vector_side:left"
BASE COUNT 63310 a 40377 c 40347 g 63732 t 1806 others
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Best Local Similarity 100.0%: Pctid.No.0.0012:
Matches 27: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 1871 ACAGCTGTAATAAAAAAAAAAAAAA 1897
|||||
Db 204291 ACAGCTGTAATAAAAAAAAAAAAAA 204317

RESULT 36
AC110232 212690 bp DNA linear HTG 15-MAY-2002
AC110232 Mus musculus clone Rp23-67H24, WORKING DRAFT SEQUENCE, 26 ordered
pieces
AC110232
AC110232.4 GI:20800203
HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 212690)
Birten,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone Rp23-67H24
Unpublished
2 (bases 1 to 212690)
Birten,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepe,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,W., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Larocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Maclean,C., McDonald,P., Major,J., Margulis,N., Matthews,C.,
McEwan,P., McKernan,K., Meldrum,J., Meneses,L., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Piere,N., Pollara,V., Raymond,C.,
Rella,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S.,
Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 212690)
Birten,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhalter,B.,
Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepe,Y., Colangelo,M., Collins,S., Collymore,A.,

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TITLE JOURNAL COMMENT

```

Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,W., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Larocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Maclean,C., McDonald,P., Major,J., Margulis,N., Matthews,C.,
McEwan,P., McKernan,K., Meldrum,J., Meneses,L., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Piere,N., Pollara,V.,
Raymond,C., Rella,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (15-MAY-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 15, 2002 this sequence version replaced g1:20531892.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green,P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Center project name: L22352
Center clone name: 67_H-24

----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 203101 bases at least Q40
Consensus quality: 204725 bases at least Q30
Consensus quality: 205415 bases at least Q20
Insert size: 210000; agarose-fp
Insert size: 210190; sum-of-ctrls
Quality coverage: 14.3 in Q20 bases; agarose-fp
Quality coverage: 14.3 in Q20 bases; sum-of-ctrls

-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1
* 619 718: gap of 100 bp
* 719 1375: contig of 618 bp in length
* 1376 1475: gap of 100 bp
* 1476 2114: contig of 638 bp in length
* 2115 2214: gap of 100 bp
* 2215 2843: contig of 629 bp in length
* 2844 2943: gap of 100 bp
* 2944 3067: contig of 124 bp in length
* 3068 3167: gap of 100 bp
* 3168 3352: contig of 185 bp in length
* 3353 3452: gap of 100 bp
* 3453 4030: contig of 578 bp in length
* 4031 4130: gap of 100 bp
* 4131 4757: contig of 627 bp in length
* 4758 4857: gap of 100 bp
* 4858 5064: contig of 207 bp in length
* 5065 5164: gap of 100 bp
* 5165 6283: contig of 1119 bp in length

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*	6284	6383:	gap of	100	bp
*	6584	7505:	contig of 1122	bp	in length
*	7506	7605:	gap of	100	bp
*	7606	8326:	contig of 721	bp	in length
*	8327	8426:	gap of	100	bp
*	8427	9838:	contig of 1412	bp	in length
*	9839	9938:	gap of	100	bp
*	9939	11695:	contig of 1757	bp	in length
*	11696	11795:	gap of	100	bp
*	11796	15821:	contig of 4026	bp	in length
*	15822	15921:	gap of	100	bp
*	15922	20158:	contig of 4237	bp	in length
*	20159	20258:	gap of	100	bp
*	20259	26711:	contig of 6453	bp	in length
*	26712	26811:	gap of	100	bp
*	26812	35766:	contig of 8949	bp	in length
*	35761	35860:	gap of	100	bp
*	35861	47391:	contig of 11531	bp	in length
*	47392	47491:	gap of	100	bp
*	47492	59604:	contig of 12113	bp	in length
*	59605	59704:	gap of	100	bp
*	59705	74256:	contig of 14554	bp	in length
*	74259	74358:	gap of	100	bp
*	74359	93680:	contig of 19322	bp	in length
*	93681	93780:	gap of	100	bp
*	93781	113564:	contig of 19784	bp	in length
*	113565	113664:	gap of	100	bp
*	113665	134201:	contig of 20537	bp	in length
*	134202	134301:	gap of	100	bp
*	134302	125666:	contig of 25367	bp	in length
*	159669	159768:	gap of	100	bp
*	159769	21690:	contig of 53922	bp	in length

FEATURES
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misc_feature	20259..26711
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Query Match		1.48;	Score 27;	DB 2;
Best Local Similarity		100.08;	Pred. No. 0.0012;	Length 212690;
Matches 27;	Conservative 0;	Mismatches 0;	Indels 0;	Caps 0;
OY	1871	ACAGGTGTAAAAAAAAAAAAAAAA	1897	
Db	42174	ACAGGTGTAAAAAAAAAAAAAAAA	42200	

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
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AC069297	linear HTG 25-MAY-2000	AC069297	AC069297	HTG. HTGS_PHASE1. HTGS_DRAFT.	Mus musculus	Mus musculus
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AC069297	DRAFT SEQUENCE, 19 unordered pieces.	AC069297	AC069297	HTG. HTGS_PHASE1. HTGS_DRAFT.	Mus musculus	Mus musculus
AC069297	1 GI:8072378	AC069297	AC069297	HTG. HTGS_PHASE1. HTGS_DRAFT.	Mus musculus	Mus musculus
AC069297	strain C57BL6/J, WORKING	AC069297	AC069297	HTG. HTGS_PHASE1. HTGS_DRAFT.	Mus musculus	Mus musculus

REFERENCE
AUTHORS
1 (bases 1 to 214411)
Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,

TITLE	NISC Mouse Sequencing Initiative
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 21441)
AUTHORS	Green, E.D.
TITLE	Direct Submission
JOURNAL	Submitted (25-MAY-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gathersburg, MD 20877, USA
COMMENT	----- Genome Center

```

Center code: NISC
Center site: http://www.nisc.nih.gov
Contact: nisc_mouse@nih.gov
-----
Project Information
Center project name: us
Center clone name: 002N07
-----
Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 204942 bases at least Q40
Consensus quality: 207550 bases at least Q30
Consensus quality: 209017 bases at least Q20
Insert size: 205000; agarose-fp
Insert size: 248000; pulse-field-gel
Insert size: 212611; sum-of-ctrls
Quality coverage: 5.40x in Q20 bases; agarose-fp
Quality coverage: 4.46x in Q20 bases; pulse-field-gel
Quality coverage: 5.20x in Q20 bases; sum-of-ctrls
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

```

* This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1	2371	contig of 2371 bp in length
2372	2471	gap of unknown length
2472	7036	contig of 4565 bp in length
7037	7136	gap of unknown length
7137	11837	contig of 4701 bp in length
11838	11937	gap of unknown length
11938	16456	contig of 4519 bp in length
16457	16556	gap of unknown length
16557	24064	contig of 7508 bp in length
24065	24164	gap of unknown length
24165	30372	contig of 6208 bp in length
30373	30472	gap of unknown length
30473	38478	contig of 8006 bp in length
38479	38578	gap of unknown length
38579	47748	contig of 9170 bp in length
47749	47848	gap of unknown length
47849	56374	contig of 8526 bp in length
56375	56474	gap of unknown length
56475	68247	contig of 11773 bp in length
68248	68347	gap of unknown length
68348	78809	contig of 10462 bp in length
78810	78909	gap of unknown length
78910	89312	contig of 10303 bp in length
89313	89312	gap of unknown length
89367	99267	contig of 9955 bp in length
99268	99367	gap of unknown length
99368	110419	contig of 11052 bp in length
110420	110519	gap of unknown length
110520	124151	contig of 13632 bp in length
124152	124251	gap of unknown length
124252	141079	contig of 16828 bp in length
141080	141179	gap of unknown length
141180	160980	contig of 19801 bp in length
160981	161080	gap of unknown length
161081	185614	contig of 24534 bp in length
185615	185714	gap of unknown length
185715	214411	contig of 28697 bp in length.

FEATURES
 source
 1. 214411
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /chromosome="12"
 /clone="RP23-2N7"
 /clone_1lb="RPC1 mouse BAC library 23"
 1. 2371
 /note="assembly-fragment"
 2472. 7036
 /note="assembly-fragment"
 7137. 11837
 /note="assembly-fragment"
 11938. 16456
 /note="assembly-fragment"
 16557. 24064
 /note="assembly-fragment"
 24165. 30372
 /note="assembly-fragment"
 clone_end:77
 vector_side:left"
 30473. 38478
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 38579. 47748
 /note="assembly-fragment"
 47849. 56374
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 56475. 68247
 /note="assembly-fragment"
 68348. 78809
 /note="assembly-fragment"
 78910. 89212
 /note="assembly-fragment"

misc_feature
 89313. 99267
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 misc_feature
 99368. 110419
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 misc_feature
 110520. 124151
 /note="assembly-fragment"
 misc_feature
 124252. 141079
 /note="assembly-fragment"
 misc_feature
 141180. 160980
 /note="assembly-fragment"
 misc_feature
 161081. 185614
 /note="assembly-fragment"
 misc_feature
 185715. 214411
 /note="assembly-fragment"
 BASE COUNT 59577 a 46639 c 46482 g 59706 t 2007 others
 ORIGIN

Query Match 1.4% Score 27; DB 2; Length 214411;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1871 ACAGTGTAAAAA 1897
 Db 80773 ACAGTGTAAAAA 80799

RESULT 38
 AL133395/c
 LOCUS
 DEFINITION
 Human DNA sequence from clone RP11-446H13 on chromosome 10.
 Contains the 3' end of the gene for a novel protein similar to
 KIAA1059 (ortholog of mouse VPS10 domain receptor protein SORCS),
 an RPL23A (60S ribosomal protein 23A) pseudogene, ESTs, STS and
 GSSs, complete sequence.

ACCESSION
 AL133395
 VERSION
 AL133395.21 GI:10045255
 KEYWORDS
 HMG; KIAA1059; RPL23A; SORCS; VPS10 domain.
 SOURCE
 ORGANISM
 human.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Submitted (11-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 On Sep 9, 2000 this sequence version replaced gi:9943953.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 only a small overlap as described above.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information
 on the WormPEP database can be found at
 http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 10, constructed by the Sanger Centre Chromosome 10
 Mapping Group. Further information can be found at
 http://www.sanger.ac.uk/HGS/Chr10

This sequence is the entire insert of clone RP11-446H13. The true
 left end of clone RP11-699H2 is at 128287 in this sequence. The
 true right end of clone RP11-41D21 is at 75932 in this sequence.
 This sequence has been finished according to sequence map criteria
 as follows. An attempt is made to resolve all sequencing problems,
 such as compressions and repeats, but not necessarily within known
 annotated repeat sequence elements. Where the sequence is
 ambiguous, there is an annotation using the 'unsure' feature key.
 RP11-446H13 is from the library RPC1-11.2 constructed by the group

repeat_region /note="MIR repeat: matches 160. .250 of consensus"
 31806. .31957
 /note="MIR repeat: matches 52. .207 of consensus"
 repeat_region 32065. .32231
 /note="LMC4 repeat: matches 6030. .6135 of consensus"
 repeat_region 32274. .32437
 /note="LMC/D repeat: matches 5559. .5728 of consensus"
 misc_feature complement(32526. .33068)
 /note="match: GSS: Em:A0277814"
 repeat_region 32562. .33031

Query Match 1.4%; Score 27; DB 9; Length 217929;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1871 ACAGTGTAAAAA 1897
 Db 204102 ACAGTGTAAAAA 204076

RESULT 39
 AF297044 1275 bp mRNA linear PLN 10-OCT-2000
 LOCUS Zea mays homocysteine S-methyltransferase-1 mRNA, complete cds.
 DEFINITION AF297044
 ACCESSION AF297044
 VERSION AF297044.1 GI:10732784
 KEYWORDS
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 1275)
 AUTHORS Li, C. and Tarczynski, M.
 TITLE Direct Submission
 JOURNAL Submitted (18-AUG-2000) T&T-D-OT, Pioneer Hi-Bred International
 Inc., 7300 NW 62nd Ave., Johnston, IA 50131, USA
 FEATURES
 source Location/Qualifiers
 1. .1275
 /organism="Zea mays"
 /db_xref="taxon:4577"
 106. .1077
 /product="homocysteine S-methyltransferase-1"
 /codon_start=1
 /protein_id="AA022537.1"
 /db_xref="GI:10732785"
 /translation="MGVLEDIVARAGCAVITDGGFATOLEALGADINDPLMSACLIT
 RPHLVKEVHMQLAGADVIITSSYQATITFGTARQMSVAEADLRTSVKLANEARD
 EFKSTLRKSPITNRALVANSISGAYIADGSEYSGADITAKLDFHRRRLQ
 VLASGPDLLAFEAIPNOMEAQLVLEELKQVQIPMWIFSSYDGNKLSGSEFADC
 LKINASEKVAVVGNCPTPQFIEGICERKQTKALAVYPNGSEVWDRAKRWLPV
 ECLGKSFDAKRMQEGASLIGCCRTPTPTIRAVSKILKRGTH"

BASE COUNT 341 a 301 c 356 g 277 t
 ORIGIN

Query Match 1.4%; Score 26; DB 8; Length 1275;
 Best Local Similarity 100.0%; Pred. No. 0.0035;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1872 CAGCTGTAAAAA 1897
 Db 1196 CAGCTGTAAAAA 1221

RESULT 40
 AF176571 1409 bp mRNA linear PLN 03-NOV-1999
 LOCUS Alternaria alternata exoglucanase (Cl) mRNA, complete cds.
 DEFINITION AF176571
 ACCESSION AF176571
 VERSION AF176571.1 GI:6179888
 KEYWORDS
 ORGANISM Alternaria alternata.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria;
 Alternaria alternata group.
 REFERENCE 1 (bases 1 to 1409)
 AUTHORS Eshel, D., Prusky, D., and Dinor, A.
 TITLE Exoglucanase of Alternaria alternata
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1409)
 AUTHORS Eshel, D., Prusky, D., and Dinor, A.
 TITLE Direct Submission
 JOURNAL Submitted (09-AUG-1999) Postharvest Sciences, Volcani Center, POB
 6, Bet-Dagan 50250, Israel
 FEATURES
 source Location/Qualifiers
 1. .1409
 /organism="Alternaria alternata"
 /db_xref="taxon:5599"
 1. .1409
 /gene="C1"
 4. .1275
 /gene="C1"
 /codon_start=1
 /product="exoglucanase"
 /protein_id="AF05699.1"
 /db_xref="GI:6179889"
 /translation="MTWOSCTAKGCTGCTNKNGKIVIDANRRLHKKEGYDNCYEMND
 ATRCPDNKACANCAVDGADYSCTTGTGSSLSKIKFTIKGISTNIGSRITLKKDD
 TTYEMFRFTGNDFTFDVVSINLPCGFNGLFVSDADAGGLKRYSTNKAGKRYGTG
 CDAQCPRLDKFTINGEGNVEGWRKSSNDANAGVGHSCCAEMDIENASVPAVPHS
 CSTIIEQSRCDGDCGGTYSADRYAGVCDGCDPNSYRMGVDRDFGKGTVPYSKFT
 VVYIFGTGDAMIKRFYVONGKTIQAPASAVGVYGENSITTKFDDOKAVRGDTYTF
 KDGGMANNAKALANGVLMVSLMDHYSNMLMLDSTYPTDKNPDTDLGTGREGETS
 SCVPADVEOHADATVYVSNIKFPLNSTRFG"

BASE COUNT 393 a 325 c 382 g 309 t
 ORIGIN

Query Match 1.4%; Score 26; DB 8; Length 1409;
 Best Local Similarity 100.0%; Pred. No. 0.0035;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1872 CAGCTGTAAAAA 1897
 Db 1383 CAGCTGTAAAAA 1408

RESULT 41
 AX056994 2481 bp DNA linear PAT 17-JAN-2001
 LOCUS Sequence 11 from Patent WO0075340.
 DEFINITION AX056994
 ACCESSION AX056994
 VERSION AX056994.1 GI:12309857
 KEYWORDS
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 REFERENCE 1 (bases 1 to 2481)
 AUTHORS Butler, K.H., Farnodu, O.O., Gutteridge, S. and Maxwell, C.A.
 TITLE Magnesium chelatease
 JOURNAL Patent: WO 0075340-A 11 14-DEC-2000;
 E.I. DU PONT DE NEMOURS AND COMPANY (US)
 FEATURES
 source Location/Qualifiers
 1. .2481
 /organism="Glycine max"
 /db_xref="taxon:3847"

BASE COUNT 783 a 489 c 589 g 620 t
 ORIGIN

Query Match 1.4%; Score 26; DB 6; Length 2481;
 Best Local Similarity 100.0%; Pred. No. 0.0037;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1872 CAGTGTAAAAA 1897
 DB 2424 CAGTGTAAAAA 2449

RESULT 42
 AF514845 2745 bp mRNA linear VRT 17-JUN-2002
 LOCUS Rana catesbeiana epithelial sodium channel ENAC beta subunit mRNA,
 complete cds.
 ACCESSION AF514845.1 GI:21435743
 VERSION AF514845.1
 KEYWORDS
 SOURCE bullfrog.
 ORGANISM Rana catesbeiana
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;
 Aquarana.

REFERENCE
 1 (bases 1 to 2745)
 Jensik, P.J., Holbird, D. and Cox, T.
 Cloning and partial characterization of an amiloride-sensitive
 sodium channel (fENaC) from adult bullfrog skin
 J. Comp. Physiol. B, Biochem. Syst. Environ. Physiol. (2002) In
 press

JOURNAL
 2 (bases 1 to 2745)
 Jensik, P.J., Holbird, D. and Cox, T.
 Direct Submission
 Submitted (22-MAY-2002) Physiology, Southern Illinois University,
 1135 Lincoln Drive, Carbondale, IL 62901, USA
 Location/Qualifiers
 1..2745
 /organism="Rana catesbeiana"
 /db_xref="taxon:8400"
 /tissue_type="skin epithelium"
 168..2135
 /codon_start=1
 /product="epithelial sodium channel ENAC beta subunit"
 /protein_id="AA053958.1"
 /db_xref="GI:21435744"
 /translation="MTTSTNISRHSSEVMIKRTKLYTRALHRMKGPGYTKELVWF
 CANNTHGPKRIVSEGPKRVRVMTLTIFALVFMGVVLOTLYSGVSLSGF
 NIMVPAVYVNVNPKYSRVKHLHLDLDLADLDLDRIOSSGSCIPAPNNNT
 VILDSPLVNMPVLVIDEHPNNTLVYINFDSTSDYSOINNAKGNQNFVAVKRVAT
 ECTNNRTOCSYRNFTSGAATKDWYLLQFNSPEKIPDEEKVKRGYAEEMITLTMF
 GGQPCSYNFTPIHODYGNCTIFPMWGGGGLSAPGADFGKMLDIDQKEYIP
 FLQSTAAARITLHQQRSTPFLKDLGITAMPGETISIAVLEDTQHLLEAPYSSCYDGS
 DIPVANIYSKENSYSIQCLSCSCFQELNMYKCAVYLFPLNGAHYCNQDEPDY
 PCYINMDIVSHREQIMCOQPCDMSNYKMTISADWPSAAEDMIRHVLSYEKDS
 LDITVNRGIMRLNIYFEENYRSISESPTNNVWLLSLNGGREGFMWGSVLCITTF
 GEIIDICIMITLIKILAMIRDRORRKRPPYVAVELVEAISNGFQHEDSNQV
 STRPGTPPPNDSRLKQIDVIDYSSDE"

BASE COUNT 853 a 581 c 545 g 766 t

ORIGIN

Query Match 1.4%; Score 26; DB 5; Length 2745;
 Best Local Similarity 100.0%; Pred. No. 0.0037;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1872 CAGTGTAAAAA 1897
 DB 2719 CAGTGTAAAAA 2744

RESULT 43
 BC034500 3889 bp mRNA linear PRI 15-JUL-2002
 LOCUS Homo sapiens, similar to RIKEN cDNA 0610013117 gene, clone
 MGC:26926 IMAGE:4838423, mRNA, complete cds.
 ACCESSION BC034500
 VERSION BC034500.1 GI:21759790
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (11-JUL-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK
 COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shihaki
 Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadan@systemsbiology.org
 Anup Madan, Jessica Fahney, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whitting

FEATURES
 source
 1..3889
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="MGC:26926 IMAGE:4838423"
 /tissue_type="testis"
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 /lab_host="DH10B"
 /note="Vector: pBluescript"
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 /codon_start=1
 /product="Similar to RIKEN cDNA 0610013117 gene"
 /protein_id="AA044500.1"
 /db_xref="GI:21759791"
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 YAPLLIRVFEKFAVSPKSGIKETRYKATPNTLENFKNRSTROPLOTDYGL
 AKCNLEPQVQERMRFRSRNOERSRKROEACMRAPFLIVAGIAFLYKDPMLYD
 LMEWVWVQYVPPPLPSQVWYVYILMSFVYSLLRLGPDYKRPFLAHITTHLAISL
 SFSCANAYISGTLVAVHVADVLESAAKMFSTAGVTCNTLFTFTFTFTSRIL
 VFPPWILYCTLLPMTVHLEPFSTYFLNTQLMLQVLAHVMGYILKMLNRCIFMKSI
 QDVNSDEDEEEEEEDEEATGKEDCDLKNGLGAEHRLIPNGOHG"

BASE COUNT 1072 a 860 c 859 g 1098 t

ORIGIN

Query Match 1.4%; Score 26; DB 9; Length 3889;
 Best Local Similarity 100.0%; Pred. No. 0.0038;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1872 CAGTGTAAAAA 1897
 DB 3844 CAGTGTAAAAA 3869

RESULT 44
 AF044209 7940 bp mRNA linear PRI 01-SEP-1998
 LOCUS Homo sapiens nuclear receptor co-repressor N-COR mRNA, complete
 cds.
 ACCESSION AF044209
 VERSION AF044209.1 GI:3510602
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 7940)
 AUTHORS Wang, J., Hoshino, T., Redner, R.L., Kajigaya, S. and Liu, J.M.
 TITLE ETO, fusion partner in t(8;21) acute myeloid leukemia, represses transcription by interaction with the human N-CoR/SMN3/HDAC1 complex
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (18), 10860-10865 (1998)
 MEDLINE 98393736
 PUBMED 9724795
 REFERENCE 2 (bases 1 to 7940)
 AUTHORS Wang, J. and Liu, J.M.
 TITLE Direct Submission
 JOURNAL Submitted (22-JAN-1998) Hematology Branch, National Heart, Lung and Blood Institute, Bldg. 10, Rm. 7C103, 9000 Rockville Pike, Bethesda, MD 20892, USA

FEATURES
 Source Location/Qualifiers
 1. 7940
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 241..7563
 /product="nuclear receptor co-repressor N-CoR"
 /protein_id="AAC33550.1"
 /db_xref="GI:3510603"
 /translation="MSSSGYPPNOGAFSTEQSRYPHVSQYTPPTRHQOEPAVDYR
 SLELEYSOASOLLQOQOLRRRLSEPHGSDRPOERTSYEPHPGSPVDH
 SLESKRRLQVDSHFQNSAVLPLVPLPGLASADKKDPAFGKHPASSPI
 SGPCGDDQNASPSKLSKEBLIDMDVRELAKEVQLKAKKQOQLEEARPE
 PERVSPPEVQKHSIVQITIDENRKAEEAKITEGGLPVELVLYNQPSDTKYH
 ENIKTNQVKKKLIFFKRNHAKQREKICQDQDLAMEKWEIENPRRAK
 ESKTREVYKQPEIKRQEQRFQVQSGAGLSATARSHESETIDGISEEN
 NEKQOLSVIPPMDFDQBRVYKINMGGLMDPKVYKQDFNMVMDHKEIKD
 KPIQHRKNGLLIYSLERKSPVCLVYLTKNENYKALVRNPKRRGNQIARP
 SOEKEVEKEDAEKTEKKEEKDEKDEKENTKEDKIDCAETEBREDO
 ATRGRKTANSQGRKGRITRSMNTNPAASAATAAATPEPPPLSTPEVE
 TSPTEEMEMVAKGLVEHGRNMAIAKAVGKSEACKNEFTNYRRNLNLDLQ
 KQTSRKPREEPRVSOEESVASTSAQEDEDISANEENDEDEEAVKPSDEPN
 ATSRGTEPAVELEPTTERAPSTPSLAVSTPADESEETQVNSISAEAEQDV
 DOOHSAGEECVQDPPATKADSDVEVREHNAKVEDNTKERDLRASKVPR
 DEDLYAQQOINQADREPQSDNSATCSADEVDGPEQRMPPMSKSLNPTSI
 LVSSPLKPNPLDIPOLQRAAYIPRYVSCPTCPICITGVSAIYQORIKMHESAL
 LEBQROQEDIDLECRSTSPGCTSSKSPNEMVLODPAPHQLITLPEVRLPTTPT
 RPPPLIPSSKTVAESKPSFIMGSIQGTPTVYLSHQASVTEPRKPSGISL
 GLPROOSESASATLPIYKQEFSPRSGNSPEGLVRAQHEGVGTAGAIQGSITR
 GTPRSKISVSIISLRGSIQGTPTALPQICITPEALVKGSIIMPIEDSGSKREA
 ASKGVHYEGKSGHILSYDNIKAREGTRSPRTAHISLRSVESEGNKQMSRE
 SPVSAPILEGICRABRSGPSHDLKERTVSGSIQGTPTATSESDGLKVPKQIR
 ESPPIRAFECAITKGRPYDGTITTEKGRSITHIPIRODITQSRKTPREVOSTRTI
 EGSIQGTPTKIFNNNGSAIKHNVSILITGPKLSRGMPLEIVEINIKVERKYE
 DVAGETVRSRHTSVSSGSPVLSLTHEAPKQSLPGIYDTSARTRPVSONTRSR
 GSPMNTSDVTITPKNSTNHERKSTLTPTQRESIPAKSPGVADVVSHPDPHR
 GTTAGEVYMSHPTPLDPAHPFALDPAAYALFOROLSPGTGYSOOLYMENTR
 OTTINDYITSOQOVNLRDVARGLSPROPLGLPYATMGITIDILNMPETILPBG
 GTSTPMDRITTYIPGDTITPPRPNYSASMPCHPHLAAASAEEREREKERER
 ERIAAASDDILRPGSEQPGRPGSHGVSPSVKRTQMTLQORVSGNIGSVI
 TPLDPTAQLRIMPLPAGPSISQGLPASRYNTADAALAVDAASAPQWDSKTES
 KHEARLEENRKSAAVSEQOLEQTELEKRSVCLITSAFSGKQPKPSVYS
 SEAGKDGPPKSYEEELRTKGTITTAFTANFDVITTRIOADNKAREGSGSSSS
 SLSKSHYEMPSAIEVISPASSAPROKLOTQOPEVYVANAENDPMPXQGLHH
 YRPOOESPFOQQLPSSQAEGMGQVPRTRHLLTLADHCITQITQDPARQVSSQTPQ
 QPTSTFQNSALVSTPVTRKTSNRSYSPSOQSVHNOHGRGSRVSPENLVSKSR
 PKGSPERSHVSSEPEIPSPQVAVHEKQDLSLLSQRAEAGVGTANTSVTSGE
 LPSEFTKLENTSPVKSQKQEFRLKNSGSGSDMAAAPGTEIFNLPLAVTSGVS
 SRGSHFADPASNGLDEDIIRKALMGSPDQDGVMAQPMGVGTANTSVTSGE
 TRREGDPPSGGVCKPKLISKSNRSKSPISIGCGYCTGTERPSSVSHSGDHR
 QTEGMANEDRPSSTGCTQFPYNPITLMALSTPTPTLACAPSAVNOAAPQQRIMER
 EPAPLISAQYETLSDSD"

BASE COUNT 2437 a 1942 c 1894 g 1667 t

Query Match 1.44; Score 26; DB 9; Length 7940;
 Best Local Similarity 100.0%; Pred. No. 0.0039;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1872 CAGGTAAAAA 1897
 Db 7909 CAGGTAAAAA 7934

RESULT 45
 AC005250/c 94336 bp DNA linear PRI 01-MAR-2002
 LOCUS Homo sapiens BAC clone CTA-318M5 from 7q22, complete sequence.
 DEFINITION
 AC005250
 AC005250.1 GI:3287719
 HTG.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 94336)
 AUTHORS Sulston, J.E. and Waterston, R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 99063792
 PUBMED 9847074

REFERENCE 2 (bases 1 to 94336)
 AUTHORS Courtney, L., Nelson, J., Wohlmann, P., Bauer, C. and Morris, M.
 TITLE The sequence of Homo sapiens BAC clone CTA-318M5
 JOURNAL Unpublished (2001)
 REFERENCE 3 (bases 1 to 94336)
 WATERSTON, R.
 DIRECT SUBMISSION
 SUBMITTED (03-JUL-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 4 (bases 1 to 94336)
 WATERSTON, R.
 DIRECT SUBMISSION
 SUBMITTED (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 REFERENCE 5 (bases 1 to 94336)
 WATERSTON, R.
 DIRECT SUBMISSION
 SUBMITTED (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc
 Contact: saplens@wustl.wustl.edu
 Summary Statistics
 Center project name: H_RG318M05

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see
 http://www.nhgrl.nih.gov/DIR/CH7/CH7 , send
 mailto:egreen@nhgrl.nih.gov , or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

Clone CTA-318M5 is from a release of the human BAC library C17B-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resgen.com).
VECTOR: pBelOBAC11
Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:

Actual start of this clone is at base position 1 of CTA-318M5.
Actual end is at base position 94336 of CTA-318M5.

FEATURES

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Query Match 1.4%: Score 26; DB 9; Length 94336;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1872 CAGCTGTAATAAAAAAAAAAAAAAAAAA 1897
 Db 83484 CAGCTGTAATAAAAAAAAAAAAAAAAAA 83459

Search completed: November 7, 2002, 23:53:12
 Job time : 7905.36 secs

507

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:52:52 : Search time 2168.96 seconds
(without alignments)
12088.965 Million cell updates/sec

Title: US-09-970-966-211
Perfect score: 1619
Sequence: 1 ggcacatttcgcatgt.....aaaaaaaaaaaaaaaaaa 1619

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estclu:*
5: em_estcov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_huv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	787.8	48.7	888	14	B0689771 AGENCOURT
2	754.2	46.6	814	9	AL567376
3	704	43.5	821	12	BG752229
4	687.8	42.5	702	14	B0006545
5	668.6	41.3	1490	11	AK012406
6	661.4	40.9	678	9	AI936826

Result No.	Score	Query Match	Length	DB ID	Description
7	661.4	40.9	596	13	BM547680
8	659.6	40.7	779	10	BE271770
9	646.6	39.9	769	10	BE385990
10	640.2	39.5	690	10	AM149665
11	615.8	38.0	649	10	AM590950
12	613.4	37.9	627	13	BM669397
13	602.8	37.2	743	10	BE395797
14	600.2	37.1	616	9	AI990500
15	599.4	37.0	666	12	BF439382
16	597.4	36.9	645	12	BF432379
17	589.2	36.4	879	14	B0689033
18	578	35.7	843	12	BF125134
19	576.4	35.6	591	12	BF126050
20	566.4	35.0	759	12	BF126050
21	549.4	33.9	578	9	AI742092
22	548.8	33.9	699	10	BE395581
23	538.4	33.3	551	12	BE858216
24	527.4	32.6	540	12	BF939693
25	526	32.5	537	12	BF954242
26	523.4	32.3	785	17	AG113832
27	522.8	32.3	538	13	BM667957
28	521.2	32.2	537	9	AI018769
29	521.2	32.2	670	12	BG753617
30	519.8	32.1	534	10	BE350014
31	518.8	32.0	540	10	AM954549
32	515.8	31.9	561	10	AM150789
33	515.8	31.9	589	9	AI859538
34	514.4	31.8	527	10	AM338938
35	514.2	31.8	920	9	AL538562
36	509.8	31.5	652	10	BE392412
37	509.2	31.5	570	13	BE181919
38	502.8	31.1	885	10	BE378674
39	502.4	31.0	515	9	AI336858
40	484.2	29.9	500	10	AM075598
41	474.2	29.3	640	10	AM148557
42	463.4	28.6	530	12	BF726459
43	462.6	28.6	480	9	AI423162
44	456	28.2	475	9	AI363261
45	455.4	28.1	457	9	AI459805

ALIGNMENTS

RESULT 1
B0689771
LOCUS B0689771
DEFINITION B0689771
ACCESSION B0689771
VERSION B0689771.1
KEYWORDS GI:21815087
SOURCE
ORGANISM human.
REFERENCE 1 (bases 1 to 888)
AUTHORS NIH-MGC
TITLE NIH-MGC
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LCM2388 row: 0 column: 21
High quality sequence stop: 665.
Location/Qualifiers
source
1. 888

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6248684"
/clone_lib="NH.MGC.110"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGCAG(C). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NH.MGC library."
BASE COUNT      217 a      219 c      264 g      187 t      1 others
ORIGIN

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Query Match      48.7%; Score 787.8; DB 14; Length 888;
Best Local Similarity 96.6%; Pred. No. 2.4e-142;
Matches 858; Conservative 0; Mismatches 23; Indels 7; Gaps 5;

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OY 571 GCATTCGTAATAATTACCTGACCTGACGATTTTCAATGATGATGAGGAAGAGGTGG 630
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 1 GCATTCGTAATAATTACCTGACCTGACGATTTTCAATGATGATGAGGAAGAGGTGG 60
OY 631 AGTGAAGTTCAACCCCATGCTGTGTAAACCGAGCTCAAGGCCAGCTGGCAGATCAGT 690
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 61 ACTGAAGTTCAACCCCATGCTGTGTAAACCGAGCTCAAGGCCAGCTGGCAGATCAGT 120
OY 691 CCTTGAAGTCACTGAGGGGGGCGATCGCTTTTAAAGCCTCCAGTGTCCATTCCTC 750
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 121 CCTTGAAGTCACTGAGGGGGGCGATCGCTTTTAAAGCCTCCAGTGTCCATTCCTC 180
OY 751 CCTGATGGGGGCGATGTTGAGACTGACAGAGTGAAGTGAAGTCTTCTTAAAGGCTGAGG 810
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 181 CCTGATGGGGGCGATGTTGAGACTGACAGAGTGAAGTGAAGTCTTCTTAAAGGCTGAGG 240
OY 811 GCCACTTCCCACTCAAGGCTCCCTGCTTGAATTCATCAACTTCATGCTCTGAAACCAT 870
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 241 GCCACTTCCCACTCAAGGCTCCCTGCTTGAATTCATCAACTTCATGCTCTGAAACCAT 300
OY 871 TCTTGCAGAGCAATTTGGCTGGTTTGGGCGTGAAGTTGGGCTAGTACTGACAGACTCA 930
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 301 TCTTGCAGAGCAATTTGGCTGGTTTGGGCGTGAAGTTGGGCTAGTACTGACAGACTCA 360
OY 931 ATGACTGGGACTTACACTGGGGCTCGGCTCTGTAAGAGTCTTAAAGAAATCTTCT 990
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 361 ATGACTGGGACTTACACTGGGGCTCGGCTCTGTAAGAGTCTTAAAGAAATCTTCT 420
OY 991 CAGTTCCTCTTCAGAGACTGGGGCGGCGGAGAGCAAGCAGCGGCGCTGCACAAAGC 1050
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 421 CAGTTCCTCTTCAGAGACTGGGGCGGCGGAGAGCAAGCAGCGGCGCTGCACAAAGC 480
OY 1051 GGGGCTCTCGGTGGTGAAGTGGCGATGTAGCGCAGGCGCTTCGCGGTGGGCGGTCT 1110
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Db 481 GGGGCTCTCGGTGGTGAAGTGGCGATGTAGCGCAGGCGCTTCGCGGTGGGCGGTCT 540
OY 1111 GCAGGACAGGCGGCGACAGCACTTTCAGCAAGAACCCCGCAAACTGCTGCGAGGAC 1170
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Db 541 GCAGGACAGGCGGCGACAGCACTTTCAGCAAGAACCCCGCAAACTGCTGCGAGGAC 599
OY 1171 ACCGCTACAGAGCGGCTGTGATGACCGAGTGAAGTGAAGAAACGCTCTCCGAGAAAGGG 1230
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
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OY 1231 AGGAGATCATGTAGCGCGGAAATAGAGACTGCTCAGAGTGT -GCTTGGGTTTGGGCGC 1289
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Db 660 AGGAGATCATGTAGCGCGGAAATAGAGACTGCTCAGAGTGTGGGTTTGGGCGC 719
OY 1290 AGCCATGATCTCTCGAATCTGGTGGGCTCAAGCATACGCAATGTCAACAATCAG 1349
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Db 720 AGCCATGATCTCTCGAATCTGGTGGGCTCAAGCATACGCAATGTCAACAATCAG 779

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OY 1350 CCTTGGCAGCAGCAGAGCA -CGAGGAGAGACAGAGAAAGAAACACAG -CATGAGA 1407
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 780 CCTTGGCAGCAGCAGAGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 839
OY 1408 CACAGTAATGAA--TAAACATTAATAATTTAGCCCTCTGTTCT 1452
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 840 CACAGTAATGAAATTAACCATTAATAATTTTAAACCCCTCTTGT 887

```

RESULT 2

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AL567376/c 814 bp mRNA linear EST 16-FEB-2001
LOCUS AL567376 LTI_FL013_Fbrn1 Homo sapiens cDNA clone GS0DP024V004 3
DEFINITION prime, mRNA sequence.
ACCESSION AL567376 GI:12920672
VERSION AL567376.1 GI:12920672
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 814)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 Evry cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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FEATURES

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/db_xref="taxon:9606"
/clone="GS0DP024V004"
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/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
/lab_host="DH10B"
/notes="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
f.liang@life.com URL :
http://fulllength.invitrogen.com"

```

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BASE COUNT      161 a      228 c      210 g      205 t      10 others
ORIGIN

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Query Match      46.6%; Score 754.2; DB 9; Length 814;
Best Local Similarity 97.4%; Pred. No. 7.6e-136;
Matches 789; Conservative 6; Mismatches 12; Indels 3; Gaps 3;

```

```

OY 636 AACGTCACCCCATCTCTGTGTAAACCGAGTCAAGGCCAGCTGGCAGATGATCTTAA 695
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Db 809 AAGTCACCCCATCTCTGTGTAAACCGAGTCAAGGCCAGCTGGCAGATGATCTTAA 751
OY 696 GAAGTCACTGAGGTGGGCAATGCTTTTGAAGGCTTCAAGTGTCCATTCAT -CCCTG 754
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Db 750 GAAGTCACTGAGGTGGGCAATGCTTTTGAAGGCTTCAAGTGTCCATTCATTCCTG 691
OY 755 ATGGGGGCAATGTTTGAAGTCAAGGAGTGAAGTACGTTTCTTAAGGCTGGAGGGCA 814
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Db 690 ATGGGGGCAATGTTTGAAGTCAAGGAGTGAAGTACGTTTCTTAAGGCTGGAGGGCA 631
OY 815 GTTCCCACTCAAGGCTCCCTGCTTGAATCAAACTTCATCTCTGTAAGCAATTCCTC 874
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Db 630 GTTCCCACTCAAGGCTCCCTGCTTGAATCAAACTTCATCTCTGTAAGCAATTCCTC 571
OY 875 TGCAGCAAGATTTGGCTGTTTGGCGCTGAGTGGGCTCTACTGACTGAGACTCAATGA 934
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```

Db 570 TGCAGAGAAATGGCTGGTTCCNCCCTGAGTGTGGGCTCTATAATACAGACTCATNA 511
QY 935 CTGGACATTAGACTGGGCTGGGCTCGCTCTGAAAAAGTCTTAAGAAATCTTCTAGT 994
Db 510 CTGGACATTAGACTGGGCTGGGCTCGCTCTGAAAAAGTCTTAAGAAATCTTCTAGT 451
QY 995 TCTCTTGCAGAGAGACTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 1054
Db 450 TCTCTTGCAGAGAGACTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 391
QY 1055 GCTGTGCGGTGTGAGTGGGCTGATGAGCGGAGCGGCTTCTGTTGGGCTGCTGAG 1114
Db 390 GCTGTGCGGTGTGAGTGGGCTGATGAGCGGAGCGGCTTCTGTTGGGCTGCTGAG 331
QY 1115 GCACAGGCGGCGACAGACCTTGCAGAGACACCCCGGAAGTCTGCGAGGACACCG 1174
Db 330 GCACAGGCGGCGACAGACCTTGCAGAGACACCCCGGAAGTCTGCGAGGACACCG 272
QY 1175 TGTACAGAGAGGCTGATGAGCGGAGCTGAGTAAAGCTTCCGAGAGGAGAGGA 1234
Db 271 TGTACAGAGAGGCTGATGAGCGGAGCTGAGTAAAGCTTCCGAGAGGAGAGGA 212
QY 1235 GATCATGATGACCCCGGAGAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1294
Db 211 GATCATGATGACCCCGGAGAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 152
QY 1295 TGTATCTCGGATCTGTTGGGCTGATGAGCTGAGTACGCTGCTGCTGCTGCTGCT 1354
Db 151 TGTATCTCGGATCTGTTGGGCTGATGAGCTGAGTACGCTGCTGCTGCTGCTGCTGCT 92
QY 1355 GGCAGACAGACAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1414
Db 91 GGCAGACAGACAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 32
QY 1415 AATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1444
Db 31 AATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2

RESULT 3
Bg752229 821 bp mRNA linear EST 15-MAY-2001
LOCUS Bg752229 60231372P1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4875113 5'
DEFINITION mRNA sequence.
ACCESSION Bg752229
VERSION Bg752229.1 GI:14062882
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 821)
NIH-MGC http://mgi.mgi.nhl.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbsr.mgi.nhl.gov
Tissue procurement: ATCC
cDNA library preparation: Ling Hong/Rubin Laboratory
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1755 row: 0 column: 18
High quality sequence stop: 770.
Location/Qualifiers
1..821
FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:4875113"
/clone_lib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"

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/!ab_host="Dh10B (phage-resistant)"
/!ote="Organ: eye; Vector: pOT87; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAAGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC library.!"
BASE COUNT 194 a 201 c 248 g 178 t
ORIGIN

```

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Query Match 43.5%; Score 704; DB 12; Length 821;
Best Local Similarity 95.1%; Pred. No. 3.8e-126;
Matches 782; Conservative 0; Mismatches 30; Indels 10; Gaps 5;

```

```

QY 555 GAAAGAGCTCGTGAAGCAATTCGATTAATTAATTAATTAATTAATTAATTAATTAAT 614
Db 2 GAAAGAGCTCGTGAAGCAATTCGATTAATTAATTAATTAATTAATTAATTAATTAAT 61
QY 615 TGAAGGAAGAGGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 674
Db 62 TGAAGGAAGAGGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 121
QY 675 GGTGAGAGAGTCAAGTCTTGAAGTCAAGTCTTGAAGTCAAGTCTTGAAGTCAAGTCTTGA 734
Db 122 GGTGAGAGAGTCAAGTCTTGAAGTCAAGTCTTGAAGTCAAGTCTTGAAGTCAAGTCTTGA 181
QY 735 CAGTGTCCATTCATCCCTGATGGGGGATGATTGAGACTGAGAGTGAAGTGAAGTGAAGT 794
Db 182 CAGTGTCCATTCATCCCTGATGGGGGATGATTGAGACTGAGAGTGAAGTGAAGTGAAGT 241
QY 795 TTTCTAGAGGCTGGAGGGGAGTCCCACTCAAGGCTCCCTGCTGATTCATTAACCTTCA 854
Db 242 TTTCTAGAGGCTGGAGGGGAGTCCCACTCAAGGCTCCCTGCTGATTCATTAACCTTCA 301
QY 855 TGTCTCTGTAAGCAATTCCTGACAGAGAAATGGCTGGTTCGCGCTGAGTGGGCTCT 914
Db 302 TGTCTCTGTAAGCAATTCCTGACAGAGAAATGGCTGGTTCGCGCTGAGTGGGCTCT 361
QY 915 AGTACTGAGAGCTCA---TGACTGGGACTTGAAGTGGGCTGGGCTGGGCTGGGCTGGGCT 967
Db 362 AGTACTGAGAGCTCA---TGACTGGGACTTGAAGTGGGCTGGGCTGGGCTGGGCTGGGCT 421
QY 968 AAAAGTCTTAAGAA -AATCTTCAGTTCCTGACAGAGAGTGGGCTGGGCTGGGCTGGGCT 1026
Db 422 AAAAGTCTTAAGAA -AATCTTCAGTTCCTGACAGAGAGTGGGCTGGGCTGGGCTGGGCT 481
QY 1027 AGAGCAAGGCGCTGCAAAAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086
Db 482 AGAGCAAGGCGCTGCAAAAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
QY 1087 GCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
Db 542 GCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
QY 1147 ACCGCCGAAGTCTGCGAGAGACCGCTGACAGAGAGCGGCTGATGACCGAGCTGAGG 1206
Db 602 ACCGCCGAAGTCTGCGAGAGACCGCTGACAGAGAGCGGCTGATGACCGAGCTGAGG 661
QY 1207 TAGAAAAAGCTCTCCGAGAGAGGAGAGATGATGATGATGATGATGATGATGATGATGAT 1266
Db 662 TAGAAAAAGCTCTCCGAGAGAGGAGAGATGATGATGATGATGATGATGATGATGATGAT 721
QY 1267 CAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
Db 722 CAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 1327 ACGGCAATGTCACAACATGACCGCTGGGAGACAGAGCA 1368
Db 781 ACGGCAATGTCACAACATGACCGCT -GGCAGACAGAGCA 821

```

RESULT 4
BQ006545/c
LOCUS
DEFINITION
UI-H-EII-aza-n-21-0-UI s1 NCI-CGAP-EII Homo sapiens cDNA clone
IMAGE:5846228 3', mRNA sequence.
ACCESSION
BQ006545
VERSION
BQ006545.1 GI:19731445
KEYWORDS
EST.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 702)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA library preparation: Dr. M. Bento Soares, University of Iowa
DNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1..702
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5846228"
/clone_lib="NCI-CGAP-EII"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pelvis; Vector: p7773-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI-CGAP-EII is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into p7773-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
ACACTTGCAC.
TAG_L1B-UI-H-EII
TAG_TISSUE="chondrosarcoma"
TAG_SEQ="ACACTTGCAC"

BASE COUNT 137 a 200 c 163 g 202 t

Query Match 42.5%, Score 687.8; DB 14; Length 702;
Best Local Similarity 99.6%; Pred. No. 5.3e-123;
Matches 700; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 915 ACTGACGAGACGCAATGACGAGCTTACGCTGGGCTCGCTCTGAAAGTG 974
|||||
DB 702 ACTGACGAGACGCAATGACGAGCTTACGCTGGGCTCGCTCTGAAAGTG 643
|||||
OY 975 CTTAGAAATCTCTCAGTTCTCTCTGACAGAGACTGGCCGGAGCGGAGAGCAAC 1034
|||||
DB 642 CTTAGAAATCTCTCAGTTCTCTCTGACAGAGACTGGCCGGAGCGGAGAGCAAC 583
|||||
OY 1035 GGGCGCTGACAAAGCGGGCGCTGTGGTGTGAGTGCAGATGTACCGCGGAGCGCTTC 1094
|||||
DB 582 GGGCGCTGACAAAGCGGGCGCTGTGGTGTGAGTGCAGATGTACCGCGGAGCGCTTC 523
|||||
OY 1095 TCGGTGTTGGGGTGTGACGAGCAGCGGGGAGCGGAGCACTTGCACGAACCCCGCG 1154

|||||
DB 522 TCGGTGTTGGGCTTGTGAGCGAGCAGCGGCGACAGACACC-TGCAGAAACCCCGCG 464
|||||
OY 1155 AAACGTGTCGAGACACACCGTGTACAGAGCGGGTGTATGACCGAGTGAAGAAAA 1214
|||||
DB 463 AAACGTGTCGAGACACACCGTGTACAGAGCGGGTGTATGACCGAGTGAAGAAAA 404
|||||
OY 1215 CGTTCGAGAAAGGGAGAGGATCATGTACGCCCGGAAGTGAAGACCTGTCAGTGTG 1274
|||||
DB 403 CGTTCGAGAAAGGGAGAGGATCATGTACGCCCGGAAGTGAAGACCTGTCAGTGTG 344
|||||
OY 1275 CTGGGTTTGGCCGAGCGATGATCTCCGAATCTGTTGGGCAATCAGATAGCGCAA 1334
|||||
DB 343 CTGGGTTTGGCCGAGCGATGATCTCCGAATCTGTTGGGCAATCAGATAGCGCAA 284
|||||
OY 1335 TGTCAACCAATTCAGCCCTGGGCGACACGACGAGGAGGAGAGACAGAAAAA 1394
|||||
DB 283 TGTCAACCAATTCAGCCCTGGGCGACACGACGAGGAGGAGAGACAGAAAAA 224
|||||
OY 1395 CACAGCATGAGACAGATTAATGAATTAATTAATTAATTAATTAATTAATTAATTAAT 1454
|||||
DB 223 CACAGCATGAGACAGATTAATGAATTAATTAATTAATTAATTAATTAATTAATTAAT 164
|||||
OY 1455 GCTTACTGGCCGAGCAATGTATCAATTTTTCAGTGTGGACTTGACAGCTCTTTTGGC 1514
|||||
DB 163 GCTTACTGGCCGAGCAATGTATCAATTTTTCAGTGTGGACTTGACAGCTCTTTTGGC 104
|||||
OY 1515 ACAAGCAAGAGAGAAATTAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAGAAA 1574
|||||
DB 103 ACAAGCAAGAGAGAAATTAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAGAAA 44
|||||
OY 1575 GACCATTAATGCTTTAGACAGTGTAAATAAAAAAAAAAAAAAAAAA 1617
|||||
DB 43 GACCATTAATGCTTTAGACAGTGTAAATAAAAAAAAAAAAAAAAAA 1

RESULT 5
AK012406
LOCUS
DEFINITION
Mus musculus 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:270050C12:BRAIN CDNA, CLONE MNCB-0671,
full insert sequence.
ACCESSION
AK012406
VERSION
AK012406.1 GI:12849129
KEYWORDS
HNC; CAP trapper.
SOURCE
Mus musculus (strain:C57BL/6J) 11 days embryo cDNA to mRNA,
clone:lib:RIKEN full-length enriched mouse cDNA library
clone:270050C12.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
AUTHORS
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636
REFERENCE
2
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20493374
PUBMED
11042159
REFERENCE
3
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneoka, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

QY 1581 TAAATGCTTTAGACAGTG 1598
|||||
Db 18 TAAATGCTTTAGACAGTG 1

RESULT 7
BM547680 696 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT_6507108 NIH_MGC_124 Homo sapiens CDNA clone IMAGE:5727798
DEFINITION 5', mRNA sequence.
ACCESSION BM547680
VERSION BM547680.1 GI:18781656
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 696)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL12722 row: h column: 07
High quality sequence stop: 641.
Location/Qualifiers
1..696
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone IMAGE:5727798"
/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1; EcoRV
(destroyed); Site 2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."
BASE COUNT 188 a 160 c 197 g 134 t 17 others
ORIGIN

Query Match 40.9%; Score 661.4; DB 13; Length 696;
Best local similarity 98.5%; Pred No. 6.6e-118;
Matches 673; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 931 ATGACTGGACTTAGACTGGGCTCGCTCGCTGAAAGTGTCTTAAGAAATCTTCT 990
|||||
Db 4 ATGACTGGAGCTTAGACTGGGCTCGCTCGCTGAAAGTGTCTTAAGAAATCTTCT 63

QY 991 CAGTTCTCTTGCAGAGCACTGGCGCGGAGCGCAAGAGCAAGGGCGCTGCACAAAGC 1050
|||||
Db 64 CAGTTCTCTTGCAGAGCACTGGCGCGGAGCGCAAGAGCAAGGGCGCTGCACAAAGC 123

QY 1051 GGGCGCTGTGCTGTGAGTGCATATGACGCGAGCGCTTCTGCTGTTGGCGTGTCT 1110
|||||
Db 124 GGGCGCTGTGCTGTGAGTGCATATGACGCGAGCGCGCTTCTGCTGTTGGCGTGTCT 183

QY 1111 GCAGCAGCAGGGGCGAGCAGCAGCAGCTTGCAGCAACCCCGGAATCTGCGAGGAC 1170
|||||
Db 184 GCAGCAGCAGGGGCGAGCAGCAGCAGC-TGCAGCAACCCCGGAATCTGCGAGGAC 242

QY 1171 ACCGTGTACAGAGCGCGGTGATGACCGAGCTGAGTAAAGTCTTCGAGAAAGGGG 1230
|||||

Db 243 ACCGTGTACAGAGCGCGGTGATGACCGAGCTGAGTAAAGTCTTCGAGAAAGGGG 302
QY 1231 AGAGATCATGTATACGCCCGGAGAGAGAGCTCGACAGTGTGGTGGTGGCGCA 1290
|||||
Db 303 AGAGATCATGTATACGCCCGGAGAGAGAGAGCTCGACAGTGTGGTGGTGGCGCA 362

QY 1291 GCCATGATCTCTCCGATCTGTGGGATCCAGCATACGCGCAATGTCTACAAATCAGC 1350
Db 363 GCCATGATCTCTCCGATCTGTGGGATCCAGCATACGCGCAATGTCTACAAATCAGC 422

QY 1351 CCTGGGCGAGACAGCGAGCGAGAGAGACAGAGAAAAAGAAACACAGTGAACAC 1410
Db 423 CCTGGGCGAGACAGCGAGCGAGAGAGAGAGAAAAAGAAACACAGTGAACAC 482

QY 1411 AGTAAATGAATAAACCTAAATATTATAGCCCTCTGTCTGTCTACGGCAGGAA 1470
|||||
Db 483 AGTAAATGAATAAACCTAAATATTATAGCCCTCTGTCTGTCTACGGCAGGAA 542

QY 1471 ATGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGCCACAGCAAGAGAAAT 1530
Db 543 ATGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGCCACAGCAAGAGAAAT 602

QY 1531 TTAACACTGTTTCAAAACCCGGGAGATTGGCTGTGTTAAGAAAGACATTAAATGCTTT 1550
Db 603 TTAACACTGTTTCAAAACCCGGGAGATTGGCTGTGTTAAGAAAGACATTAAATGCTTT 662

QY 1591 AGACAGTGTAAAGAAAAA 1613
Db 663 AGACAGTGTAAAGAAAAA 685

RESULT 8
BE271770 799 bp mRNA linear EST 26-OCT-2000
LOCUS BE271770
DEFINITION 601141674F1 NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3141450 5',
mRNA sequence.
ACCESSION BE271770
VERSION BE271770.1 GI:9145793
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 799)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCPD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CMI11 row: c column: 19
High quality sequence stop: 721.
Location/Qualifiers
1..799
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone IMAGE:3141450"
/clone_lib="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 171 a 225 c 199 g 204 t
ORIGIN

Query Match 40.7%; Score 659.6; DB 10; Length 799;

Best Local Similarity 96.9%; Pred. No. 1.4e-117;
Matches 769; Conservative 0; Mismatches 14; Indels 11; Gaps 9;

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OY 215 ATGCGCTCGCGGAGTACAGTCTTCTGCTCCCAAGGAACTGACATGCTTGGCATC 274
    |||||||
DB 1 ATGCGCTCGCGGAGTACAGTCTTCTGCTCCCAAGGAACTGACATGCTTGGCATC 59
OY 275 AGCTGTCGACACACCCCTTTTGAACGGGCGCAAGGCCCAAGAAAAGGGAAGTTCTGCC 334
    |||||||
DB 60 AGCTGTCGACACACCCCTTTTGAACGGGCGCAAGGCCCAAGAAAAGGGAAGTTCTGCC 119
OY 335 TGGGCGCTTACGCGGAGGCTCGGACACACATCTCTTCTTAAATTAAGCTCTTCTG 394
    |||||||
DB 120 TGGGCGCTTACGCGGAGGCTCGGACACACATCTCTTCTTAAATTAAGCTCTTCTG 178
OY 395 GCACACTGCTGAAGCTGAAGGAGATGCGCAC--CCCTCTGCTGATTTGTTCTGACGCTTC 452
    |||||||
DB 179 GCACACTGCTGAAGCTGAAGGAGATGCGCACCGGCTCTGCTGATTTGTTCTGACGCTTC 238
OY 453 GCGCCCAACCCCGCCACCTCCCTGAGTGAATTTCTTGGGTCCTTTATTTCTGGTAG 512
    |||||||
DB 239 GCGCCCAACCCCGCCACCTCCCTGAGTGAATTTCTTGGGTCCTTTATTTCTGGTAG 298
OY 513 GGAAGCGGAGTCCGCTTCTTCTTTGCTTCTGCAATATGAAGAAAGCTCGTAAAGC* 572
    |||||||
DB 299 GGAAGCGGAGTCCGCTTCTTCTTTGCTTCTGCAATATGAAGAAAGCTCGTAAAGC 358
OY 573 ATTCGTAATTAATTAATTCAGCTGATGATTTTCAATGATGATTTGAAGAGAGGCTGGAG 632
    |||||||
DB 359 ATTCGTAATTAATTAATTCAGCTGATGATTTTCAATGATGATTTGAAGAGAGGCTGGAG 418
OY 633 TGAAGCTTACCCCGCCATGCTGTGTGAACCGAGTCAAGGCGGCTGGCAGAGTCAATCC 692
    |||||||
DB 419 TGAAGCTTACCCCGCCATGCTGTGTGAACCGAGTCAAGGCGGCTGGCAGAGTCAATCC 478
OY 693 TTGAAGTACAGTGAAGTGGGATCTGCTTTTGTAAAGCTTCCATGCTCATCTCC 752
    |||||||
DB 479 TTGAAGTACAGTGAAGTGGGATCTGCTCC--TTTGTAAAGCTTCCATGCTCATCTCC 537
OY 753 TGAATGGGCGCATAGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 812
    |||||||
DB 538 TGAATGGGCGCATAGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 596
OY 813 CAGTTCCTCACTCAAGGCTCCCT--CGCTTGACATTCAAACCTTCATGCTGAAAACCAT 871
    |||||||
DB 597 CAGTTCCTCACTCAAGGCTCCCTCAAGCTTGACATTCAAACCTTCATGCTGAAAACCAT 656
OY 872 CTCTGAGAGAAATTTGGCTGCTTGGCGCTGAGTTGGGCTCTAG--TGACTGGAATCTCA 930
    |||||||
DB 657 CTCTGAGAGAAATTTGGCTGCTTGGCGCTGAGTTGGGCTCTAG--TGACTGGAATCTCA 716
OY 931 ATGA--CTGGAGACTTGAAGTGGGCTCGGCTCGCTCTGAAAGTGGCTTGAAGAAATCTTC 989
    |||||||
DB 717 ATGACCTGGGACTTAACTTGGGCTGGGCTCTG--TCTGAAGTGGCTTGAAGCAATCTTC 774
OY 990 TCAGTTCTCTCTTGC 1003
    |||||||
DB 775 TCAGTTCTCTCTTGC 788

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RESULT 9
BE385990 676 bp mRNA linear EST 21-JUL-2000
LOCUS 601276636f1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617696 5',
DEFINITION mRNA sequence.
ACCESSION BE385990
VERSION BE385990.1 GI:9331355
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 676)

AUTHORS

NIH-MGC http://mgc.ncl.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph. D.

Email: ggapbs-remail.nih.gov

FEATURES

source

1..676

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3617696"

/clone_id="NIH_MGC_20"

/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: pORF7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCAAGAGG(g). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

Location/Qualifiers

1..676

High quality sequence stop: 653.

Plate: LICM285 row: 9 column: 09

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

DNA sequencing by: Incyte Genomics, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Tissue Procurement: ATCC/DCT/DRP

Email: ggapbs-remail.nih.gov

Unpublished (1999)

Contact: Robert Strausberg, Ph. D.

Unpublished (1999)

Unpublished (1999)

BASE COUNT 168 a 172 c 199 g 137 t
ORIGIN

Query Match

Best Local Similarity 39.9%; Score 646.6; DB 10; Length 676;
Matches 672; Conservative 0; Mismatches 4; Indels 3; Gaps 2;

```

OY 830 TCCCTGCTGACATTCNAACCTTATGCTCTGAAACCAATTCCTGACAGCAATTTGCC 889
    |||||||
DB 1 TCCCTGCTGACATTCNAACCTTATGCTCTGAAACCAATTCCTGACAGCAATTTGCC 60
OY 890 TGGTTTGGCGCTGAGTTGGGCTCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 949
    |||||||
DB 61 TGGTTTGGCGCTGAGTTGGGCTCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
OY 950 GGGCTGGGCTGCTCTGAAAGTGTGAAGAAATCTTCTCAAGTCTCTCTGAGAGGA 1009
    |||||||
DB 121 GGGCTGGGCTGCTCTGAAAGTGTGAAGAAATCTTCTCAAGTCTCTCTGAGAGGA 180
OY 1010 CTGGGCGCGGAGCGCAAGAGCAAGGCGCTGCAAAAGCGGGCGCTGCGGTGTGGA 1069
    |||||||
DB 181 CTGGGCGCGGAGCGCAAGAGCAAGGCGCTGCAAAAGCGGGCGCTGCGGTGTGGA 240
OY 1070 GTGGGCAATGTGCGGCGGCGCTCTGCTGTTGGGCTGCTGCAAGGAGGCGGAGCA 1129
    |||||||
DB 241 GTGGGCAATGTGCGGCGGCGCTCTGCTGTTGGGCTGCTGCAAGGAGGCGGAGCA 300
OY 1130 CAGCAGCTTGCAGCAGACACCGCGGAAGTGTGCGAGAGACACCGTGTACAGAGCGG 1189
    |||||||
DB 301 CAGCAGCTTGCAGCAGACACCGCGGAAGTGTGCGAGAGACACCGTGTACAGAGCGG 359
OY 1190 TGATGACCGAGCTGAGTGAAGAAAGCTTTCGAGAAAGGAGAGAGATCATGTAGCCC 1249
    |||||||
DB 360 TGATGACCGAGCTGAGTGAAGAAAGCTTTCGAGAAAGGAGAGAGATCATGTAGCCC 419
OY 1250 GGAGTGAAGACCTGCTCAGTGTGCTTGGTTGGCGGAGGAGCATATCTCGAATCT 1309
    |||||||
DB 420 GGAGTGAAGACCTGCTCAGTGTGCTTGGTTGGCGGAGGAGCATATCTCGAATCT 479
OY 1310 GGTGGGCAATCAGCAGATACGCGCAATGTCAACAAATCAGCCCTGGGAGAGAGAG 1369

```

Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/INL at: image.llnl.gov/image/html/iresources.shtml

Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Glibco
High quality sequence stop: 457.
Location/Qualifiers

FEATURES

Source

1. 649
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/db_xref="taxon:9606"
/clone="IMAGE:2949166"
/clone_lib="NCI CGAP GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pTR73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 132 a 189 c 155 g 173 t
ORIGIN

Query Match 38.0%; Score 615.8; DB 10; Length 649;
Best Local Similarity 98.6%; Pred. No. 4.3e-109;
Matches 642; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

OY 949 GGGGCTGGCCGCTCGTGAAGAGTCTTAAAGAAATCTCTCAGTTCTCTTCAGAGG 1008
DB 649 GGGGCTGGCCGCTCGTCTG-AAAGTCTTTTAAACAATCTCTCAGTTCTCTTCAGAGG 591
OY 1009 ACTGCGCCGCGGACGCAAGACGCGGCGCTGCACAAAGCGGCGCTGTCGGTGGG 1068
DB 590 ACTGCGCGCGGACGCAAGATCAACGGGCGCTGCACAAAGCGGCGCTGTCGGTGGG 531
OY 1069 AGTGGCATGTACGGGCGGCGCTCTCTGTTGGCTGCTGCAGCAGCAGCGGCGGCG 1128
DB 530 AGTGGCATGTACGGGCGGCGCTCTCTGTTGGCTGCTGCAGCAGCAGCGGCGGCG 471
OY 1129 ACAGCACCCTTCACGACCAACCCGCGCAACTGCTGCGAGACACCGTGTACAGAGCGGG 1188
DB 470 ACAGCACC-TCGACGACCAACCCGCGCAACTGCTGCGAGACACCGTGTACAGAGCGGG 412
OY 1189 TTGATGACCGAGCTGAGTAAAGAAAGCTCTCCGAGAAAGGAGAGGATCATGTACGCC 1248
DB 411 TTGATGACCGAGCTGAGTAAAGAAAGCTCTCCGAGAAAGGAGAGGATCATGTACGCC 352
OY 1249 CGGAGTGGGACCTGCTCAGTCTGCTTGGGTTGGCGGAGCATGATCTCCGAAATC 1308
DB 351 CGGAGTGGGACCTGCTCAGTCTGCTTGGGTTGGCGGAGCATGATCTCCGAAATC 292
OY 1309 TGGTTGGCATTCACGATACGGCCCAATGTCAACAATCAGCCCTGGGCGAGACGAGCA 1368
DB 291 TGGTTGGCATTCACGATACGGCCCAATGTCAACAATCAGCCCTGGGCGAGACGAGCA 232
OY 1369 GGAGGAGAGCAGAGAAAGAAAGAAACACAGCATGAGAAACAGTAAATGAATAAACCA 1428
DB 231 GGAGGAGAGCAGAGAAAGAAAGAAACACAGCATGAGAAACAGTAAATGAATAAACCA 172
OY 1429 TAAATATTTACCCCTCTGCTTCTGCTTACTGCGCAGAGAAATGTCAATTTTTCAG 1488
DB 171 TAAATATTTACCCCTCTGCTTCTGCTTACTGCGCAGAGAAATGTCAATTTTTCAG 112
OY 1489 TGTGGACTTGACAGCTTCTTTTGCACAGACAGAGAAATTTAACTCTTTTCAAC 1548
DB 111 TGTGGACTTGACAGCTTCTTTTGCACAGACAGAGAAATTTAACTCTTTTCAAC 52
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RESULT 12

BM669397/c

LOCUS

DEFINITION

BM669397

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

CONTACT: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

Tissue Procurement: Dr. Gregg Hagaman

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

Seq primer: M13 Forward

POLYA-Tes.

Location/Qualifiers

1. 627

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="UI-E-DWI-and-c-11-0-UI"

/clone_lib="UI-E-DWI"

/tissue_type="adult"

/dev_stage="adult"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/note="Organ: eye; Vector: pTR73-Pac (Pharmacia) with a modified polylinker. Site 1: EcoR I; Site 2: Not I;

UI-E-DWI is a normalized cDNA library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTR73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGATGAGCA. This library was created for the program 'Gene Discovery in the Visual System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

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System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

System, supported by National Eye Institute (NEI).

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QY 1050 CCGGCCCTGTCGGTGGTGGAGTGCATGTACGCGAGGCGCTTCTGCTGTTGGCTGC 1109
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Db 567 CCGGCCCTGTCGGTGGTGGAGTGCATGTACGCGAGGCGCTTCTGCTGTTGGCTGC 508
QY 1110 TCGAGGACAGGCGGAGCAGCAGCACCCTTGCACGAACCCCGCAACTGCTGCAGGA 1169
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Db 507 TCGAGGACAGGCGGAGCAGCAGCACCCTTGCACGAACCCCGCAACTGCTGCAGGA 449
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QY 1470 AATGATACCAATTTTCACTGTTGACCTTGACAGCTTCTTTGCCACAGAGAGAGAA 1529
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RESULT 13
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 VERSION BE395797.1 GI:9341162
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 SOURCE human.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 743)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
 http://image.llnl.gov
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 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"

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/clone="IMAGE:3631543"
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/lab_host="DH10B (phage-resistant)"
/notes="Organ: uterus; Vector: pOTB7; Site:1; XhoI; Site:2;
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAAGAG(G). Library constructed by Ling Hong
in the Laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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BASE COUNT 160 a 189 c 214 g 180 t
 ORIGIN

Query Match	Score	DB	Length
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QY 529 TTCTCTTTTGTTCCTGCTCAATATGAAGAGCTCGGTAAAGCATTCGTAATTAATCA 588
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Db 121 TTCTCTTTTGTTCCTGCTCAATATGAAGAGCTCGGTAAAGCATTCGTAATTAATCA 180
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Db 181 GCGTACTGAATTTTCACTATGACTTGAAGAGAGAGTGAAGTGAAGTCAACCCCA 240
QY 649 TGTCTGTAAACCGAGAGTCAAGCCAGGCTGGCAGAGTCACTCTTGAAGTCACTAGG 708
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Db 301 TGGGATCTGCTTTTGAAGCCCTCAAGTGTCCATTCCTGATTTGGGGATAGTT 360
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Db 720 ACAC 723

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 VERSION AI990500.1 GI:5837381
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 SOURCE human.
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 616)
 NCBI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/dbp/image/image.html
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 High quality sequence stop: 459.
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 from the normalized library NCI_CGAP_G64 was prepared, and
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 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clonoids)
 1257096-1258631, 1469064-1470983, and 1473592-1476743).
 Subtraction by Bento Soares and M. Fatima Bonaldo. "
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 Db 556 CACAAAGCGCGCTGCTGCTGAGTGGCATGTACGGCGCGCTTCTGCTGTT 497
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 Db 496 GCGGTGCTGACGAGCGGCGCGACAGCACTTGACGAACACCGCGGAACAGTCT 438
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 Db 377 AGAAGGAGAGAGATCATGTACGCCCGGAAGTAGAGACTGTCAGTCTGCTGGGTT 318

Oy 1283 TGGCCGACGACCATGATTCCTCCGATCTGGTGGGCATCCAGCATCGGCCAATGTCACA 1342
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 Db 317 TGGCCGACGACCATGATTCCTCCGATCTGGTGGGCATCCAGCATCGGCCAATGTCACA 258
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 Db 257 CATCAGCCCTGGGAGACAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 198
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 Db 197 GAGAACACAGTAAATGATTAATAAATATTTAGCCCTCTGTTCTGCTTACTG 138
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 Db 137 GCGAGAAATGTGATCAATTTTTCAGTGTGACCTTGACAGCTGTTTGCACAGCAA 78
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 Db 77 GAGAGATTTAACAATGTTTCAACCCCGGAGAGTGGCTGTGTTAAGAGAGACATTA 18
 Oy 1583 AATGCTTTAGACAGTGT 1599
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 Db 17 AATGCTTTAGACAGTGT 1
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 PROTEIN-COUPLED RECEPTOR GPR39. ; mRNA sequence.
 ACCESSION BF439382
 VERSION BF439382.1 GI:11451899
 EST.
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 696)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -400P from Gibco
 High quality sequence stop: 459.
 Location/Qualifiers
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 /note="Organ: pooled; Vector: p773D-pac (Pharmacia) with
 a modified polylinker. Site.1: Not I; Site.2: Eco RI;
 Equal amounts of plasmid DNA from five normalized
 libraries were mixed, and ss circles were made in vitro.
 Following HAP purification, this DNA was used as tracer in
 a subtractive hybridization reaction. The driver was
 PCR-amplified cDNAs from pools of 5,000 clones made from
 the same 5 libraries. The pools consisted of the following
 libraries and clonoids: Soares NBHF pool 1:
 309384-310919, 323208-325895 Soares NB2HP pool 1:
 145032-147335, 147720-148103, 148872-149255, 15002 -
 150407, 151176-152327 Soares NB2HP-9W pool 1:
 758280-760583, 772104-774407 Soares NBHP pool 1:
 304776-306311, 320136-322823, 326280-326663 Soares NBHP
 pool 1: 723720-726407, 739080-740999 Subtraction by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT 138 a 202 c 164 g 192 t
ORIGIN

Query Match 37.0%; Score 599.4; DB 12; Length 696;
Best Local Similarity 97.4%; Pred. No. 6, 2e-106;
Matches 663; Conservative 0; Mismatches 11; Indels 7; Gaps 5;

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Db 674 AGATTCATGACT-GGACTTAGACT-GGGCTCGGCTCGCTTAATAA---GTGCTAAAA 620
QY 984 ATCTCTCAGTTCCTTCGAGAGACTGGCGCGCGGAGCGCGAAGACAAGCGGCTGC 1043
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Db 619 AATCTCTCACTTCC-TGCAGAGACTGGCGCGGAGCGCGAAGACAAGCGGCTGC 561
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Db 321 GCGCGAGCATGATCTCCGAATCTGTTGGGCAATCCAGATACGCGCAATGTCAACA 262
QY 1344 AATCAGCCCTGGGACAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1403
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Db 141 CCAGGAAATGTAACCAATTTTTCAGTGTGGACTGTACAGCTTCTTTGCCAAGCAAG 82
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Db 21 ATGCTTTAGACAGTGAATAA 1
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Search completed: November 7, 2002, 15:02:50
J00 Time : 2182.96 secs

412

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 15:03:08 ; Search time 373.511 Seconds
(without alignments)
11437.514 Million cell updates/sec

Title: US-09-970-966-214

Perfect score: 1897
Sequence: 1 gcccaactccgagagctctg.....aaaaaaaaaaaaaaaaaaaa 1897

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 10

Total number of hits satisfying chosen parameters: 1368953

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1897	100.0	1897	24	ABT03284
2	1897	100.0	1897	24	ABT03284
3	1897	100.0	1897	24	ABT03284
4	1897	100.0	1897	24	ABT03284
5	1897	100.0	1897	24	ABT03284
6	1897	100.0	1897	24	ABT03284
7	1897	100.0	1897	24	ABT03284
8	1897	100.0	1897	24	ABT03284
9	1897	100.0	1897	24	ABT03284

10	1344	70.8	1890	22	AAE93845	Human CDNA encoding
11	1218	64.2	2528	22	AAO18690	Human G protein co
12	1150	60.6	1608	24	ABD14231	Human ovarian anti
13	606	31.9	625	24	ABT03280	Human ovarian carc
14	606	31.9	625	24	ABT03280	Human ovarian carc
15	606	31.9	625	24	ABT03280	Human ovarian carc
16	511	26.9	591	22	AAE94044	Human ovarian carc
17	506	26.7	1362	24	ABT03279	Human ovarian carc
18	506	26.7	1362	24	ABT03279	Human ovarian carc
19	425	22.4	480	24	ABT03283	Human ovarian carc
20	425	22.4	480	24	ABT03283	Human ovarian carc
21	366	19.3	587	22	AAE94186	Human ovarian carc
22	364	19.2	444	22	AAH50766	Human ovarian carc
23	316	16.7	396	22	AAE94818	Human ovarian carc
24	316	16.7	396	22	AAE94818	Human ovarian carc
25	316	16.7	396	22	AAE94818	Human ovarian carc
26	315	16.6	369	22	AAE95007	Human ovarian carc
27	315	16.6	369	22	AAE95007	Human ovarian carc
28	315	16.6	369	22	AAE95007	Human ovarian carc
29	315	16.6	369	22	AAE95007	Human ovarian carc
30	307	16.2	349	24	ABT03274	Human ovarian carc
31	271	14.3	1010	24	ABT03282	Human ovarian carc
32	271	14.3	1010	24	ABT03282	Human ovarian carc
33	264	13.9	409	24	ABT03282	Human ovarian carc
34	166	8.8	201	24	ABT03282	Human ovarian carc
35	154	8.1	390	24	ABT03282	Human ovarian carc
36	125	6.6	381	24	ABT03282	Human ovarian carc
37	120	6.3	430	24	ABT03282	Human ovarian carc
38	120	6.3	430	24	ABT03282	Human ovarian carc
39	60	3.2	60	24	ABT03282	Human ovarian carc
40	27	1.4	1368	22	AAE94186	Human ovarian carc
41	26	1.4	50	22	AAE94186	Human ovarian carc
42	26	1.4	50	22	AAE94186	Human ovarian carc
43	26	1.4	50	22	AAE94186	Human ovarian carc
44	26	1.4	50	22	AAE94186	Human ovarian carc
45	25	1.3	51	22	AAE94186	Human ovarian carc

ALIGNMENTS

RESULT 1	ABT03284	standard; CDNA; 1897 BP.
ID	ABT03284	
XX	ABT03284	
AC	ABT03284	
XX	ABT03284	
DT	05-SEP-2002	(first entry)
DE	Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.	
DE	Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.	
DE	Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.	
KW	Human ovarian carcinoma; gene therapy; immunotherapy;	
KW	Cyclostatin; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	MO200239885-A2.	
PD	23-MAY-2002.	
XX		
XX	13-NOV-2001; 2001MO-US45395.	
XX	14-NOV-2000; 2000US-0713550.	
PR	03-APR-2001; 2001US-0825294.	
PR	02-OCT-2001; 2001US-0970966.	
XX		
PA	(CORI-) CORIXA CORP.	
XX		
PI	Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;	
XX	WPI; 2002-500186/53.	
DR		
XX		
PT	Novel ovarian cancer polypeptide and polynucleotide, useful for	

ID	AB140352	standard; cDNA; 1897 BP.
XX	AB140352;	
XX	28-JUN-2002	(first entry)
XX	Ovarian carcinoma O1034C/O591S	consensus nucleotide sequence.
XX	Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer; ss.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	CDS	260..685
XX	FT	/*tag= a
XX	FT	/product= "Ovarian carcinoma protein O1034C/O591S"
XX	US2002004491-A1.	
XX	10-JAN-2002.	
XX	03-APR-2001; 2001US-0825294.	
XX	10-SEP-1999; 99US-0394374.	
XX	01-MAY-2000; 2000US-0561778.	
XX	15-AUG-2000; 2000US-0640173.	
XX	07-SEP-2000; 2000US-0656668.	
XX	14-NOV-2000; 2000US-0713550.	
XX	(XUJ/) XU J.	
XX	(STOL/) STOLK J A.	
XX	(ALGA/) ALGATE P A.	
XX	(FLIN/) FLING S P.	
XX	XU J, STOLK JA, ALGATE PA, FLING SP;	
XX	WPI; 2002-117027/22.	
XX	P-PSDB; ABB09417.	
XX	Ovarian tumour polypeptide and polynucleotide useful in diagnosis, prevention and/or treatment of cancer, especially ovarian cancer.	
XX	Claim 1a; Page 127-128; 131pp; English.	
XX	The invention relates to ovarian tumour polynucleotides and polypeptides that may be utilised in cancer therapy, for example in a vaccine or gene therapy. Polypeptides and polynucleotides of the invention are useful for detecting a cancer in a patient, for stimulating and/or expanding T-cells specific for a tumour protein, and for inhibiting the development of a cancer in a patient. They are also useful for stimulating an immune response in a patient, and for treating a cancer in a patient and for determining the presence of a cancer in a patient. The isolated polynucleotides of the invention are useful for their ability to selectively form duplex molecules with complementary stretches of the entire desired gene or gene fragments, and for designing and preparing ribozyme molecules for inhibiting expression of tumour polypeptides in tumour cells. Polypeptides and polynucleotides of the invention are also useful in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. The current sequence represents the ovarian carcinoma O1034C/O591S consensus nucleotide sequence.	
XX	Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other;	
XX	Query Match	100.0%; Score 1897; DB 24; Length 1897;
XX	Best Local Similarity	100.0%; Pred. No. 0;
XX	Matches 1897; Conservative	0; Mismatches 0; Indels 0; Gaps 0

Db	1	GCACAACTCCGGAGGCGCTGTGHCCTCGGCCCGGGAGCGCGAGCGGAGGAGCAGAGACCCG	60
Qy	61	CAGCCGGGAGGCCGCAAGCGGGGGCGATCAGGCTCCGCGAGCGGCACTCGGCTCCTCTA	120
Db	61	CAGCCGGGAGGCCGCAAGCGGGGGCGATCAGGCTCCGCGAGCGGCACTCGGCTCCTCTA	120
Qy	121	AGCTACGACCTCTCTCCGCGGAGCAGCGCGGGGCCAGCAGCCTCTGGGAGCCACAC	180
Db	121	AGCTACGACCTCTCTCCGCGGAGCAGCGCGGGGCCAGCAGCCTCTGGGAGCCACAC	180
Qy	181	CGCTCAGCCGGGGCAGCTCCGCTGTGCGCTCTCTGATGGCTTGGCCTCCCG	240
Db	181	CGCTCAGCCGGGGCAGCTCCGCTGTGCGCTCTCTGATGGCTTGGCCTCCCG	240
Qy	241	GCCCCGGGACCTCGGGGAAATGTGGGTCCTAAGGCATTCGGGCAACTTTTGGGAAATGT	300
Db	241	GCCCCGGGACCTCGGGGAAATGTGGGTCCTAAGGCATTCGGGCAACTTTTGGGAAATGT	300
Qy	301	CTTGCTTCCAGGCTTTTGCGGTGCAAAATCAGTCTACAGTGTGAAGAAATTCACACTAA	360
Db	301	CTTGCTTCCAGGCTTTTGCGGTGCAAAATCAGTCTACAGTGTGAAGAAATTCACACTAA	360
Qy	361	CAAGGACTGCTCTCTCCCGGAGTTCAATGTGAATTGCACGGGTGAACGTTCAAGACATGTG	420
Db	361	CAAGGACTGCTCTCTCCCGGAGTTCAATGTGAATTGCACGGGTGAACGTTCAAGACATGTG	420
Qy	421	TCAGAAAGAAATGTATGGAGAAATGGCCGGGATCATGTACCCGCAAGTCTGTGCATATC	480
Db	421	TCAGAAAGAAATGTATGGAGAAATGGCCGGGATCATGTACCCGCAAGTCTGTGCATATC	480
Qy	481	AGCGCGCTGTCTCATCGCTCTGCCGGGTAACAGTCTTCTGCTCCCGAGGAAATGAA	540
Db	481	AGCGCGCTGTCTCATCGCTCTGCCGGGTAACAGTCTTCTGCTCCCGAGGAAATGAA	540
Qy	541	CTCAGTTTGGATCAGCGTGCAGCAACCCCTCTTTTAACGGGGCCAAAGGCCCAAGAAAG	600
Db	541	CTCAGTTTGGATCAGCGTGCAGCAACCCCTCTTTTAACGGGGCCAAAGGCCCAAGAAAG	600
Qy	601	GGGAAGTTCTGCGCTCGGCCCTCAAGGCGAGGCGTCCGACACACATCTGTGTTCTCAATT	660
Db	601	GGGAAGTTCTGCGCTCGGCCCTCAAGGCGAGGCGTCCGACACACATCTGTGTTCTCAATT	660
Qy	661	AGCCCTCTTCTCGGCAACACTGCTGAAGCTGAAGAGATGCCACCCCTCTCGCATTTGTC	720
Db	661	AGCCCTCTTCTCGGCAACACTGCTGAAGCTGAAGAGATGCCACCCCTCTCGCATTTGTC	720
Qy	721	TTCCAGCGCTCGGCCCAACCCGCCACCTCCGATGATGTTCTTCTGGGGTGGCTCTTT	780
Db	721	TTCCAGCGCTCGGCCCAACCCGCCACCTCCGATGATGTTCTTCTGGGGTGGCTCTTT	780
Qy	781	ATTCTGGGTAGGGAGCGGGAGTCCGTCTCTTTTGTCTCTGTGCAAAATATGAAGAG	840
Db	781	ATTCTGGGTAGGGAGCGGGAGTCCGTCTCTTTTGTCTCTGTGCAAAATATGAAGAG	840
Qy	841	CTCGCTTAAGCATTTGGAATAAATTAAGGATACAGTAATTTCACTATGTACTGAAAGA	900
Db	841	CTCGCTTAAGCATTTGGAATAAATTAAGGATACAGTAATTTCACTATGTACTGAAAGA	900
Qy	901	AGGAGGTGGAATGAATTACCCCATCTCTGTGTAAACCGAGTCAAGGCGCAGGCTGGC	960
Db	901	AGGAGGTGGAATGAATTACCCCATCTCTGTGTAAACCGAGTCAAGGCGCAGGCTGGC	960
Qy	961	AGAGTCTGTCTTGAAGATCACTGAGGTGGCATCTGCCCTTTGTAAGCCTCCAGTGTG	1020
Db	961	AGAGTCTGTCTTGAAGATCACTGAGGTGGCATCTGCCCTTTGTAAGCCTCCAGTGTG	1020
Qy	1021	CATTCATTCCTATATGGGGCAGATGTTTAGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	1080
Db	1021	CATTCATTCCTATATGGGGCAGATGTTTAGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	1080
Qy	1081	GGCTGAGGGGCCATTTCCACTCAAGGCTCCCTCGCTTGACATTTCAAACTCATGCTCT	1140
Db	1081	GGCTGAGGGGCCATTTCCACTCAAGGCTCCCTCGCTTGACATTTCAAACTCATGCTCT	1140

Oy	1141	GAAACCACTTCTCTGACAGCAGAAATGGCTGCTTTCGCGCTTGAAGTTGGCTCTAGTGACT	1200
Db	1141	GAAACCACTTCTCTGACAGCAGAAATGGCTGCTTTCGCGCTTGAAGTTGGCTCTAGTGACT	1200
Oy	1201	CGAAGCTCAATGACTGGGAGCTTACACTGGGGGCTCGGCTGCTGCTGAAAAAGTCTTAAGA	1260
Db	1201	CGAAGCTCAATGACTGGGAGCTTACACTGGGGGCTCGGCTGCTGCTGAAAAAGTCTTAAGA	1260
Oy	1261	AAATCTTCTCAGTTCCTCTTGACAGAGACTGCGCCCGGAGCGGAAAGACAGCGGCGCT	1320
Db	1261	AAATCTTCTCAGTTCCTCTTGACAGAGACTGCGCGCGGAGCGGAAAGACAGCGGCGCT	1320
Oy	1321	GCACAAAGCGGGCCCTGTCGCTGTGTGAATGCGCATATACCGCAGCGCTTCTCTGGT	1380
Db	1321	GCACAAAGCGGGCCCTGTCGCTGTGTGAATGCGCATATACCGCAGCGCTTCTCTGGT	1380
Oy	1381	TGGCGTGTGTGAAGGACAGCGGGGAGCAACAGCACTCTCACAAACCCCGCGAAACTGCT	1440
Db	1381	TGGCGTGTGTGAAGGACAGCGGGGAGCAACAGCACTCTCACAAACCCCGCGAAACTGCT	1440
Oy	1441	GCAGAGCACCCGTCGTACAGAGCGGGTGTGATGACCGAGCTGAGGTAGAAAAAGTCTCG	1500
Db	1441	GCAGAGCACCCGTCGTACAGAGCGGGTGTGATGACCGAGCTGAGGTAGAAAAAGTCTCG	1500
Oy	1501	AGMAGGGAAGAGATCATCTTACGCCCGGGAAGTAGACCTCTGCTCACTCGCTTGGGTT	1560
Db	1501	AGMAGGGAAGAGATCATCTTACGCCCGGGAAGTAGACCTCTGCTCACTCGCTTGGGTT	1560
Oy	1561	TGGCGCGCAGCATGATCCTCCGAACTTGTTGGGCTATCCAGCATACGGCCAAATGTCAGAA	1620
Db	1561	TGGCGCGCAGCATGATCCTCCGAACTTGTTGGGCTATCCAGCATACGGCCAAATGTCAGAA	1620
Oy	1621	CAATCAGCCCTGGGCGAGCACGAGCAGAGGAGGAGAGACAGAGAAAAACACACACAT	1680
Db	1621	CAATCAGCCCTGGGCGAGCACGAGCAGAGGAGGAGAGACAGAGAAAAACACACACAT	1680
Oy	1681	GAGAACACAGTAATGATTAATAACCATTAATATTTGGCCCTGTGTTCTGCTTACTG	1740
Db	1681	GAGAACACAGTAATGATTAATAACCATTAATATTTGGCCCTGTGTTCTGCTTACTG	1740
Oy	1741	GCCAGGAATGGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGGCCACAAGCAA	1800
Db	1741	GCCAGGAATGGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGGCCACAAGCAA	1800
Oy	1801	GAGACAATTTTAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAACCATTA	1860
Db	1801	GAGACAATTTTAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAACCATTA	1860
Oy	1861	AATGCTTAGACAGTGTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1897
Db	1861	AATGCTTAGACAGTGTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1897
RESULT 3			
ID	AAFP22400/c		
XX	AAFP22400 standard; cDNA; 1953 BP.		
AC	AAFP22400;		
XX			
DT	26-MAR-2001 (first entry)		
XX			
DE	Human secreted protein gene 28 SRQ ID NO:38.		
XX			
KM	Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;		
KM	antirheumatic; antiproliferative; cyostatic; cardiant; vasotropic;		
KM	cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;		
KM	fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;		
KM	rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;		
KM	cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;		
KM	angiogenesis; nervous system disorder; Alzheimer's disease; infection;		
KM	ocular disorder; corneal infection; wound healing; skin aging;		
KM	food additive; preservative; ss.		

QY 259 AATGGGCTCTAAGGCAATCGGCAACTTTTGGGATGTTCTGCTCCAGGCTTTC 318
 |||||
 Db 1695 AATGGGCTCTAAGGCAATCGGCAACTTTTGGGATGTTCTGCTCCAGGCTTTC 1636
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 QY 319 GGTGCAATTCAGTGTACCAAGTGTGAAGAATTCCAGCTGAACAAGACTGCTCC 378
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 Db 1635 GGTGCAATTCAGTGTACCAAGTGTGAAGAATTCCAGCTGAACAAGACTGCTCC 1576
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 QY 379 CGAGTTCATTGTGAATTGCAAGGTTGAAGCTTCAAGACATGTGTGAGAAAGTGTGGA 438
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 Db 1575 CGAGTTCATTGTGAATTGCAAGGTTGAAGCTTCAAGACATGTGTGAGAAAGTGTGGA 1516
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 QY 439 GCAAAATGCGGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCTGTCTATCG 498
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 Db 1515 GCAAAATGCGGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCTGTCTATCG 1456
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 QY 499 CTGTGCGGGGTACAGTCTGTGCTGCTCCGAGGAAATGAACTCATGTTGCTACGCTG 558
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 Db 1455 CTGTGCGGGGTACAGTCTGTGCTGCTCCGAGGAAATGAACTCATGTTGCTACGCTG 1396
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 QY 559 CTGCAACACCCCTCTTGTGAACGGGCAAGGCCCAAGAAAGGGGAAAGTTCTGCTCGG 618
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 Db 1395 CTGCAACACCCCTCTTGTGAACGGGCAAGGCCCAAGAAAGGGGAAAGTTCTGCTCGG 1336
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 QY 619 CCTCAGGCGAGGGCTCCGCAACCACTCTGTTCTCAAAATTAAGCCCTCTTCTCGGACA 678
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 Db 1335 CCTCAGGCGAGGGCTCCGCAACCACTCTGTTCTCAAAATTAAGCCCTCTTCTCGGACA 1277
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 QY 679 CTGCTAGAGTGAAGAGATGCAACCCCTCTGATGTTGTTCTCCAGGCTCGGCCCA 738
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 QY 799 GAGTCCGTCTCTTGTGCTGCAAAATTAAGAAAGACTCGGTAAGACTTCTGA 858
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 Db 1156 GAGTCCGTCTCTTGTGCTGCAAAATTAAGAAAGACTCGGTAAGACTTCTGA 1097
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 QY 859 ATAAATTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 918
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 Db 1096 ATAAATTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1037
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 QY 919 TCACCCCATGCTGTGTACCGGAGTCAAGGCTGCGAGAGTCTGCTTGAAG 978
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 QY 979 TCAGTGAAGTGGGCAATCTGCTTTGTAAAGCTCAGTGTCCATTCCTCATGAGG 1038
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 QY 1039 GGCATAGTGTGAGACTGAGAGTGAAGAGTGAAGTGTGTTTGAAGGCTGAGGCGCATGCC 1098
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 QY 1099 CACTCAAGGCTCCGCTGCTGATCAATTCATTCCTGTAAGAACCATCTCTGAG 1158
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 Db 736 ACTTGAAGTGGGCTGCGCTGCTGTGAAAAGTCTTAAGAAAATCTTCTCAAGTTCTCC 677
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 QY 1279 TTGCAAGAGACTGGGCGGCGGAGAGCAAGGCGCTGCAACAAGGCGGCTGT 1338
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 Db 676 TTGCAAGAGACTGGGCGGCGGAGAGCAAGGCGCTGCAACAAGGCGGCTGT 617
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 QY 1339 CGGTGGTGAAGTGCAGATGACGCGAGGCGCTTCTGCTGGTGGCGTGTGACGACACA 1398
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Db 616 CGGTGGTGAAGTGGCCATGATACCGGAGGCTTCTGCTGGTGGCGGTGACGACGACA 557
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 QY 1399 GCGGCGAGCAGACACCTGTCAGCAACACCGCGGAAATGCTGCGAGAGACACCGTGTCA 1458
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 Db 496 GGAAGGCGTGTGATGACCGAGTGTAGAGTGAAGAAAGTGTCTCGAGAAAGGAGAGATCA 437
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 QY 1519 TGTAGCCCGGAAATGAGACCTGTCAGTGTGCTGGTGGTGGCCGACCATGATGCC 1578
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 Db 436 TGTAGCCCGGAAATGAGACCTGTCAGTGTGCTGGTGGTGGCCGACCATGATGCC 377
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 Db 316 CACGAGCAGAGGAG 257
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 Db 256 TAAACCATTAATAATTTAAGCCCTCTGTTCTGCTTACTGAGGCGAAGTGTACCA 197
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 Db 196 TTTTTCAGTGTGACCTTGACACTTCTTTTGCACAAGAGAGAGATTTAACACTGT 137
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 QY 1819 TTCAACCCGGGAGGAGTGGCTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTGA 1878
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 Db 136 TTCAACCCGGGAGGAGTGGCTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTGA 77
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RESULT 4
 AAF64188/c
 ID AAF64188 standard; cDNA; 1956 BP.
 XX
 AC AAF64188;
 DT 06-APR-2001 (first entry)
 XX
 DE Human secreted protein gene I3 SRQ ID NO:23.
 XX
 KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
 KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
 KW nootropic; neuroprotective; antibacterial; virucide; fungicide;
 KW ophthalmological; vulnary; autoimmune disease; cardiovascular disorder;
 KW hyperproliferative disorders; cerebrovascular disorder; wound healing;
 KW nervous system disorder; ocular disorder; skin aging; chemotaxis;
 KW food additive; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200077026-A1.
 XX
 PD 21-DEC-2000.
 XX
 PF 01-JUN-2000; 2000WC-US14973.
 XX
 PR 11-JUN-1999; 99US-0138630.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 PI Rosen CA, Ruben SM, Komatsoulis GA;
 XX
 DR WPI: 2001-071258/08.
 DR P-PSDB; AAB75518.
 XX
 PT Nucleic acid molecules encoding human secreted proteins, used in

QY 1639 CACGACGAGGAGGAGACAGAGAAAAAGAAAAACACAGCATGAGAAACACAGTAATGAA 1698
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 DB 316 CACGACGAGGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGAAACACAGTAATGAA 257
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 QY 1699 TAAACCATTAATATTTAGCCCCCTGTTCTGTCTACTGGCCAGGAATGTAACCA 1758
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 DB 256 TAAACCATTAATATTTAGCCCCCTGTTCTGTCTACTGGCCAGGAATGTAACCA 197
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 QY 1759 TTTTTCAGTTGAGCTTGCACCTCTTTTGCACACAGAGAGAAATTAACCTGT 1818
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 DB 196 TTTTTCAGTTGAGCTTGCACCTCTTTTGCACACAGAGAGAAATTAACCTGT 137
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 QY 1819 TTCAAAACCCGGGAGTGGCTGTGTTAAAGAAACATTAATGCTTTAGACAGTGA 1878
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 DB 136 TTCAAAACCCGGGAGTGGCTGTGTTAAAGAAACATTAATGCTTTAGACAGTGA 77
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 RESULT 5
 ABR33543
 ID ABR33543 standard; cDNA; 1524 BP.
 AC ABR33543;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE cDNA encoding human PRO protein, Seq ID No 15.
 XX
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha; gene: ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200208288-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US21066.
 XX
 XX 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23528.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2000WO-US34956.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001WO-US17092.
 XX
 PA (GENE) GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gerlitsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 PI WPI: 2002-172001/22.
 DR P-PSDB; AAU83599.
 XX
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal

PT tumour or liver tumour -
 XX
 PS Claim 2; Figure 15; 359pp; English.
 XX
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABR33543-ABR33567 represent human
 CC PRO protein coding sequences of the invention.
 CC
 SQ Sequence 1524 BP; 321 A; 433 C; 435 G; 335 T; 0 other;
 Query Match 75.0%; Score 1422; DB 24; Length 1524;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1522; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 140 GCGGACGAGCGCGGCGCCAGACAGCTCGGACACAGCGCGTGCAGCGGCGAGCC 199
 DB 1 GCGGACGAGCGCGGCGCCAGACAGCTCGGACACAGCGCGTGCAGCGGCGAGCC 60
 QY 200 TCCGCTGCTGTCGCTCCTCGATGCGCTTGCCTCCCGCGCGCGGACTCGGGAGA 259
 DB 61 TCCGCTGCTGTCGCTCCTCGATGCGCTTGCCTCCCGCGCGGACTCGGGAGA 120
 QY 260 ATGTTGGTCTAGGACATCGCGCACTTTTGGCATTTGTTCTTCCAGGCTTGGC 319
 DB 121 ATGTTGGTCTAGGACATCGCGCACTTTTGGCATTTGTTCTTCCAGGCTTGGC 180
 QY 320 CTGCAATCCAGTCTCTACAGTGTGAAGAAATTCAGTGAACAAGCTCTCTCCCC 379
 DB 181 CTGCAATCCAGTCTCTACAGTGTGAAGAAATTCAGTGAACAAGCTCTCTCCCC 240
 QY 380 GAGTTCAATTGATTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 439
 DB 241 GAGTTCAATTGATTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300
 QY 440 CAAAGTGGGGATCATGATCCGCAAGTCTGTGCATCATCAGCGGCTGTCTATGCC 499
 DB 301 CAAAGTGGGGATCATGATCCGCAAGTCTGTGCATCATCAGCGGCTGTCTATGCC 360
 QY 500 TCTGCGGGATACAGTCTCTGCTCCCGAGGAAATGAAATCATGATCATGATCATG 559
 DB 361 TCTGCGGGATACAGTCTCTGCTCCCGAGGAAATGAAATCATGATCATGATCATG 420
 QY 560 TGCAACACCCCTTTTGAACGGGCGCAAGGCCCAAGAAAGGGAAGTTGCTCGGCG 619
 DB 421 TGCAACACCCCTTTTGAACGGGCGCAAGGCCCAAGAAAGGGAAGTTGCTCGGCG 480
 QY 620 CTCAGGCGAGGGCTCGGACACCATCTCTCTCAATTAAGCCCTCTTCTGGGACAC 679
 DB 481 CTCAGGCGAGGGCTCGGACACCATCTCTCTCAATTAAGCCCTCTTCTGGGACAC 540
 QY 680 TGCTGAAGCTGAAGGAGATGCCACCCCTCTGATGTTCTTCCAGGCGCTCGCCCA 739
 DB 541 TGCTGAAGCTGAAGGAGATGCCACCCCTCTGATGTTCTTCCAGGCGCTCGCCCA 600
 QY 740 CCCCCACCTCCCTGATGAGTTCTTCTGAGTGTCTTTATCTTGGGTAAGGAGCGGG 799
 DB 601 CCCCCACCTCCCTGATGAGTTCTTCTGAGTGTCTTTATCTTGGGTAAGGAGCGGG 660
 QY 800 AGTCCGTTCTCTTTGTTCTCTGCAATTAAGAGCTCGGTAAGCATTTGAA 859
 |||||||

Db 661 AGTCCGTTCTCTTTTGTCTCTGTCGCAATTAATGAAGAGCTCGTAAAGCATTTCTGAA 720
 QY 860 TAAATTCAGCTYAGTAATTTTCATGATGACTTGAAGAGAGAGGTGAGTGAAGTT 919
 Db 721 TAAATTCAGCTYAGTAATTTTCATGATGACTTGAAGAGAGAGGTGAGTGAAGTT 780
 QY 920 CACCCCATCTCTGTGTAACCGAGTCAAGGCCAGGCTGGCAGAGTGTGCTTGAAGT 979
 Db 781 CACCCCATCTCTGTGTAACCGAGTCAAGGCCAGGCTGGCAGAGTGTGCTTGAAGT 840
 QY 980 CACTGAGTGGGCAATCGCTTTTGTAAAGCCTCAGTGTCCATCTCATCCCTGATGGG 1039
 Db 841 CACTGAGTGGGCAATCGCTTTTGTAAAGCCTCAGTGTCCATCTCATCCCTGATGGG 900
 QY 1040 GCATAGTTTGAAGTGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1099
 Db 901 GCATAGTTTGAAGTGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 960
 QY 1100 ACTCAAGGCTCCCTCGCTGATCAATTAACCTTCATGCTCCGAAAGACCATTTCTGAGC 1159
 Db 961 ACTCAAGGCTCCCTCGCTGATCAATTAACCTTCATGCTCCGAAAGACCATTTCTGAGC 1020
 QY 1160 AGAATTTGGCTGTTTCGCGCTGAGTGGGCTCTAGTACTGAGACTCAATGATGAGGA 1219
 Db 1021 AGAATTTGGCTGTTTCGCGCTGAGTGGGCTCTAGTACTGAGACTCAATGATGAGGA 1080
 QY 1220 CTYAGACTGGGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1279
 Db 1081 CTYAGACTGGGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 QY 1280 TGCAGAGGAGTGGGCTCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1339
 Db 1141 TGCAGAGGAGTGGGCTCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 QY 1340 GGTGTTGAGTGGTCCGATCTAGCGCGAGGCGCTCTCTGTTGGTGGCTGCTGCTGCTGCT 1339
 Db 1201 GGTGTTGAGTGGTCCGATCTAGCGCGAGGCGCTCTCTGTTGGTGGCTGCTGCTGCTGCT 1260
 QY 1400 GCGGAG 1459
 Db 1261 GCGGAG 1320
 QY 1460 GAGCGGTTGATGACCGAGCTGAGGTAGAAAACGCTCCGAGAAAGGAGAGAGAGATCAT 1519
 Db 1321 GAGCGGTTGATGACCGAGCTGAGGTAGAAAACGCTCCGAGAAAGGAGAGAGATCAT 1380
 QY 1520 GTACGCGCGGAAATGAGACCTGCTCAGTCTGCTGGGTTTGGCCGAGAGCATGATCCT 1579
 Db 1381 GTACGCGCGGAAATGAGACCTGCTCAGTCTGCTGGGTTTGGCCGAGAGCATGATCCT 1440
 QY 1580 CCGAATCTGGTGGGCAATCCAGCATGAGGCCAATGTCAACAATCAGCCCTGGGAGAC 1639
 Db 1441 CCGAATCTGGTGGGCAATCCAGCATGAGGCCAATGTCAACAATCAGCCCTGGGAGAC 1500
 QY 1640 ACGAGCAG 1663
 Db 1501 ACGAGCAG 1524
 RESULT 6
 ABR03277
 ID ABR03277 standard; cDNA; 1619 BP.
 XX ABR03277;
 DT 05-SEP-2002 (first entry)
 DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 205.
 XX Human ovarian cancer; gene therapy; immunotherapy;
 KW cytostatic; gene; ss.
 OS Homo sapiens.

XX MO200239885-A2.
 PN 23-MAY-2002.
 PD 13-NOV-2001; 2001WO-US45395.
 PF 14-NOV-2000; 2000US-0713550.
 PR 03-APR-2001; 2001US-0825294.
 PR 02-OCT-2001; 2001US-0970966.
 PA (CORI-) CORIXA CORP.
 XX Xu J, Stolk JA, Albate PA, Fling SP, Molesh DA;
 PI WPI; 2002-500186/53.
 DR Novel ovarian cancer polypeptide and polynucleotide, useful for
 XX detecting the presence of ovarian cancer in a patient, and in
 XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
 PT
 PS Claim 2; Page 189-190; 197pp; English.
 CC The present invention provides human ovarian cancer associated proteins
 CC and coding sequences. The sequences can be used in the diagnosis and
 CC treatment of ovarian cancers. The present sequence is a coding sequence
 CC of the invention.
 SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other:
 Query Match 73.6%; Score 1396; DB 24; Length 1619;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1616; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 280 GGCACATTTTGGGATGTTGTTGCTTCCAGGCTTTCGCTGCAAAATCAGTGTCTACCA 339
 Db 1 GGCACATTTTGGGATGTTGTTGCTTCCAGGCTTTCGCTGCAAAATCAGTGTCTACCA 60
 QY 340 GTGTGAAGATTCAGGTGAGCAACAGACGCTCTCCCGAGTTCATTTGTGATGAC 399
 Db 61 GTGTGAAGATTCAGGTGAGCAACAGACGCTCTCCCGAGTTCATTTGTGATGAC 120
 QY 400 GGTGAACGTTCAAGACATGTGTGAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 459
 Db 121 GGTGAACGTTCAAGACATGTGTGAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180
 QY 460 CCGCAATCTGTGATCATCAGCGGCTGTCTCATCGGCTGTGGGGGATCAGTCTT 519
 Db 181 CCGCAATCTGTGATCATCAGCGGCTGTCTCATCGGCTGTGGGGGATCAGTCTT 240
 QY 520 CTGCTCCCGAGGAACTGCACTGATTTGATCAGCTGCTGCAACACCCCTTTGTAA 579
 Db 241 CTGCTCCCGAGGAACTGCACTGATTTGATCAGCTGCTGCAACACCCCTTTGTAA 300
 QY 580 CCGGCAAGGCCCAAGAAAGGGAAGTTTGGCTGCGCCCTTAGGCGAGAGGCTCGGCAC 639
 Db 301 CCGGCAAGGCCCAAGAAAGGGAAGTTTGGCTGCGCCCTTAGGCGAGAGGCTCGGCAC 360
 QY 640 CACCATCTGTCTCTCAATTAAGTCTCTGAGGCACTGCTGAAGGAGAGAGAG 699
 Db 361 CACCATCTGTCTCTCAATTAAGTCTCTGAGGCACTGCTGAAGGAGAGAGAG 420
 QY 700 CCACCCCTCTCGATGTTCTTCCAGCCCTGCGCCCAACCCCAACCTCCCTGAGTGA 759
 Db 421 CCACCCCTCTCGATGTTCTTCCAGCCCTGCGCCCAACCCCAACCTCCCTGAGTGA 480
 QY 760 GTTCTCTCTGGGTGCTCTTTTATCTGAGGAGAGGAGAGGAGTCTTCTTTTGT 819
 Db 481 GTTCTCTCTGGGTGCTCTTTTATCTGAGGAGAGGAGAGGAGTCTTCTTTTGT 540
 QY 820 CTTGTCAATTAAGAAAGCTCGTAAAGCATTTGATTAATTCAGTCAAT 879
 Db 540 CTTGTCAATTAAGAAAGCTCGTAAAGCATTTGATTAATTCAGTCAAT 879

Db	541	CGTGGCAAAATAAATGAAGAGAGCTGGGTAAAGCAATTCGAAATTAATTCACCTGACTGAAT	600
Qy	880	TTTCAGATGTACTTTGAAGAAGAGGTGGAGTGAAGATTCAACCCCATGTCTGTATAAC	939
Db	601	TTTTAGTATGTACTTTGAAGAAGAGGTGGAGTGAAGATTCAACCCCATGTCTGTATAAC	660
Qy	940	CGGACTCAAGGCCAAGGCGGGAGAGTGMWRCCTTAAAGTCACTAGAGGTGGGCACTGGC	999
Db	661	CGGACTCAAGGCCAAGGCGGGAGAGTGMWRCCTTAAAGTCACTAGAGGTGGGCACTGGC	720
Qy	1000	TTTTTAAAGCCTCCAGTGTCCATTTCCATCCCTGATAGGGGGCAATAGTTTGAAGTGCAGA	1059
Db	721	TTTTTAAAGCCTCCAGTGTCCATTTCCATCCCTGATAGGGGGCAATAGTTTGAAGTGCAGA	780
Qy	1060	GTGAGAGTACGCTTTTCTTAGGGCTGGAGGGCCAGTTCCOACTCAAGGCTCCCTGCTTG	1119
Db	781	GTGAGAGTACGCTTTTCTTAGGGCTGGAGGGCCAGTTCCOACTCAAGGCTCCCTGCTTG	840
Qy	1120	ACATTCAAACTTCATGTCTCCGAAAACCAATTCCTGTACAGAGAAATTTGGTGGTTCCGGC	1179
Db	841	ACATTCAAACTTCATGTCTCCGAAAACCAATTCCTGTACAGAGAAATTTGGTGGTTCCGGC	900
Qy	1180	CTGAGTTGGGCTCTTAGTGACTCGAGACTCAATGACCTGGAGCTTAGCTGGGCTGGGCT	1239
Db	901	CTGAGTTGGGCTCTTAGTGACTCGAGACTCAATGACCTGGAGCTTAGCTGGGCTGGGCT	960
Qy	1240	CGCTCTGAAAAGTGCCTTAACAAAATCTTCCACTTCTCTTCCAGAGACTGCGCCGGG	1299
Db	961	CGCTCTGAAAAGTGCCTTAACAAAATCTTCCACTTCTCTTCCAGAGACTGCGCCGGG	1020
Qy	1300	ACCGGAAGAGCAACGAGGCGCTGCACAAGCGGGCGCTGCGGTGGAGTCCGCATTA	1359
Db	1021	ACCGGAAGAGCAACGAGGCGCTGCACAAGCGGGCGCTGCGGTGGAGTCCGCATTA	1080
Qy	1360	CGCGAGGCGGTTCTCGTGGTTGGGCTGCTGCAGAGCAACGCGGCGAGCAACACCTTGC	1418
Db	1081	CGCGAGGCGGTTCTCGTGGTTGGGCTGCTGCAGAGCAACGCGGCGAGCAACACCTTGC	1140
Qy	1419	ACGAACACCCGCGAAACTCTCCGAGAGACACCCTTACAGAGCGGGTTGATACCGAG	1478
Db	1141	ACGAACACCCGCGAAACTCTCCGAGAGACACCCTTACAGAGCGGGTTGATACCGAG	1200
Qy	1479	CTGAGGTGAAGAAAACGTCCTCCGAGAAAGGAGAGGATCATGCGCCGGAAGTAGGAC	1538
Db	1201	CTGAGGTGAAGAAAACGTCCTCCGAGAAAGGAGAGGATCATGCGCCGGAAGTAGGAC	1260
Qy	1539	CTCTCCAGTGTGCTTGGGTTTGGCGGAGGCAATGATCCTCCGAATCTGGTTGGGATC	1598
Db	1261	CTCTCCAGTGTGCTTGGGTTTGGCGGAGGCAATGATCCTCCGAATCTGGTTGGGATC	1320
Qy	1599	CAGCATACGGCCCAATGTCAACAAATCAGCCCTGGGCGAGACACGACGAGAGGAGAGAC	1658
Db	1321	CAGCATACGGCCCAATGTCAACAAATCAGCCCTGGGCGAGACACGACGAGAGGAGAGAC	1380
Qy	1659	AGAGAAAAGAAAACACACGATGAGAAACACAGTAAATGAATTAACCATTAATATTTAG	1718
Db	1381	AGAGAAAAGAAAACACACGATGAGAAACACAGTAAATGAATTAACCATTAATATTTAG	1440
Qy	1719	CCCTCTGTCTGTCTTACTGGCCGAGAAATGTATACCAATTTTTCAGTGTGGACTTGA	1778
Db	1441	CCCTCTGTCTGTCTTACTGGCCGAGAAATGTATACCAATTTTTCAGTGTGGACTTGA	1500
Qy	1779	CAGCTTCTTTGGCCACAGCAAGAGAAATTTAACACTGTTTCAAAACCCGGGGAGTTGG	1838
Db	1501	CAGCTTCTTTGGCCACAGCAAGAGAAATTTAACACTGTTTCAAAACCCGGGGAGTTGG	1560
Qy	1839	CTGTGTTTAAAGAAAGCAATTAATGTCTTTATACAGTGTAAAAAATTTTTAAAAA	1897
Db	1561	CTGTGTTTAAAGAAAGCAATTAATGTCTTTATACAGTGTAAAAAATTTTTAAAAA	1619

ID	ABT03281 standard; cDNA; 1619 BP.	
XX		
AC	ABT03281:	
XX		
DT	05-SEP-2002 (first entry)	
XX		
DE	Human ovarian carcinoma associated coding sequence SEQ ID NO: 211.	
XX		
KW	Human: Ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;	
KW	cytostatic; gene; ss.	
OS	Homo sapiens.	
XX		
PN	W0200239885-A2.	
XX		
PD	23-MAY-2002.	
XX		
PF	13-NOV-2001; 2001WO-US45395.	
XX		
PR	14-NOV-2000; 2000US-0713550.	
PR	03-APR-2001; 2001US-0825294.	
XX	02-OCT-2001; 2001US-0970966.	
PA	(CORI-) CORIXA CORP.	
XX		
PI	Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;	
XX	WPI; 2002-500186/53.	
DR		
XX		
PT	Novel ovarian cancer polypeptide and polynucleotide, useful for	
PT	detecting the presence of ovarian cancer in a patient, and in	
PT	pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer	
XX		
PS	Claim 2: Page 195; 197pp; English.	
XX		
CC	The present invention provides human ovarian cancer associated proteins	
CC	and coding sequences. The sequences can be used in the diagnosis and	
CC	treatment of ovarian cancers. The present sequence is a coding sequence	
CC	of the invention.	
XX		
XX	Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other:	
XX		
Query Match	73.6%; Score 1396; DB 24; Length 1619;	
Best Local Similarity	99.8%; Pred. No. 0;	
Matches 1616; Conservative	0; Mismatches 2; Indels 1; Gaps	
1;		
QY	280 GGCACCTTTTGGCGGATGCTCTTCCTCCAGCTTGGCGTCAATCCAGTGTACCA	339
Db	1 GGCACCTTTTGGCGGATGCTCTTCCTCCAGCTTGGCGTCAATCCAGTGTACCA	60
QY	340 GGTGAAGATTCACGCTGCAACACGACTGCTCCGCCGAGTTCATTGTAATTGCAC	399
Db	61 GGTGAAGATTCACGCTGCAACACGACTGCTCCGCCGAGTTCATTGTAATTGCAC	120
QY	400 GGTGAAGTTCACGATGTGTCAAGAAAGATGTAGTAGAGCAAGTGGCGGATCATGTA	459
Db	121 GGTGAAGTTCACGATGTGTCAAGAAAGATGTAGTAGAGCAAGTGGCGGATCATGTA	180
QY	460 CCGCAAGTCTGTGATATACAGCGGCTGTCTATGCGCTTGGCGGATACCACTTCCT	519
Db	161 CCGCAAGTCTGTGATATACAGCGGCTGTCTATGCGCTTGGCGGATACCACTTCCT	240
QY	520 CTGCTCCCGAGGAAACGAACTCAGTTGGATCGATCGATCGCAACACCCCTTTGTAA	579
Db	241 CTGCTCCCGAGGAAACGAACTCAGTTGGATCGATCGATCGCAACACCCCTTTGTAA	300
QY	560 CGGCGCAAGGCCCAAGAAAGGGGAACTTCGCTCGGCGCCCTCAAGGCCAGGCTCCGAC	639
Db	301 CGGCGCAAGGCCCAAGAAAGGGGAACTTCGCTCGGCGCCCTCAAGGCCAGGCTCCGAC	360
QY	640 CACCATCTGTTCCCAATATAGCCCTTTCTCGGCAACACTGCTGAAGCTAAGAGATG	699

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Db 361 CACATTCCTGTTCCTCAATTAAGCCCTCTTCGGGACACACTGTAAGCTGAAGGATG 420
Qy 700 CCAACCCCTCTGCATGTTGTTTCAGACCCCTGCCCCCAACCCCTCCCTGAGTGA 759
Db 421 CCAACCCCTCTGCATGTTGTTTCAGACCCCTGCCCCCAACCCCTCCCTGAGTGA 480
Qy 760 GTTTCCTTCGGGTCCTTTTATTCGGGTAGGAGGAGGAGTCCGTTCTCTTTGTT 819
Db 481 GTTTCCTTCGGGTCCTTTTATTCGGGTAGGAGGAGGAGTCCGTTCTCTTTGTT 540
Qy 820 CCTGTGCAATTAATGAAGAAGCTCGTAAAGCATTTCTGAATTAATTCAGCTGAT 879
Db 541 CCGTGTGAATTAATGAAGAAGCTCGTAAAGCATTTCTGAATTAATTCAGCTGAT 600
Qy 880 TTTTCAGTATGACTTGAAGAAGAGAGTGAAGTGAAGTTCACCCCATCTCTGTGAAC 939
Db 601 TTTTCAGTATGACTTGAAGAAGAGAGTGAAGTGAAGTTCACCCCATCTCTGTGAAC 660
Qy 940 CGGAGTCAAGGCGCAGGCTGGGAGAGTGMGTCTTGAAGTCACTGAGGTGGCATCGCC 999
Db 661 CGGAGTCAAGGCGCAGGCTGGGAGAGTGMGTCTTGAAGTCACTGAGGTGGCATCGCC 720
Qy 1000 TTTTGTAAAGCCCTCAGTGTCCATTCCTGATGCGGAGCATAGTTGAGACTGCAGA 1059
Db 721 TTTTGTAAAGCCCTCAGTGTCCATTCCTGATGCGGAGCATAGTTGAGACTGCAGA 780
Qy 1060 GTGAGAGTGAAGTCTTTCTTGAAGGCTGAGAGGCGCATCCACATCAAGGCTCCGCTG 1119
Db 781 GTGAGAGTGAAGTCTTTCTTGAAGGCTGAGAGGCGCATCCACATCAAGGCTCCGCTG 840
Qy 1120 ACATTCAAACTTCATGCTCTGAAACCAATCTCTGCAGAGAGATTTGGCTTCGCGC 1179
Db 841 ACATTCAAACTTCATGCTCTGAAACCAATCTCTGCAGAGAGATTTGGCTTCGCGC 900
Qy 1180 CTGAGTGGGCTCTGATGACTCGAGACTCAATGACTGCGACTTGAAGTGGGCTCGGCT 1239
Db 901 CTGAGTGGGCTCTGATGACTCGAGACTCAATGACTGCGACTTGAAGTGGGCTCGGCT 960
Qy 1240 CGCTGTGAAGTGTGTTAAGAAATCTTCTGATGTTCTGCTGAGAGAGTGGGCGCGG 1299
Db 961 CGCTGTGAAGTGTGTTAAGAAATCTTCTGATGTTCTGCTGAGAGAGTGGGCGCGG 1020
Qy 1300 ACGGAAAGAGCAAGGCGGCTGCAAAAGGCGGCTGTGCGTGGTGGAGTGCAGTGA 1359
Db 1021 ACGGAAAGAGCAAGGCGGCTGCAAAAGGCGGCTGTGCGTGGTGGAGTGCAGTGA 1080
Qy 1360 CGCGCAGCGCTTCTGCTGTTGGGCTGCTGACGAGAGCGCGCAGCAGCAGC-TCG 1418
Db 1081 CGCGCAGCGCTTCTGCTGTTGGGCTGCTGACGAGAGCGCGCAGCAGCAGCCTTGC 1140
Qy 1419 ACGAAGACCGCGCGAACTGTGCGAGAGACCGGTGTACAGAGCGGGTGTATGACGAG 1478
Db 1141 ACGAAGACCGCGCGAACTGTGCGAGAGACCGGTGTACAGAGCGGGTGTATGACGAG 1200
Qy 1479 CTGAGGTGAAGAAACGTCTCGAAGAGGAGAGATCATGTACGCCGGAAGTAGAC 1538
Db 1201 CTGAGGTGAAGAAACGTCTCGAAGAGGAGAGATCATGTACGCCGGAAGTAGAC 1260
Qy 1539 CTGCTGCAAGTGTGTTGGGTTGGCCGACGACATGATCCCTCCAAATGTTGGTGGCATC 1598
Db 1261 CTGCTGCAAGTGTGTTGGGTTGGCCGACGACATGATCCCTCCAAATGTTGGTGGCATC 1320
Qy 1599 CAGCATACGCGCAATGTACAAATCAGCCCTGGGAGACAGCAGAGGAGGAGAGAC 1658
Db 1321 CAGCATACGCGCAATGTACAAATCAGCCCTGGGAGACAGCAGAGGAGGAGAGAC 1380
Qy 1659 AGAGAAAGAAAGAAACAGACATGAGACAGTAATGAATTAATTAATTTAG 1718
Db 1381 AGAGAAAGAAAGAAACAGACATGAGACAGTAATGAATTAATTAATTTAG 1440
Qy 1719 CCGCTCTGTTGCTTACCTGAGAGAAATGTTACAAATTTTTCATGTTGGACTTGA 1778
Db 1441 CCGCTCTGTTGCTTACCTGAGAGAAATGTTACAAATTTTTCATGTTGGACTTGA 1500

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Qy 1779 CAGCTTCCTTTTCCACAGAGAGAGATTTAACACTGTTTCAAAACCCGGGGAGTTGG 1838
Db 1501 CAGCTTCCTTTTCCACAGAGAGAGATTTAACACTGTTTCAAAACCCGGGGAGTTGG 1560
Qy 1839 CTGTGTTAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAAGAAAAA 1897
Db 1561 CTGTGTTAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAAGAAAAA 1619

RESULT 8
ABL40345
ID ABL40345 standard: cDNA; 1619 BP.
XX
AC ABL40345;
XX
DT 28-JUN-2002 (first entry)
XX
DE Ovarian carcinoma sequence isolate 57887 extended cDNA.
XX
KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX
SS.
XX
Homo sapiens.
XX
US2002004491-A1.
XX
PD 10-JAN-2002.
XX
PE 03-APR-2001; 2001US-0825294.
XX
PR 10-SEP-1999; 99US-0394374.
XX
PR 01-MAY-2000; 2000US-0561778.
XX
PR 15-MAY-2000; 2000US-0640173.
XX
PR 07-SEP-2000; 2000US-0656668.
XX
PR 14-NOV-2000; 2000US-0713550.
XX
XX
PA (XUJ/) XU J.
PA (STOL/) STOLK J A.
PA (ALGM/) ALGATE P A.
PA (FLIN/) FLING S P.
XX
PI Xu J, Stolk JA, Algate PA, Fling SP;
XX
DR WPI; 2002-171027/22.
XX
PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX
PT prevention and/or treatment of cancer, especially ovarian cancer.
XX
PS Claim 1a: Page 119-120; 131pp; English.
XX
XX
The invention relates to ovarian tumour polynucleotides and polypeptides
CC that may be utilised in cancer therapy, for example in a vaccine or
CC gene therapy. Polypeptides and polynucleotides of the invention are
CC useful for detecting a cancer in a patient, for stimulating and/or
CC expanding T-cells specific for a tumour protein, and for inhibiting the
CC development of a cancer in a patient. They are also useful for
CC stimulating an immune response in a patient, and for treating a cancer in
CC a patient and for determining the presence of a cancer in a patient.
CC The isolated polynucleotides of the invention are useful for their
CC ability to selectively form duplex molecules with complementary stretches
CC of the entire desired gene or gene fragments, and for designing and
CC preparing ribozyme molecules for inhibiting expression of tumour
CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
CC invention are also useful in recombinant DNA molecules to direct
CC expression of a polypeptide in appropriate host cells. The current
CC sequence represents the extended cDNA sequence of ovarian carcinoma
CC isolate 57887 given in record ABL48956.
XX
SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;
Query Match 73.6%; Score 1396; DB 24; Length 1619;
Best Local Similarity 99.8%; Pred. No. 0;

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Matches 1616; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 280 GGCACATTTTGGCGATTGTTCTTCCAGAGCTTTGGCCCTCAATCATGTCACCA 339
    |||||
Db 1 GGCACATTTTGGCGATTGTTCTTCCAGAGCTTTGGCCCTCAATCATGTCACCA 60
QY 340 GTTGAAGAAATTCACCTGAAACAGACAGTCTCCGCCGAGTTGTAATGAC 399
    |||||
Db 61 GTTGAAGAAATTCACCTGAAACAGACAGTCTCCGCCGAGTTGTAATGAC 120
QY 400 GGTGAAGCTTCAAGACATGTGTGAGAAAGAGTGTGAGCAAGTCCGGGATCATGTA 459
    |||||
Db 121 GGTGAAGCTTCAAGACATGTGTGAGAAAGAGTGTGAGCAAGTCCGGGATCATGTA 180
QY 460 CCGCAAGTCTGTGATCATATCAGCGGCTGTCTCATCGGCTGCGGGATACAGTCTT 519
    |||||
Db 181 CCGCAAGTCTGTGATCATATCAGCGGCTGTCTCATCGGCTGCGGGATACAGTCTT 240
QY 520 CTGCTCCCGAGGAAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 579
    |||||
Db 241 CTGCTCCCGAGGAAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 580 CCGGCAAGGCCCCAAGAAAGGGGAGTGTGCTGCGGCTGAGGCTCAGGCTCCGAC 639
    |||||
Db 301 CCGGCAAGGCCCCAAGAAAGGGGAGTGTGCTGCGGCTGAGGCTCAGGCTCCGAC 360
QY 640 CACCATCTGTCTCCTCAATTAAGCTCTTCTGCGACACTGTGAAGCTGAAGAGATG 699
    |||||
Db 361 CACCATCTGTCTCCTCAATTAAGCTCTTCTGCGACACTGTGAAGCTGAAGAGATG 420
QY 700 CACACCCCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 759
    |||||
Db 421 CACACCCCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 760 GTTCTTCTGGGCTGCTTTTATTCGGGTAGGAGGAGGAGTCTGTTCTTTGTT 819
    |||||
Db 481 GTTCTTCTGGGCTGCTTTTATTCGGGTAGGAGGAGGAGTCTGTTCTTTGTT 540
QY 820 CCGTGCATAATATGAAGAGCTCGGTAAAGCATTCGTGAATTAATCAGCTGATGAT 879
    |||||
Db 541 CCGTGCATAATATGAAGAGCTCGGTAAAGCATTCGTGAATTAATCAGCTGATGAT 600
QY 880 TTTCACTATGATCTTGAAGAGAGGAGTGAAGTCAACCCCATGTTGTGTAAAC 939
    |||||
Db 601 TTTCACTATGATCTTGAAGAGAGGAGTGAAGTCAACCCCATGTTGTGTAAAC 660
QY 940 CCGAGTCAAGGCGGAGCTGCGAGAGTCTGCTGTAAGATCTGAGGGGAGCATCTGCC 999
    |||||
Db 661 CCGAGTCAAGGCGGAGCTGCGAGAGTCTGCTGTAAGATCTGAGGGGAGCATCTGCC 720
QY 1000 TTTTGTAAAGCTCCAGTGTCCATTCATCCGTGATGGGGCATAGTTGAGATGACGA 1059
    |||||
Db 721 TTTTGTAAAGCTCCAGTGTCCATTCATCCGTGATGGGGCATAGTTGAGATGACGA 780
QY 1060 GTGAGAGTACCTTTTCTTAGGGCTGAGAGGCGCAGTTCCCATCAAGGCTCCCTGCTTG 1119
    |||||
Db 781 GTGAGAGTACCTTTTCTTAGGGCTGAGAGGCGCAGTTCCCATCAAGGCTCCCTGCTTG 840
QY 1120 ACATTCAAATTCATGCTCTGAAACCAATCTCTGACAGCAATTTGGTGGTTCCGGC 1179
    |||||
Db 841 ACATTCAAATTCATGCTCTGAAACCAATCTCTCTGACAGCAATTTGGTGGTTCCGGC 900
QY 1180 CTGAGTGTGGGCTCTAGTACCTGAGACCTCAATGACTGGGACTTAGACTGGGCTCGGCT 1239
    |||||
Db 901 CTGAGTGTGGGCTCTAGTACCTGAGACCTCAATGACTGGGACTTAGACTGGGCTCGGCT 960
QY 1240 CGCTCGAAGAAAGTGTGAAGAAATCTTCTGAGTCTCTTCAAGAGACTGGCCCGG 1299
    |||||
Db 961 CGCTCGAAGAAAGTGTGAAGAAATCTTCTGAGTCTCTTCAAGAGACTGGCCCGG 1020
QY 1300 ACGCAAGAGCAAGCGGCGCTGACAAAGCGGCGCTGCGGTGGTGGAGTGGCATGTA 1359
    |||||
Db 1021 ACGCAAGAGCAAGCGGCGCTGACAAAGCGGCGCTGCGGTGGTGGAGTGGCATGTA 1080

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QY 1360 GCGCAGGCGCTTCTGNGTTGGCTGCTGACAGCAGCGGCGACAGCACACC-TGC 1418
    |||||
Db 1081 GCGCAGGCGCTTCTGNGTTGGCTGCTGACAGCAGCGGCGACAGCACACC-TTGC 1140
QY 1419 ACGAACCACCGCGCAATGCTGCGAGGACACCGGTACAGAGCGGGTTATGACCGAG 1478
    |||||
Db 1141 ACGAACCACCGCGCAATGCTGCGAGGACACCGGTACAGAGCGGGTTATGACCGAG 1200
QY 1479 CTGAGTGTGAAGAAAGCTTCCGAGAAAGGAGAGATCATGTACGCCCGGAATAGAG 1538
    |||||
Db 1201 CTGAGTGTGAAGAAAGCTTCCGAGAAAGGAGAGATCATGTACGCCCGGAATAGAG 1260
QY 1539 CTGCTTCAGTGTGCTTGGGTTGGCCGACCATGATCTCCGAAATGTGTTGGCATC 1598
    |||||
Db 1261 CTGCTTCAGTGTGCTTGGGTTGGCCGACCATGATCTCCGAAATGTGTTGGCATC 1320
QY 1599 CAGCATACGGCCATGTGACAAACATCAGCCCTGGGCGAGACGAGAGGAGAGAC 1658
    |||||
Db 1321 CAGCATACGGCCATGTGACAAACATCAGCCCTGGGCGAGACGAGAGGAGAGAC 1380
QY 1659 AGAGAAAGAAAGAACACAGCATGAGACACAGTAATGATTAATTAATTAATTAAT 1718
    |||||
Db 1381 AGAGAAAGAAAGAACACAGCATGAGAACACAGTAATGATTAATTAATTAATTAAT 1440
QY 1719 CCCCCTGTCTGCTGCTTACGCGCAGGAATGATTAATTTTCACTGTGACCTTGA 1778
    |||||
Db 1441 CCCCCTGTCTGCTTACGCGCAGGAATGATTAATTTTCACTGTGACCTTGA 1500
QY 1779 CAGCTTCTTTTGCACAGCAGAGAGATTTAACACTGTTTCAACCCGGGAGATTGG 1838
    |||||
Db 1501 CAGCTTCTTTTGCACAGCAGAGAGATTTAACACTGTTTCAACCCGGGAGATTGG 1560
QY 1839 CTGCTTTAAAGAAAGCATTAATGCTTTAGACAGTGTAAAGAAAAA 1897
    |||||
Db 1561 CTGCTTTAAAGAAAGCATTAATGCTTTAGACAGTGTAAAGAAAAA 1619

```

RESULT 9
 ABL40349
 ID ABL40349 standard; cDNA; 1619 BP.
 ABL40349;
 AC 28-JUN-2002 (first entry)
 DE Ovarian carcinoma O591S nucleotide sequence.
 KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
 OS ss.
 XX Homo sapiens.
 PN US2002004491-A1.
 PD 10-JAN-2002.
 PE 03-APR-2001; 2001US-0825294.
 PR 10-SEP-1999; 99US-0394374.
 PR 01-MAY-2000; 2000US-0561778.
 PR 15-AUG-2000; 2000US-0640173.
 PR 07-SEP-2000; 2000US-0656668.
 PR 14-NOV-2000; 2000US-0713550.
 PA (XUJ/) XU J.
 PA (STOL/) STOLK J A.
 PA (ALGA/) ALGATE P A.
 PA (FLIN/) FLIN S P.
 PI XU J, Stolk JA, Algate PA, Flin SP;
 DR WPI; 2002-171027/22.

XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
 PT prevention and/or treatment of cancer, especially ovarian cancer -
 XX
 XX Claim 1a: Page 125-126; 131pp: English.

CC The invention relates to ovarian tumour polynucleotides and polypeptides
 CC that may be utilised in cancer therapy, for example in a vaccine or
 CC gene therapy. Polypeptides and polynucleotides of the invention are
 CC useful for detecting a cancer in a patient, for stimulating and/or
 CC expending T-cells specific for a tumour protein, and for inhibiting the
 CC development of a cancer in a patient. They are also useful for
 CC stimulating an immune response in a patient, and for treating a cancer in
 CC a patient and for determining the presence of a cancer in a patient.
 CC The isolated polynucleotides of the invention are useful for their
 CC ability to selectively form duplex molecules with complementary stretches
 CC of the entire desired gene or gene fragments, and for designing and
 CC preparing ribozyme molecules for inhibiting expression of tumour
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
 CC invention are also useful in recombinant DNA molecules to direct
 CC expression of a polypeptide in appropriate host cells. The current
 CC sequence represents the ovarian carcinoma 05915 nucleotide sequence.
 CC
 XX
 SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 73.6%; Score 1396; DB 24; Length 1619;

Beet Local Similarity 99.8%; Pred. No. 0; Mismatches 2; Indels 1; Gaps 1;

Matches 1616; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 280 GGCACATTTTTCGCGATTTGCTTCCTCCAGCTTTGGCTGCAATTCAGTGTACCA 339
 DB 1 GGCACATTTTTCGCGATTTGCTTCCTCCAGCTTTGGCTGCAATTCAGTGTACCA 60
 QY 340 GTGTGAAGAAATTCACAGCTAACAAGACGCTGCTCTCCCGAGTTCATTGTGAATTGCAC 399
 DB 61 GTGTGAAGAAATTCACAGCTAACAAGACGCTGCTCTCCCGAGTTCATTGTGAATTGCAC 120
 QY 400 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 459
 DB 121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 180
 QY 460 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTCTGCGGGTACAGTCTT 519
 DB 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTCTGCGGGTACAGTCTT 240
 QY 520 CTGCTCCGAGGAAATCACTAGTTGATCAGCTGCTGCAACACCCCTTGTGA 579
 DB 241 CTGCTCCGAGGAAATCACTAGTTGATCAGCTGCTGCAACACCCCTTGTGA 300
 QY 580 CGGCGCAAGGCCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCAGGCCAGGGCTCCGAC 639
 DB 301 CGGCGCAAGGCCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCAGGCCAGGGCTCCGAC 360
 QY 640 CACCATCTGTTCTCAAAATTAAGCCCTTCTGCGCACACTGCTCAAGCTGAGAGATG 699
 DB 361 CACCATCTGTTCTCAAAATTAAGCCCTTCTGCGCACACTGCTCAAGCTGAGAGATG 420
 QY 700 CACACCCCTCCGATGTTCTTCAAGCCCTGCGCCCAACCCCACTCCCTAGTGA 759
 DB 421 CACACCCCTCCGATGTTCTTCAAGCCCTGCGCCCAACCCCACTCCCTAGTGA 480
 QY 760 GTTCTTCTGCGGTCCTTTTATTCGTGAGGAGCGGAGTCCGTTCTCTTTTGT 819
 DB 481 GTTCTTCTGCGGTCCTTTTATTCGTGAGGAGCGGAGTCCGTTCTCTTTTGT 540
 QY 820 CCTGTGCAAAATTAAGAAAGAGCTCGGTAAAGCAATTCGAATTAATTCAGCTGAAT 879
 DB 541 CCTGTGCAAAATTAAGAAAGAGCTCGGTAAAGCAATTCGAATTAATTCAGCTGAAT 600
 QY 880 TTTTCAATGATCTGTAAGCAAGAGAGTGAAGAAAGTCAACCCCACTGTGTGTAC 939
 DB 601 TTTTCAATGATCTGTAAGCAAGAGAGTGAAGAAAGTCAACCCCACTGTGTGTAC 660

QY 940 CGGAGTCAAGGCCAGGCTGCGACAGTCMTGCTTTAGAAAGTCACTAGTGGCCATCTGCC 999
 DB 661 CGGAGTCAAGGCCAGGCTGCGACAGTCMTGCTTTAGAAAGTCACTAGTGGCCATCTGCC 720
 QY 1000 TTTTGAAGCCCTCCAGTGTCCATTCATTCCTCGATGAGGAGCATTAATTGAGACTGCA 1059
 DB 721 TTTTGAAGCCCTCCAGTGTCCATTCATTCCTCGATGAGGAGCATTAATTGAGACTGCA 780
 QY 1060 GTGAGATGAGCTTTTCTTGAAGGCTGAGGAGCCAGTTCCACATCAAGGCCCTCGCTTG 1119
 DB 781 GTGAGATGAGCTTTTCTTGAAGGCTGAGGAGCCAGTTCCACATCAAGGCCCTCGCTTG 840
 QY 1120 ACATTCAAATTCATGCTCTCTGAAACCAATTCCTGACAGCAATTTGGCTGTTTGGCC 1179
 DB 841 ACATTCAAATTCATGCTCTCTGAAACCAATTCCTGACAGCAATTTGGCTGTTTGGCC 900
 QY 1180 CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACTGAGCTTAAGACTGGGCTCGGCT 1239
 DB 901 CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACTGAGCTTAAGACTGGGCTCGGCT 960
 QY 1240 CGCTCTGAAAGAGCTTAAAGAAATCTTTCAGTTCTCTTGGCAGAGGACTGGCGCGGG 1299
 DB 961 CGCTCTGAAAGAGCTTAAAGAAATCTTTCAGTTCTCTTGGCAGAGGACTGGCGCGGG 1020
 QY 1300 ACGGAGAGAGCAAGCGGCGCTGACCAAAAGCGGCGCTGCTGCTGAGTGGCATGTA 1359
 DB 1021 ACGGAGAGAGCAAGCGGCGCTGACCAAAAGCGGCGCTGCTGCTGAGTGGCATGTA 1080
 QY 1360 CGGCGAGGCGCTTCTGCTGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1418
 DB 1081 CGGCGAGGCGCTTCTGCTGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 QY 1419 ACGAAGACCCGCGCAACCTGCTGAGAGACACCGTGTACAGAGAGGAGTGTATGACGAG 1478
 DB 1141 ACGAAGACCCGCGCAACCTGCTGAGAGACACCGTGTGTACAGAGAGGAGTGTATGACGAG 1200
 QY 1479 CTGAGGTAGAAAACGTTCTCGAGAAAGGAGAGAGATCATGTACGCCGGAATGAGAC 1538
 DB 1201 CTGAGGTAGAAAACGTTCTCGAGAAAGGAGAGAGATCATGTACGCCGGAATGAGAC 1260
 QY 1539 CTGCTCCAGTGTGCTGTTGGCTGCGGAGCCATGATCTCCGAATCTGTTGGGCTATC 1598
 DB 1261 CTGCTCCAGTGTGCTGTTGGCTGCGGAGCCATGATCTCCGAATCTGTTGGGCTATC 1320
 QY 1599 CAGCATACGGCCATGTCTCAACAAATCAGCCCTGAGCAGACAGAGAGGAGAGAGAC 1658
 DB 1321 CAGCATACGGCCATGTCTCAACAAATCAGCCCTGAGCAGACAGAGAGGAGAGAGAC 1380
 QY 1659 AGAGAAAAGAAAACACAGCATGAGAACACATGAATGAATGAATGAATGAATGAAT 1718
 DB 1381 AGAGAAAAGAAAACACAGCATGAGAACACATGAATGAATGAATGAATGAATGAAT 1440
 QY 1719 CCGCTGCTGTGCTGTACGCGCAGAGAAATGTTTTCATGTTTTCATGTTTTCATG 1778
 DB 1441 CCGCTGCTGTGCTGTACGCGCAGAGAAATGTTTTCATGTTTTCATGTTTTCATG 1500
 QY 1779 CAGCTTCTTTGCGACAAAGCAAGAGAAATTTAACTGTTTTCAAACCCGCGGAGTTGG 1838
 DB 1501 CAGCTTCTTTGCGACAAAGCAAGAGAAATTTAACTGTTTTCAAACCCGCGGAGTTGG 1560
 QY 1839 CTGTGTTAAGAAAGACATTAATTAATGCTTTAGACAGTGTAAAAAATTAATTAAT 1897
 DB 1561 CTGTGTTAAGAAAGACATTAATTAATGCTTTAGACAGTGTAAAAAATTAATTAAT 1619

RESULT 10

AA93845

ID AA93845 standard; cDNA; 1890 BP.

XX AA93845:

XX

XX 23-MAY-2001 (first entry)

XX

DE Human cDNA encoding a membrane or secretory protein clone PSEC0181.
XX
XX Human; secretory protein; membrane protein; vaccine; gene therapy;
KM rheumatoid arthritis; diabetes; ss.
XX Homo sapiens.
OS
XX EP1067182-A2.
XX
XX 10-JAN-2001.
PD
XX
XX 07-JUL-2000; 2000EP-0114090.
PE
XX
XX 08-JUL-1999; 99JP-0194179.
PR 11-JAN-2000; 2000JP-0118775.
PR 02-MAY-2000; 2000JP-0183766.
XX
XX (HELI-) HELIX RES INST.
PA
XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
PI
XX WPI; 2001-093989/71.
DR
XX P-PSDB; AAB88418.
XX
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development -
PS
XX Claim 1; SEQ ID 203; 609pp + CD ROM; English.
XX
XX This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by
CC AAB88317 - AAB88419. Included in the invention are primers
CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
CC cDNA sequences of the invention. The invention also includes methods for
CC the production of antibodies directed against the proteins, and cDNA
CC sequences, which can be used in vaccines. The polynucleotide sequences
CC can be used in gene therapy. The polynucleotide sequences and the
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate secretory
CC protein/membrane protein expression. The nucleic acids and complementary
CC sequences may also be used as DNA probes in diagnostic assays
CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC presence of similar nucleic acid sequences in samples. They may also be
CC used to study the expression and function of secretory proteins/membrane
CC polypeptides and their role in metabolism. The polypeptides may be used
CC as antigens in the production of antibodies against them and in assays to
CC identify modulators (agonists and antagonists) of expression and
CC activity. The antibodies and antagonists may also be used as therapeutic
CC agents to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA)). Examples of diseases which may be treated include rheumatoid
CC arthritis and diabetes.
XX
XX Sequence 1890 BP; 419 A; 528 C; 533 G; 410 T; 0 other:
SQ

Query Match 70.8%; Score 1344; DB 22; Length 1890;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1854; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Db 213 CTCGCTGCTGTCGCCCTCTGATGGCGCTTCCGCCGCCCGGAGATCCGGAG 272
Qy 259 AATGGGCTCTAGGCAATGCGGCACTTTTGGGATGTTCTTCTCCAGGCTTTC 318
Db 273 AATGGGCTCTAGGCAATGCGGCACTTTTGGGATGTTCTTCTCCAGGCTTTC 332
Qy 319 GCTGCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACAGAGCTGCTCC 378
Db 333 GCTGCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACAGAGCTGCTCC 392
Qy 379 CGAGTTATTGTGATTTGACAGGTGAACGTTCAAGACATGTGACAAAGATGTA 438
Db 393 CGAGTTATTGTGATTTGACAGGTGAACGTTCAAGACATGTGACAAAGATGTA 452
Qy 439 GCAAGTCCGGGGATCATATGACGCAAGTCTGTGATCATGAGGCGGCTCATGCG 498
Db 453 GCAAGTCCGGGGATCATATGACGCAAGTCTGTGATCATGAGGCGGCTCATGCG 512
Qy 499 CTCTGCCGGGTACAGTCTTCTGCTCCAGGGAACCTGAATGATTTGATCAGCTG 558
Db 513 CTCTGCCGGGTACAGTCTTCTGCTCCAGGGAACCTGAATGATTTGATCAGCTG 572
Qy 559 CTGCAACACCCCTCTTTTGAACGGGCCAAGGCCCAAGAAAAGGGAATTCCTCGC 618
Db 573 CTGCAACACCCCTCTTTTGAACGGGCCAAGGCCCAAGAAAAGGGAATTCCTCGC 632
Qy 619 CCTAGGCGAAGGGGTCCGCAACCAATCCTGTTCTCAATTAATGCTCTCTCCGCA 678
Db 633 CTTAGGCGAAGGGGTCCGCAACCAATCCTGTTCTCAATTAATGCTCTCTCCGCA 691
Qy 679 CTGCTGAAGCTGAAGAGATGCAACCCCTCTGATTTGTTTCCAGCCCTGCCCA 738
Db 692 CTGCTGAAG-CTGAAGAGATGCAACCCCTCTGATTTGTTTCCAGCCCTGCCCA 750
Qy 739 ACCCCCAACCTCTCTGATGATTTCTTGGGTTCTTTTATTTGGGTAGGAGCG 798
Db 751 ACCCCCAACCTCTCTGATGATTTCTTGGGTTCTTTTATTTGGGTAGGAGCG 810
Qy 799 GAGTCGCTGCTCTTTTGTTCCTGCAATTAATGAAGTCCGGTAAAGATTCGA 858
Db 811 GAGTCGCTGCTCTTTTGTTCCTGCAATTAATGAAGTCCGGTAAAGATTCGA 870
Qy 859 ATAAATTCAGCTGATGAATTTTCACTATGTAAGGAAGAGGTGAGTGAAGT 918
Db 871 ATAAATTCAGCTGATGAATTTTCACTATGTAAGGAAGAGGTGAGTGAAGT 930
Qy 919 TCACCCCAATGCTGTGTAAACCGAGTCAAGGCCAGGCTGCAAGTCACTTGAAG 978
Db 931 TCACCCCAATGCTGTGTAAACCGAGTCAAGGCCAGGCTGCAAGTCACTTGAAG 990
Qy 979 TCACCTGAAGTGGGATGCTTTTGAAGCCCTGATTCATTCATTCCTGATGG 1038
Db 991 TCACCTGAAGTGGGATGCTTTTGAAGCCCTGATTCATTCATTCCTGATGG 1050
Qy 1039 GGCATGATTTGAGACTCAGAGTGAAGTGAAGTTCCTTAGGGCTGAGGGCCAGTTC 1098
Db 1051 GGCATGATTTGAGACTCAGAGTGAAGTGAAGTTCCTTAGGGCTGAGGGCCAGTTC 1110
Qy 1099 CACTCAAGGCTCCTCGCTTGAACATTCATTCATTCATTCATTCATTCATTC 1158
Db 1111 CACTCAAGGCTCCTCGCTTGAACATTCATTCATTCATTCATTCATTCATTC 1170
Qy 1159 CAGAAATGGGCTGCTTGGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1218
Db 1171 CAGAAATGGGCTGCTTGGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1230
Qy 1219 ACTTAGACTGGGGCTCGGCTGCTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGT 1277
Db 1231 ACTTAGACTGGGGCTCGGCTGCTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGT 1290
Qy 1278 CTTGCAAGGACTGGGCGGAGCGGAGAGCAAGCGGCGCTGCAAAAGCGGCGCTG 1337
Db 1290 CTTGCAAGGACTGGGCGGAGCGGAGAGCAAGCGGCGCTGCAAAAGCGGCGCTG 1337

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Db 1291 CTTCAGAGAGACTGCGCCGCGGACGCGAAGCAACGGGCGCTGCACAAAGCGGCGCTG 1350
OY 1338 TCGGTGTGAGTGGCATGACCGCGCAGCGCTTCTCGTGGTGGCCGTGACAGCGAC 1397
Db 1351 TCGGTGTGAGTGGCATGACCGCGCAGCGCTTCTCGTGGTGGCCGTGACAGCGAC 1410
OY 1398 AGCGGCGACACAGCACTGACAGAACACCCCGCAAACTGCTGGGAGGACACCGTGTAC 1457
Db 1411 AGCGGCGACACAGCACTGACAGAACACCCCGCAAACTGCTGGGAGGACACCGTGTAC 1470
OY 1458 AGAGCGGGTGTATGACCCAGCTGAGGTGAGAAAACGTCTCCGAGAGGGAGAGAGATC 1517
Db 1471 AGAGCGGGTGTATGACCCAGCTGAGGTGAGAAAACGTCTCCGAGAGGGAGAGATC 1530
OY 1518 ATGTACGCCCGGAGTGAAGCACTGCTCAGTGTGCTGGTGGTGGCCGACCATGATC 1577
Db 1531 ATGTACGCCCGGAGTGAAGCACTGCTCAGTGTGCTGGTGGTGGCCGACCATGATC 1590
OY 1578 CTCGGAATCTGTTGGGCACTCCAGCATGCGCAATGTCAACAATCAGCCCTGGGCGAG 1637
Db 1591 CTCGGAATCTGTTGGGCACTCCAGCATGCGCAATGTCAACAATCAGCCCTGGGCGAG 1650
OY 1638 ACACGACGACGAGGAGACACAGAGAAAAGAAAACACAGCATGAGAACAGTAAATGA 1697
Db 1651 ACACGACGACGAGGAGACACAGAGAAAAGAAAACACAGCATGAGAACAGTAAATGA 1710
OY 1698 ATAAACCATTAATAATTTAGCCCTCTGTTCTGCTTACTGAGGCGAGAAATGTAACA 1757
Db 1711 ATAAACCATTAATAATTTAGCCCTCTGTTCTGCTTACTGAGGCGAGAAATGTAACA 1770
OY 1758 ATTTTCAAGTGTGACCTTGACAGCTTCTTTTGCACAGACAGAGAGAAATTAACATG 1817
Db 1771 ATTTTCAAGTGTGACCTTGACAGCTTCTTTTGCACAGAGAGAGAAATTAACATG 1830
OY 1818 TTTCGAACCGGGGGAGTGGTGTGTTAAGAAAGACCATTAATTCCTTACAGAGTGT 1877
Db 1831 TTTCGAACCGGGGGAGTGGTGTGTTAAGAAAGACCATTAATTCCTTACAGAGTGT 1890

RESULT 11
AADI8690/c
ID AADI8690 standard; cDNA; 2528 BP.
XX
AC AADI8690;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human G protein coupled receptor (GPCR) 4941 cDNA.
XX
KW Human; cardiovascular; tumorigenic disorder; aberrant angiogenesis;
KW gene therapy; aberrant vascularisation; atherosclerosis; ovarian cancer;
KW ischaemia/reperfusion injury; hypertension; arterial inflammation;
KW psoriasis; endothelial cell disorder; diabetic retinopathy; restenosis;
KW myocardial infarction; Grave's disease; G protein coupled receptor;
KW GPCR 4941; vasodilator; hypotensive; antiinflammatory; cytosolic;
KW antidiabetic; antipsoriatic; leukemia; ss.
XX
OS Homo sapiens.
XX
FH Key 42.1403 Location/Qualifiers
FT CDS
FT /tag= a
FT /product= "Human GPCR 4941"
FT /note= "The CDS is specifically claimed in claim 1 of
FT the specification."
XX
PN WO200181634-A2.
PD 01-NOV-2001.
XX
PF 25-APR-2001; 2001WO-US13788.
XX
PR 26-APR-2000; 2000US-199908P.

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PR 09-AUG-2000; 2000US-0635521.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Galvin KA, Rudolph-owen LA;
XX
DR WPI: 2001-611743/70.
XX
DR P-PSDB: AAE11751.
XX
PT Identifying nucleic acids for the diagnosis and treatment of
PT cardiovascular and tumorigenic disorders, comprises identifying G
PT protein coupled receptor (GPCR)-4941
XX
PS Example 1; Fig 1; 118bp; English.
XX
CC The present invention relates to a method for identifying a nucleic acid
CC molecule (G protein coupled receptor gene, GPCR 4941) associated with a
CC cardiovascular or tumorigenic disorder. The method comprising contacting
CC a sample containing a nucleic acid molecule with a hybridisation probe or
CC amplification primers and detecting the presence. The invention is used
CC in gene therapy. The method of the invention is used for identifying
CC nucleic acids or polypeptides associated with a cardiovascular or
CC tumorigenic disorder such as aberrant angiogenesis, aberrant
CC vascularisation, atherosclerosis, or ovarian cancer, ischaemia/
CC reperfusion injury, hypertension, restenosis, arterial inflammation,
CC endothelial cell disorders, diabetic retinopathy, psoriasis, myocardial
CC infarction, Grave's disease and leukemia. The methods can also detect
CC mRNA or genomic DNA in a sample. The present sequence is G protein
CC coupled receptor (GPCR) 4941 cDNA.
XX
SQ Sequence 2528 BP; 516 A; 766 C; 677 G; 567 T; 2 other;
XX
Query Match 64.2%; Score 1218; DB 22; Length 2528;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1318; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 310 AGGCTTTGCGGTGCAAAATCCAGTCTACAGTGTGAAGAAATTCAGCTGAACAAGCACTG 369
Db 2217 AGGCTTTGCGGTGCAAAATCCAGTCTACAGTGTGAAGAAATTCAGCTGAACAAGCACTG 2158
OY 370 CTCCTCCCCCGAGTTCATTTGCAATTTGCACCGGTGAACGTTCAAGACATGTGTGTAAGA 429
Db 2157 CTCCTCCCCCGAGTTCATTTGCAATTTGCACCGGTGAACGTTCAAGACATGTGTGTAAGA 2098
OY 430 AGTATGAGCAAAAGTGGCGGATCATGTACCCGCAAGTCTGTCATCATCAGCGGCTG 489
Db 2097 AGTATGAGCAAAAGTGGCGGATCATGTACCCGCAAGTCTGTCATCATCAGCGGCTG 2038
OY 490 TGTGATCGCTCTGCGGGGTACAGTCTCTGCTCTCCGAGGAACGTGACATGCTTGG 549
Db 2037 TGTGATCGCTCTGCGGGGTACAGTCTCTGCTCTCCGAGGAACGTGACATGCTTGG 1978
OY 550 CATGAGCTGCTGCAACACCCCTTTTAAACGGGCAAGGCCCAAGAAAGGGAAGTTC 609
Db 1977 CATGAGCTGCTGCAACACCCCTTTTAAACGGGCAAGGCCCAAGAAAGGGAAGTTC 1918
OY 610 TGCCTGGCCCTCAAGGCGAGGGCTCCGACACCATCTCTTCCCTCAAAATTAAGCCCTCT 669
Db 1917 TGCCTGGCCCTCAAGGCGAGGGCTCCGACACCATCTCTTCCCTCAAAATTAAGCCCTCT 1858
OY 670 CTGGGACACACTGTGAAGCTGAAGAGATGCCACCCCTCTGCAATTTGTTCCAGCC 729
Db 1857 CTGGGACACACTGTGAAGCTGAAGAGATGCCACCCCTCTGCAATTTGTTCCAGCC 1798
OY 730 TCGCCCCCAACCCCGCAACCTCCGATGAGTGTCTTCTGGGTGCTCTTTATTCGGGT 789
Db 1797 TCGCCCCCAACCCCGCAACCTCCGATGAGTGTCTTCTGGGTGCTCTTTATTCGGGT 1738
OY 790 AGGAGCGGAGTCCGTTCTCTTTTGTCTCTGTGCAATTAATGAAGAGCTCGGTA 849
Db 1737 AGGAGCGGAGTCCGTTCTCTTTTGTCTCTGTGCAATTAATGAAGAGCTCGGTA 1678
OY 850 GCATTCGTGAATTAATTCAGCTGACTGAATTTTCAGTATGTAAGGAAGAGAGTGG 909

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Db 1677 GGAATCTGAAATAAATTCACCTTGAGTAATTTTCAATATGTAAGAGAGAGAGTGG 1618
Oy 910 AGTGAAGATTCACCCCAATGCTGTGTACCGAGTCAAGGCGAGCGGAGATCMT 969
Db 1617 AGTGAAGATTCACCCCAATGCTGTGTGTACCGAGTCAAGGCGAGCGGAGTCAAGT 1558
Oy 970 CCTTGAAGATTCACCGAGTGGGATCTGCTTTTGTAAAGCTCCAGTGTCCATTCATC 1029
Db 1557 CCTTGAAGATTCACCGAGTGGGATCTGCTTTTGTAAAGCTCCAGTGTCCATTCATC 1498
Oy 1030 CCTGATGGGGGATAGTTGTGACATGACAGTGAAGTGAAGCTTTTCTTAAAGCTGGAG 1089
Db 1497 CCTGATGGGGGATAGTTGTGACATGACAGTGAAGTGAAGCTTTTCTTAAAGCTGGAG 1438
Oy 1090 GCGAGTCCCACTCAAGGCTCCCTGCTGACATCAAACTCAAGCTCCCAAAACCAT 1149
Db 1437 GCGAGTCCCACTCAAGGCTCCCTGCTGACATCAAACTCAAGCTCCCAAAACCAT 1378
Oy 1150 TCTTGCACAGCAATTTGGCTGTTTGGCGCTGAGTTGGGCTTGTAGTACAGACATCA 1209
Db 1377 TCTTGCACAGCAATTTGGCTGTTTGGCGCTGAGTTGGGCTTGTAGTACAGACATCA 1318
Oy 1210 ATGACTGGGACTTACAGTGGGCTGCGCTGCTGAAAAGTGGTTAAGAAATCTTCT 1269
Db 1317 ATGACTGGGACTTACAGTGGGCTGCGCTGCTGAAAAGTGGTTAAGAAATCTTCT 1258
Oy 1270 CAGTCTCTCTTCAGAGAGCTGGGCGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1329
Db 1257 CAGTCTCTCTTCAGAGAGCTGGGCGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1198
Oy 1330 GGGGCTGTGGTGTGAGAGTGGCATGTACCGAGCGGCTTCTGTTGGGCTGCT 1389
Db 1197 GGGGCTGTGGTGTGAGAGTGGCATGTACCGAGCGGCTTCTGTTGGGCTGCT 1138
Oy 1390 GAGGAGACAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1449
Db 1137 GAGGAGACAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1078
Oy 1450 CCGTGTACAGAGCGGCTGTGATGACAGGCTGAGTGAAGAAAGCTCCGAGAGAGAG 1509
Db 1077 CCGTGTACAGAGCGGCTGTGATGACAGGCTGAGTGAAGAAAGCTCCGAGAGAGAG 1018
Oy 1510 GAGGATCATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1569
Db 1017 GAGGATCATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 958
Oy 1570 CCATGATCCTCCGAAATGCTGTTGGGATCCAGCAATGCTCAACAATCAAGCC 1629
Db 957 CCATGATCCTCCGAAATGCTGTTGGGATCCAGCAATGCTCAACAATCAAGCC 898

```

RESULT 12

AB054231
ID AB054231 standard; cDNA: 1608 BP.

XX AB054231:

DT 22-AUG-2002 (first entry)

DE Human ovarian antigen HVCAG04 cDNA, SEQ ID NO:111.

XX Human: ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive; chromosome 2q21-22;
 KW gene; ss.

XX Homo sapiens.
 OS
 PN W020020677-A1.
 XX
 PD 03-JAN-2002.
 XX
 XX 07-JUN-2001; 2001WO-US18569.
 XX
 PR 07-JUN-2000; 2000US-209467P.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Blaise CE, Rosen CA;
 DR WPI: 2002-147878/19.
 DR P-PSDB: ABP41154.
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.
 PT ovarian cancer), immune disorders, cardiovascular disorders and
 PT neurological diseases -
 PS
 XX
 XX Claim 1; SEQ ID NO 111; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-
 ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents cDNA encoding a human ovarian antigen of the
 CC invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX

SO Sequence 1608 BP; 402 A; 402 C; 417 G; 381 T; 6 other;

Query Match 60.6%; Score 1150; DB 24; Length 1608;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Oy 627 CAGGCGTCCGACACCATCTGCTTCAAAATTAACCCCTTCTGGCAGACACTGTGA 686
Db 281 CAGGCGTCCGACACCATCTGCTTCAAAATTAACCCCTTCTGGCAGACACTGTGA 340
Oy 687 GCTGAAGAGATGCACACCCCTCTGATGTTCTTCAGACCCCTCCCAACCCCA 746
Db 341 GCTGAAGAGATGCACACCCCTCTGATGTTCTTCAGACCCCTCCCAACCCCA 400
Oy 747 CTTCCCGATGATGTTCTTCTGCGTCTCTTTATTTGAGGAGAGCGGAGTCCGT 806
Db 401 CTTCCCGATGATGTTCTTCTGCGTCTCTTTATTTGAGGAGAGCGGAGTCCGT 460

```


DE Ovarian carcinoma GPR39 cDNA.
 XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
 KW ss.
 OS Homo sapiens.
 XX
 XX
 FT Key Location/Qualifiers
 FT CDS 1..1362
 FT /tag= a
 FT /product= "Ovarian carcinoma protein GPR39"
 XX
 PN US2002004491-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 03-APR-2001; 2001US-0825294.
 XX
 PR 10-SEP-1999; 99US-0394374.
 PR 01-MAY-2000; 2000US-0561778.
 PR 15-AUG-2000; 2000US-0640173.
 PR 07-SEP-2000; 2000US-0656668.
 PR 14-NOV-2000; 2000US-0713550.
 XX
 PA (XUJ/) XU J.
 PA (SLOL/) STOLK J A.
 PA (ALGA/) ALGATE P A.
 PA (FLIN/) FLING S P.
 XX
 PI Xu J, Stolk JA, Algate PA, Fling SP;
 XX
 DR WPI: 2002-171027/22.
 DR P-PSDB; ABB09416.
 XX
 PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
 XX prevention and/or treatment of cancer, especially ovarian cancer
 PS
 PS Claim 1a; Page 123-124; 131pp; English.
 XX
 CC The invention relates to ovarian tumour polynucleotides and polypeptides
 CC that may be utilised in cancer therapy, for example in a vaccine or
 CC gene therapy. Polypeptides and polynucleotides of the invention are
 CC useful for detecting a cancer in a patient, for stimulating and/or
 CC expanding T-cells specific for a tumour protein, and for inhibiting the
 CC development of a cancer in a patient. They are also useful for
 CC stimulating an immune response in a patient, and for treating a cancer in
 CC a patient and for determining the presence of a cancer in a patient.
 CC The isolated polynucleotides of the invention are useful for their
 CC ability to selectively form duplex molecules with complementary stretches
 CC of the entire desired gene or gene fragments, and for designing and
 CC preparing ribozyme molecules for inhibiting expression of tumour
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
 CC invention are also useful in recombinant DNA molecules to direct
 CC expression of a polypeptide in appropriate host cells. The current
 CC sequence represents the ovarian carcinoma GPR39 cDNA.
 CC
 XX
 SO Sequence 1362 BP; 263 A; 435 C; 362 G; 302 T; 0 other;
 XX
 XX Query Match 26.7%; Score 506; DB 24; Length 1362;
 XX Best Local Similarity 100.0%; Pred. No. 7.8e-194;
 XX Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1124 TCMAACTCATGCTCTGTAACCATTCCTGACAGCAATGAGGCTGGTGGCCCTGA 1183
 DB 1362 TCAAACTTATGCTCTGTAACCATTCCTGACAGCAATGAGGCTGGTGGCCCTGA 1303
 QY 1184 GTTGGCTCTAGTACTGAGACTGAGACTGAGACTTGAAGTGGGCTGGCCCTGCT 1243
 DB 1302 GTTGGCTCTAGTACTGAGACTGAGACTGAGACTTGAAGTGGGCTGGCCCTGCT 1243
 QY 1244 CTGAAAGTGTGTTAGAAATCTTCTCACTTCTCTTGAGAGAGACTGGCGCGGAGACG 1303
 DB 1242 CTGAAAGTGTGTTAGAAATCTTCTCACTTCTCTTGAGAGAGACTGGCGCGGAGACG 1183

QY 1304 GAAGAGCAACGGGCGCTGCACAAAGCGGCGCTGTCGTTGTGAGATGGCATGTACGG 1363
 DB 1182 GAAGAGCAACGGGCGCTGCACAAAGCGGCGCTGTCGTTGTGAGATGGCATGTACGG 1123
 QY 1364 CAGGCGCTTCTGCTGTTGGCTGCTGCAGCAGCAGCGGCGACACAGCAGCTGCACGAA 1423
 DB 1122 CAGGCGCTTCTGCTGTTGGCTGCTGCAGCAGCAGCGGCGACACAGCAGCTGCACGAA 1063
 QY 1424 CACCCGCGAACTGCTGCAGAGACACCGTGTACAGAGCGGGTTATATACGAGCTGAG 1483
 DB 1062 CACCCGCGAACTGCTGCAGAGACACCGTGTACAGAGCGGGTTATATACGAGCTGAG 1003
 QY 1484 GTAGAAAACGCTCCGAGAGAGGAGAGATCATGTACGCCCGGAGTAGACCTGCT 1543
 DB 1002 GTAGAAAACGCTCCGAGAGAGGAGAGATCATGTACGCCCGGAGTAGACCTGCT 943
 QY 1544 CCACTGCTGCTGTTGGCTGCTGCAGCAGCAGCATGATCTCCGAATCTGTTGGCATCCAGCA 1603
 DB 942 CCACTGCTGCTGTTGGCTGCTGCAGCAGCAGCATGATCTCCGAATCTGTTGGCATCCAGCA 883
 QY 1604 TAGGCGCAATGTCAACAATCAGCC 1629
 DB 882 TAGGCGCAATGTCAACAATCAGCC 857
 XX
 XX RESULT 19
 XX ABR03283
 XX ID ABR03283 standard; cDNA; 480 BP.
 XX
 XX ABR03283;
 XX
 XX 05-SEP-2002 (first entry)
 XX
 XX Human ovarian carcinoma associated coding sequence SEQ ID NO: 213.
 XX
 XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
 XX cytosolic; gene; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO200239885-A2.
 XX
 XX 23-MAY-2002.
 XX
 XX 13-NOV-2001; 2001WO-US45395.
 XX
 XX 14-NOV-2000; 2000US-0713550.
 XX 03-APR-2001; 2001US-0825294.
 XX 02-OCT-2001; 2001US-0970966.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 XX Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
 XX
 XX WPI: 2002-500186/53.
 XX
 XX Novel ovarian cancer polypeptide and polynucleotide, useful for
 XX detecting the presence of ovarian cancer in a patient, and in
 XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
 XX
 XX Claim 2; Page 196; 197pp; English.
 XX
 XX The present invention provides human ovarian cancer associated proteins
 XX and coding sequences. The sequences can be used in the diagnosis and
 XX treatment of ovarian cancers. The present sequence is a coding sequence
 XX of the invention.
 XX
 XX Sequence 480 BP; 86 A; 154 C; 153 G; 87 T; 0 other;
 XX
 XX Query Match 22.4%; Score 425; DB 24; Length 480;
 XX Best Local Similarity 99.8%; Pred. No. 3.3e-161;
 XX

Matches 475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCAACTCCGAGGCTCTGTGCTCTGCGCCGCGAGCGGAGCGGAGAGAGAGACCCG 60
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 GCCAACTCCGAGGCTCTGTGCTCTGCGCCGCGAGCGGAGCGGAGAGAGAGACCCG 60
 QY 61 CACCCGGAGAGCCGAGCGGCGGAGATGACAGGCTCCCGAGCGGACCTCGGCTCTCTA 120
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 CACCCGGAGAGCCGAGCGGCGGAGATGACAGGCTCCCGAGCGGACCTCGGCTCTCTA 120
 QY 121 AGCTAGACCGTCTGTCCGCGGAGAGCGGCGGCGGAGCGGAGCGGAGCGGAGCGG 180
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 AGCTAGACCGTCTGTCCGCGGAGAGCGGCGGCGGAGCGGAGCGGAGCGGAGCGG 180
 QY 181 CGCTGACCGCGGAGCGGAGCTCGCTCTGTGAGCGCTCTGAGCGCTCTGCGG 240
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 CGCTGACCGCGGAGCGGAGCTCGCTCTGTGAGCGCTCTGAGCGCTCTGCGG 240
 QY 241 GCCCGGGAGCTCCGCGGAGAGATGAGGCTCTAGGAGTCCGCGGACCTTTTGGGATGTT 300
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 GCCCGGGAGCTCCGCGGAGAGATGAGGCTCTAGGAGTCCGCGGACCTTTTGGGATGTT 300
 QY 301 CTGTCTCCAGGCTTTCGCTGCAATCCAGTCTACAGTCTGAGAGATTCAGCTGAA 360
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 CTGTCTCCAGGCTTTCGCTGCAATCCAGTCTACAGTCTGAGAGATTCAGCTGAA 360
 QY 361 CAACGACTGCTCTCCCGGAGTTCATTTGTAATTCAGCGGTGAACGTTCAAGACATGTG 420
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 CAACGACTGCTCTCCCGGAGTTCATTTGTAATTCAGCGGTGAACGTTCAAGACATGTG 420
 QY 421 TCAGAAAGAGATGATGAGCAAAAGTCCGCGGATCATGTACCCGAGTCTGTGAT 476
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 TCAGAAAGAGATGATGAGCAAAAGTCCGCGGATCATGTACCCGAGTCTGTGAT 476

RESULT 20
 ABL40351
 ID ABL40351 standard; cDNA; 480 BP.
 AC ABL40351;
 DT 28-JUN-2002 (first entry)
 DE Ovarian carcinoma BE336607 nucleotide sequence.
 KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
 KM ss.
 OS Homo sapiens.
 PN US2002004491-A1.
 PD 10-JAN-2002.
 PF 03-APR-2001; 2001US-0825294.
 PR 10-SEP-1999; 99US-0394374.
 PR 01-MAY-2000; 2000US-0561778.
 PR 15-AUG-2000; 2000US-0640173.
 PR 07-SEP-2000; 2000US-0656668.
 PR 14-NOV-2000; 2000US-0713550.
 PA (XUJ/) XU J.
 PA (STOL/) STOLK J A.
 PA (ALGA/) ALGATE P A.
 PA (FLIN/) FLING S P.
 PI Xu J, Stolk JA, Algate PA, Fling SP;
 DR WPI; 2002-171027/22.
 PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
 prevention and/or treatment of cancer, especially ovarian cancer.

XX XX
 PS Claim 1a; Page 127; 131p; English.
 CC The invention relates to ovarian tumour polynucleotides and polypeptides
 CC that may be utilised in cancer therapy, for example in a vaccine or
 CC gene therapy. Polypeptides and polynucleotides of the invention are
 CC useful for detecting a cancer in a patient, for stimulating and/or
 CC expanding T-cells specific for a tumour protein, and for inhibiting the
 CC development of a cancer in a patient. They are also useful for
 CC stimulating an immune response in a patient, and for treating a cancer in
 CC a patient and for determining the presence of a cancer in a patient.
 CC The isolated polynucleotides of the invention are useful for their
 CC ability to selectively form duplex molecules with complementary stretches
 CC of the entire desired gene or gene fragments, and for designing and
 CC preparing ribozyme molecules for inhibiting expression of tumour
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
 CC invention are also useful in recombinant DNA molecules to direct
 CC expression of a polypeptide in appropriate host cells. The current
 CC sequence represents the ovarian carcinoma BE336607 nucleotide sequence.
 CC
 SQ Sequence 480 BP; 86 A; 154 C; 153 G; 87 T; 0 other;

Query Match 22.4%; Score 425; DB 24; Length 480;
 Best Local Similarity 99.8%; Pred. No. 3.3e-161;
 Matches 475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCAACTCCGAGGCTCTGTGCTCTGCGCCGCGAGCGGAGCGGAGAGAGAGACCCG 60
 Db 1 GCCAACTCCGAGGCTCTGTGCTCTGCGCCGCGAGCGGAGCGGAGAGAGAGACCCG 60
 QY 61 CACCCGGAGAGCCGAGCGGCGGAGATGACAGGCTCCCGAGCGGACCTCGGCTCTCTA 120
 Db 61 CACCCGGAGAGCCGAGCGGCGGAGATGACAGGCTCCCGAGCGGACCTCGGCTCTCTA 120
 QY 121 AGCTAGACCGTCTGTCCGCGGAGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 180
 Db 121 AGCTAGACCGTCTGTCCGCGGAGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 180
 QY 181 CGCTGACCGCGGAGCGGAGCTCGCTCTGTGAGCGCTCTGAGCGCTCTGCGG 240
 Db 181 CGCTGACCGCGGAGCGGAGCTCGCTCTGTGAGCGCTCTGAGCGCTCTGCGG 240
 QY 241 GCCCGGGAGCTCCGCGGAGAGATGAGGCTCTAGGAGTCCGCGGACCTTTTGGGATGTT 300
 Db 241 GCCCGGGAGCTCCGCGGAGAGATGAGGCTCTAGGAGTCCGCGGACCTTTTGGGATGTT 300
 QY 301 CTGTCTCCAGGCTTTCGCTGCAATCCAGTCTACAGTCTGAGAGATTCAGCTGAA 360
 Db 301 CTGTCTCCAGGCTTTCGCTGCAATCCAGTCTACAGTCTGAGAGATTCAGCTGAA 360
 QY 361 CAACGACTGCTCTCCCGGAGTTCATTTGTAATTCAGCGGTGAACGTTCAAGACATGTG 420
 Db 361 CAACGACTGCTCTCCCGGAGTTCATTTGTAATTCAGCGGTGAACGTTCAAGACATGTG 420
 QY 421 TCAGAAAGAGATGATGAGCAAAAGTCCGCGGATCATGTACCCGAGTCTGTGAT 476
 Db 421 TCAGAAAGAGATGATGAGCAAAAGTCCGCGGATCATGTACCCGAGTCTGTGAT 476

RESULT 21
 AAF94186/c
 ID AAF94186 standard; DNA; 587 BP.
 AC AAF94186;
 DT 23-MAY-2001 (first entry)
 DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 620.
 DE Human; secretory protein; membrane protein; vaccine; gene therapy;
 KW rheumatoid arthritis; diabetes; PCR primer; ss.
 KM Synthetic.

XX EP1067182-A2.
 XX 10-JAN-2001.
 XX 07-JUL-2000; 2000EP-0114090.
 XX 08-JUL-1999; 99JP-0194179.
 PR 11-JAN-2000; 2000JP-0118775.
 PR 02-MAY-2000; 2000JP-0183766.
 XX (HELI-) HELIX RES INST.
 XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
 DR WPI; 2001-093989/11.
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
 PT gene therapy or as candidate target molecules in drug development -
 XX Claim 5; SEQ ID 620; 609pp + CD ROM; English.
 PS
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by
 CC AAB88317 - AAB88419. Included in the invention are primers
 CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
 CC cDNA sequences of the invention. The invention also includes methods for
 CC the production of antibodies directed against the proteins, and cDNA
 CC sequences, which can be used in vaccines. The polynucleotide sequences
 CC can be used in gene therapy. The polynucleotide sequences and the
 CC proteins they encode may be used in the prevention, treatment and
 CC diagnosis of diseases associated with inappropriate secretory
 CC protein/membrane protein expression. The nucleic acids and complementary
 CC sequences may also be used as DNA probes in diagnostic assays
 CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
 CC presence of similar nucleic acid sequences in samples. They may also be
 CC used to study the expression and function of secretory proteins/membrane
 CC polypeptides and their role in metabolism. The polypeptides may be used
 CC as antigens in the production of antibodies against them and in assays to
 CC identify modulators (agonists and antagonists) of expression and
 CC activity. The antibodies and antagonists may also be used as therapeutic
 CC agents to down regulate expression and activity. The antibodies may also
 CC be used as diagnostic agents for detecting the presence of the
 CC polypeptides in samples (e.g. by enzyme linked immunosorbent assay
 CC (ELISA). Examples of diseases which may be treated include rheumatoid
 CC arthritis and diabetes.
 CC
 XX
 XX Sequence 587 BP; 117 A; 162 C; 140 G; 162 T; 6 other;
 SQ
 Query Match 19.3%; Score 366; DB 22; Length 587;
 Best Local Similarity 99.8%; Pred. No. 1.7e-137;
 Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1761 TTTCAGTGTGGAGCTTGACAGCTTCCTTTGCGACAGAGAGAGAAATTAACACTGTTT 1820
 |||||||
 DB 117 TTTCAGTGTGGAGCTTGACAGCTTCCTTTGCGACAGAGAGAGAAATTAACACTGTTT 58
 |||||||
 OY 1821 CAACCCGGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAGACAGTGT 1877
 |||||||
 DB 57 CAACCCGGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAGACAGTGT 1
 |||||||
 RESULT 22
 AAH50766/c
 ID AAH50766 standard; cDNA; 444 BP.
 XX
 AC AAH50766;
 XX
 DT 23-AUG-2001 (first entry)
 XX
 DE Human tumour associated cDNA #95.
 XX
 KW Human: cancer specific gene expression: gene therapy;
 KW age related differential expression: ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200136685-A2.
 PD 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-US31809.
 XX
 PR 17-NOV-1999; 99US-0166056.
 PR 17-NOV-1999; 99US-0166106.
 XX
 PA (NYXT-) NYXTS NEURO THERAPIES INC.
 XX
 PI Kroes RA, Moskal JR, Yamamoto H;
 PI
 DR WPI; 2001-355647/37.
 XX
 PT Novel nucleic acid molecules differentially expressed in brain cancers,
 PT useful for ascertaining propensity of cell for malignant phenotype or
 PT ascertaining suitability of anti-neoplastic drug candidate -
 XX Claim 28; Page 50; 82pp; English.
 CC
 CC The present invention provides the sequences of 184 cDNA fragments which
 CC are differentially expressed in cancer cell depending on the age of the
 CC patient. They can be used to diagnose and identify treatments for
 CC cancers, particularly brain cancers such as haemangioblastoma, teratoma,
 CC haemangioma, glioblastoma, schwannoma, osteoma and pinealoma. The
 CC present sequence is a cancer-associated cDNA of the invention.
 CC
 XX
 XX Sequence 444 BP; 95 A; 113 C; 94 G; 142 T; 0 other;
 SQ
 Query Match 19.2%; Score 364; DB 22; Length 444;
 Best Local Similarity 99.8%; Pred. No. 1.1e-136;
 Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1714 TTATGCCCTCTGTTCTGTTCTACTGCGCAGGAATGTACCAATTTTTCAGTGTGA 1773
 |||||
 Db 191 TTATGCCCTCTGTTCTGTTCTACTGCGCAGGAATGTACCAATTTTTCAGTGTGA 132
 QY 1774 CTTGACAGCTTCTTTTCCACAGAGAGAAATTTTAACTGTTTCAACCCGGGGGA 1833
 |||||
 Db 131 CTTGACAGCTTCTTTTCCACAGAGAGAAATTTTAACTGTTTCAACCCGGGGGA 72
 QY 1834 GTTGGCTGTGTAAAGAACATTAATGCTTTGACAGTGTAAAAA 1888
 |||||
 Db 71 GTTGGCTGTGTAAAGAACATTAATGCTTTGACAGTGTAAAAA 17

RESULT 23

AAF94818
 ID AAF94818 standard; cDNA: 396 BP.

AC AAF94818;

DT 23-MAY-2001 (first entry)

DE Human ovarian cancer associated coding sequence SEQ ID NO: 9.

KW Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.

OS Homo sapiens.

PN WO200118046-A2.

PD 15-MAR-2001.

PF 08-SEP-2000; 2000WO-US24827.

PR 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.

PR 15-AUG-2000; 2000US-0640173.

PR 07-SEP-2000; 2000US-0656668.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA;

DR WPI: 2001-211395/21.

PT Isolated polypeptides associated with ovarian carcinomas, and the

PT nucleic acids that encode them, useful for the prevention diagnosis and

PT treatment of ovarian cancers.

PS Claim 5; Page 119; 189pp; English.

XX The present invention provides a number of coding sequences and proteins,

CC the over-expression of which is associated with ovarian carcinoma/cancer.

CC These can be used in the diagnosis, treatment and prevention of ovarian

CC cancer, optionally by gene therapy or in the form of a vaccine. The

CC present sequence is an example of one of these sequences.

CC Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other;

QY Query Match 16.7%; Score 316; DB 22; Length 396;

Best Local Similarity 100.0%; Pred. No. 2.3e-117;

Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 125 TTGCACGGTGAACGTTTCAAGACATGTGTACAGAAAGAACTGATGACGAACAGTCCCGGAT 184
 QY 454 CATGATCCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATTCGCTTGGCGGTACCA 513
 |||||
 Db 185 CATGATCCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATTCGCTTGGCGGTACCA 244
 QY 514 GTCCCTTGTGCTCCCGGCAAGTGAACACTGATTGATCATGCGTCCGACACCCCTCT 573
 |||||
 Db 245 GTCCCTTGTGCTCCCGGCAAGTGAACACTGATTGATCATGCGTCCGACACCCCTCT 304
 QY 574 TTGTAAACGGGCCAAGG 589
 |||||
 Db 305 TTGTAAACGGGCCAAGG 320

RESULT 24

ABT03085
 ID ABT03085 standard; cDNA: 396 BP.

AC ABT03085;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 9.

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

OS Homo sapiens.

PN WO200239885-A2.

PD 23-MAY-2002.

PF 13-NOV-2001; 2001WO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825284.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

DR WPI: 2002-500186/53.

PT Novel ovarian cancer polypeptide and polynucleotide, useful for

PT detecting the presence of ovarian cancer in a patient, and in

PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

PS Example 1; Page 116; 197pp; English.

XX The present invention provides human ovarian cancer associated proteins

CC and coding sequences. The sequences can be used in the diagnosis and

CC treatment of ovarian cancers. The present sequence is a coding sequence

CC of the invention.

CC Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other;

QY Query Match 16.7%; Score 316; DB 24; Length 396;

Best Local Similarity 100.0%; Pred. No. 2.3e-117;

Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

|||||
Db 125 TTGCACGGTGAACGTTCAAGACATGTGCAGAAAGATGAGCAAGTCCGGAT 184
Oy 454 CATGTACCGCAAGTCTCTGCATCATCAGCGGCTGTCTCATCGCTTGGCGGTACCA 513
Db 185 CATGTACCGCAAGTCTCTGCATCATCAGCGGCTGTCTCATCGCTTGGCGGTACCA 244
Oy 514 GTCTTGTGCTCCCGAGGAACGTGACTGATTGTCATCAGCTGCTCAACACCCCTCT 573
Db 245 GTCTTGTGCTCCCGAGGAACGTGACTGATTGTCATCAGCTGCTCAACACCCCTCT 304
Oy 574 TTGTACGGGGCCCAAG 589
Db 305 TTGTACGGGGCCCAAG 320

RESULT 25
ABLA8768
ID ABLA8768 standard; cDNA: 396 BP.
AC ABLA8768;
XX 18-JUN-2002 (first entry)
DE Ovarian carcinoma sequence isolate 21920.
XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
KW ss.
XX Homo sapiens.
OS
XX US2002004491-A1.
XX 10-JAN-2002.
XX 03-APR-2001; 2001US-0825294.
XX 10-SEP-1999; 99US-0394374.
XX 01-MAY-2000; 2000US-0561778.
XX 15-AUG-2000; 2000US-0640173.
XX 07-SEP-2000; 2000US-0656668.
XX 14-NOV-2000; 2000US-0713550.
XX
XX (XUJ/J) XU J.
XX (STOL/J) STOLK J A.
XX (ALCA/P) ALGATE P A.
XX (FLIN/S) FLING S P.
XX Xu J, Stolk JA, Algate PA, Fling SP;
XX WPI: 2002-171027/22.
XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX prevention and/or treatment of cancer, especially ovarian cancer.
XX Claim 1a; Page 41-42; 131pp; English.
XX
XX The invention relates to ovarian tumour polynucleotides and polypeptides
XX that may be utilised in cancer therapy, for example in a vaccine or
XX gene therapy. Polypeptides and polynucleotides of the invention are
XX useful for detecting a cancer in a patient, for stimulating and/or
XX expanding T-cells specific for a tumour protein, and for inhibiting the
XX development of a cancer in a patient. They are also useful for
XX stimulating an immune response in a patient, and for treating a cancer in
XX a patient and for determining the presence of a cancer in a patient.
XX The isolated polynucleotides of the invention are useful for their
XX ability to selectively form duplex molecules with complementary stretches
XX of the entire desired gene or gene fragments, and for designing and
XX preparing ribozyme molecules for inhibiting expression of tumour
XX polypeptides in tumour cells. Polypeptides and polynucleotides of the
XX invention are also useful in recombinant DNA molecules to direct
XX expression of a polypeptide in appropriate host cells. The sequences
XX given in records ABLA8760-ABLA8956 represent polynucleotides encoding

```

```

CC ovarian carcinoma proteins.
XX
SQ Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other:
Query Match 16.7%; Score 316; DB 24; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 274 CATCGGGGCAACTTTTGGCGATTGTTCTGTCCAGGCTTGGCGCTCAATCCAGTG 333
Db 5 CATCGGGGCAACTTTTGGCGATTGTTCTGTCCAGGCTTGGCGCTCAATCCAGTG 64
Oy 334 CTACCACTGTGAAGAAATTCAGCTGAGCAACAGACTCTCTCCCGAGTTCATTGTGA 393
Db 65 CTACCACTGTGAAGAAATTCAGCTGAGCAACAGACTCTCTCCCGAGTTCATTGTGA 124
Oy 394 TTGCACGGTGAAGCTTCAACATGTGTCAAGAAAGATGATGACCAAGTCCGGAT 453
Db 125 TTGCACGGTGAAGCTTCAACATGTGTCAAGAAAGATGATGACCAAGTCCGGAT 184
Oy 454 CATGTACCGCAAGTCTCTGCATCATCAGCGGCTGTCTCATCGCTTGGCGGTACCA 513
Db 185 CATGTACCGCAAGTCTCTGCATCATCAGCGGCTGTCTCATCGCTTGGCGGTACCA 244
Oy 514 GTCTTGTGCTCCCGAGGAACGTGACTGATTGTCATCAGCTGCTCAACACCCCTCT 573
Db 245 GTCTTGTGCTCCCGAGGAACGTGACTGATTGTCATCAGCTGCTCAACACCCCTCT 304
Oy 574 TTGTACGGGGCCCAAG 589
Db 305 TTGTACGGGGCCCAAG 320

RESULT 26
AAF95007
ID AAF95007 standard; DNA: 369 BP.
XX
XX AAF95007;
XX 23-MAY-2001 (first entry)
DE Human ovarian cancer associated coding sequence SEQ ID NO: 199.
XX Human, ovarian cancer; vaccine; gene therapy; carcinoma; ds.
XX Homo sapiens.
XX
XX NO200118046-A2.
XX 15-MAR-2001.
XX 08-SEP-2000; 2000WO-US24827.
XX 10-SEP-1999; 99US-0394374.
XX 01-MAY-2000; 2000US-0561778.
XX 15-AUG-2000; 2000US-0640173.
XX 07-SEP-2000; 2000US-0656668.
XX
XX (CORI-) CORIXA CORP.
XX Xu J, Stolk JA;
XX WPI: 2001-211395/21.
XX
XX Isolated polypeptides associated with ovarian carcinomas, and the
XX nucleic acids that encode them, useful for the prevention diagnosis and
XX treatment of ovarian cancers.
XX Claim 18; Page 189; 189pp; English.
XX
XX The present invention provides a number of coding sequences and proteins,
XX the over-expression of which is associated with ovarian carcinoma/cancer.
XX These can be used in the diagnosis, treatment and prevention of ovarian

```

CC cancer, optionally by gene therapy or in the form of a vaccine. The
CC present sequence is an example of one of these sequences.
XX
XX
SQ Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;

Query Match 16.6%; Score 315; DB 22; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.7e-117;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 CAGGCTTTCGCGTCAATCCAGTGTACAGTGTGAAGAAATTCACGCTGAACACGACT 368
DB 30 CAGGCTTTCGCGTCAATCCAGTGTACAGTGTGAAGAAATTCACGCTGAACACGACT 89
QY 369 GCTCTCTCCCGGAGTTCATTTGTAATTCAGCGGTGAACCTTCAAGCATGTGTGCAAG 428
DB 90 GCTCTCTCCCGGAGTTCATTTGTAATTCAGCGGTGAACCTTCAAGCATGTGTGCAAG 149
QY 429 AAGTGTGAGCAAGAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 488
DB 150 AAGTGTGAGCAAGAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
QY 489 GTCTCATCGCTCTGCGGGGTACAGTCTCTGCTCCCGGAGAACTGAATCAGTTT 548
DB 210 GTCTCATCGCTCTGCGGGGTACAGTCTCTGCTCCCGGAGAACTGAATCAGTTT 269
QY 549 GCATCAGCTGTGCAACACCCCTTTTGTAAAGGGGCCAAGGCCCAAGAAAGGGGAATT 608
DB 270 GCATCAGCTGTGCAACACCCCTTTTGTAAAGGGGCCAAGGCCCAAGAAAGGGGAATT 329
QY 609 CTGCCTCGGCGCTCA 623
DB 330 CTGCCTCGGCGCTCA 344

RESULT 27
ABT03274

ID ABT03274 standard; cDNA; 369 BP.

XX AC ABT03274;

XX DT 05-SEP-2002 (first entry)

XX DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 199.

XX KM Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

XX OS cytoskeletal; gene; ss.

XX OS Homo sapiens.

XX PN W0200239885-A2.

XX PD 23-MAY-2002.

XX PF 13-NOV-2001; 2001WO-US45395.

XX PR 14-NOV-2000; 2000US-0713550.

XX PR 03-APR-2001; 2001US-0825294.

XX PR 02-OCT-2001; 2001US-0970966.

XX PA (CORI-) CORIXA CORP.

XX PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

XX DR WPI: 2002-500186/53.

XX PT Novel ovarian cancer polypeptide and polynucleotide, useful for

XX PT detecting the presence of ovarian cancer in a patient, and in

XX PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

XX PT Example 1; Page 187; 197pp; English.

CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention.
XX
XX
SQ Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;

Query Match 16.6%; Score 315; DB 24; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.7e-117;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 CAGGCTTTCGCGTCAATCCAGTGTACAGTGTGAAGAAATTCACGCTGAACACGACT 368
DB 30 CAGGCTTTCGCGTCAATCCAGTGTACAGTGTGAAGAAATTCACGCTGAACACGACT 89
QY 369 GCTCTCTCCCGGAGTTCATTTGTAATTCAGCGGTGAACCTTCAAGCATGTGTGCAAG 428
DB 90 GCTCTCTCCCGGAGTTCATTTGTAATTCAGCGGTGAACCTTCAAGCATGTGTGCAAG 149
QY 429 AAGTGTGAGCAAGAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 488
DB 150 AAGTGTGAGCAAGAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
QY 489 GTCTCATCGCTCTGCGGGGTACAGTCTCTGCTCCCGGAGAACTGAATCAGTTT 548
DB 210 GTCTCATCGCTCTGCGGGGTACAGTCTCTGCTCCCGGAGAACTGAATCAGTTT 269
QY 549 GCATCAGCTGTGCAACACCCCTTTTGTAAAGGGGCCAAGGCCCAAGAAAGGGGAATT 608
DB 270 GCATCAGCTGTGCAACACCCCTTTTGTAAAGGGGCCAAGGCCCAAGAAAGGGGAATT 329
QY 609 CTGCCTCGGCGCTCA 623
DB 330 CTGCCTCGGCGCTCA 344

RESULT 28
ABL48956

ID ABL48956 standard; cDNA; 369 BP.

XX AC ABL48956;

XX DT 18-JUN-2002 (first entry)

XX DE Ovarian carcinoma sequence isolate 57887.

XX KM Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;

XX OS ss.

XX OS Homo sapiens.

XX PN US2002004491-A1.

XX PD 10-JAN-2002.

XX PF 03-APR-2001; 2001US-0825294.

XX PR 10-SEP-1999; 99US-0394374.

XX PR 01-MAY-2000; 2000US-0561778.

XX PR 15-AUG-2000; 2000US-0640173.

XX PR 07-SEP-2000; 2000US-0656668.

XX PR 14-NOV-2000; 2000US-0713550.

XX PA (XUJ/) XU J,

XX PA (STOL/) STOLK J A.

XX PA (ALGA/) ALGATE P A.

XX PA (FLIN/) FLING S P.

XX PI Xu J, Stolk JA, Algate PA, Fling SP;

XX DR WPI: 2002-171027/22.

XX PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,

XX PT prevention and/or treatment of cancer, especially ovarian cancer

XX PS Claim 1a; Page 116; 131pp; English.

XX CC The invention relates to ovarian tumour polynucleotides and polypeptides

XX CC that may be utilised in cancer therapy, for example in a vaccine or

XX CC gene therapy. Polypeptides and polynucleotides of the invention are

XX CC useful for detecting a cancer in a patient, for stimulating and/or

XX CC expanding T-cells specific for a tumour protein, and for inhibiting the

XX CC development of a cancer in a patient. They are also useful for

XX CC stimulating an immune response in a patient, and for treating a cancer in

XX CC a patient and for determining the presence of a cancer in a patient.

XX CC The isolated polynucleotides of the invention are useful for their

XX CC ability to selectively form duplex molecules with complementary stretches

XX CC of the entire desired gene or gene fragments, and for designing and

XX CC preparing ribozyme molecules for inhibiting expression of tumour

XX CC polypeptides in tumour cells. Polypeptides and polynucleotides of the

XX CC invention are also useful in recombinant DNA molecules to direct

XX CC expression of a polypeptide in appropriate host cells. The sequences

XX CC given in records ABL48760-ABL48956 represent polynucleotides encoding

XX CC ovarian carcinoma proteins.

XX SQ Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other:

Query Match 16.6%; Score 315; DB 24; Length 369;

Best Local Similarity 100.0%; Pred. No. 5.7e-117;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 CAGGCTTGGCGTGAATCCAGTCCAGTGTGAGAAATCCAGTGAACAACGACT 368

DB 30 CAGGCTTGGCGTGAATCCAGTGTGAGAAATCCAGTGAACAACGACT 89

QY 369 GCTCTCCGCCGAGTTCATTGTGAAATTCACAGGTTCAACAGCATGTCTGAGAAG 428

DB 90 GCTCTCCGCCGAGTTCATTGTGAAATTCACAGGTTCAACAGCATGTCTGAGAAG 149

QY 429 AAGTATGAGAGCAAGAGTCCGAGTCAATGATCCGCAAGTCTCTGATCATCAGCGCT 488

DB 150 AAGTATGAGAGCAAGAGTCCGAGTCAATGATCCGCAAGTCTCTGATCATCAGCGCT 209

QY 489 GTCTATGAGCGCTCTGCGGAGTCAAGTCTCTGCTCCCGAGGAAACTGAAGTACTT 548

DB 210 GTCTATGAGCGCTCTGCGGAGTCAAGTCTCTGCTCCCGAGGAAACTGAAGTACTT 269

QY 549 GCATCAGCTGTGTCAACACCCCTTTTGTAAAGGGGCAAGGCCCAAGAAAGGGGAAGTT 608

DB 270 GCATCAGCTGTGTCAACACCCCTTTTGTAAAGGGGCAAGGCCCAAGAAAGGGGAAGTT 329

QY 609 CTGCTCGGCGCTCA 623

DB 330 CTGCTCGGCGCTCA 344

RESULT 29

ABL78538/c

ID ABL78538 standard; cDNA; 373 BP.

XX AC ABL78538;

XX DT 17-MAY-2002 (first entry)

XX DE Human ovarian cancer related CDNA clone SEQ ID NO.1516.

XX KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

XX OS Homo sapiens.

XX PM WO200192581-A2.

XX PD 06-DEC-2001.

XX PF 29-MAY-2001; 2001WO-US17756.

XX PR 26-MAY-2000; 2000US-207484P.

XX PA (CORI-) CORIXA CORP.

XX PI Algate PA, Harlocker SL, Jones R;

XX DR WPI; 2002-122075/16.

XX PT Composition for therapy and diagnosis of ovarian cancer comprising

XX PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding

XX PT polypeptide, antibody specific to polypeptide or T cell expressing

XX PS polypeptide

XX SQ Claim 1; SEQ ID 1516; 489pp; English.

XX CC The present invention describes a composition (I) comprising: carriers

XX CC and immunostimulants; and a polypeptide (II) of a ovarian tumour

XX CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence

XX CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to

XX CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell

XX CC population of (II), or antigen presenting cells that express (II).

XX CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to

XX CC (S1) can be used for detecting ovarian cancer in a patient's biological

XX CC sample preferably serum or ovarian tissue. The method comprises

XX CC contacting a biological sample from a patient with (IV), detecting the

XX CC amount of polynucleotide hybridising to (IV) and comparing the amount to

XX CC a predetermined cutoff value and thereby detecting ovarian cancer in the

XX CC patient, where the amount of polynucleotide hybridising to (IV) is

XX CC detected preferably by polymerase chain reaction (PCR). (I) comprising

XX CC (III) and/or (II) is useful for stimulating and/or expanding T cells

XX CC specific for an ovarian tumour protein comprising contacting T cells

XX CC with (III) or (II). (III) is useful in design and preparation of

XX CC ribozyme molecules for inhibiting expression of the tumour polypeptides

XX CC and proteins in tumour cells; and to isolate a full length gene from a

XX CC suitable library e.g., a tumour cDNA library using well known

XX CC techniques.

XX SQ Sequence 373 BP; 83 A; 96 C; 80 G; 114 T; 0 other:

Query Match 16.6%; Score 315; DB 24; Length 373;

Best Local Similarity 100.0%; Pred. No. 5.7e-117;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1563 GCCGAGCAGTATCTCGAATCTGTTGGCATCCAGTACGCCAATGTCAACA 1622

DB 315 GCCGAGCAGTATCTCGAATCTGTTGGCATCCAGTACGCCAATGTCAACA 256

QY 1623 ATCAGCCCTGGGAGACAGCAGGAGGAGAGACAGAAAGAAAACACAGCATGA 1682

DB 255 ATCAGCCCTGGGAGACAGCAGGAGGAGAGACAGAAAGAAAACACAGCATGA 196

QY 1683 GAAACAGTAATGATTAACATTAATATTTAGCCCTCTGTTCTGTACTTGGC 1742

DB 195 GAAACAGTAATGATTAACATTAATATTTAGCCCTCTGTTCTGTACTTGGC 136

QY 1743 CAGGAAATGGTACCAATTTTCACTGTGACATTTCTTTTGGCACAAGCA 1802

DB 135 CAGGAAATGGTACCAATTTTCACTGTGACATTTCTTTTGGCACAAGCA 76

QY 1803 GAGAAATTAACATGTTTCAACCCGGGAGTGGCTGTGTTAAAGAAACATTTAA 1862

DB 75 GAGAAATTAACATGTTTCAACCCGGGAGTGGCTGTGTTAAAGAAACATTTAA 16

QY 1863 TGCTTTAGACAGTGT 1877

DB 15 TGCTTTAGACAGTGT 1

RESULT 30

ABL79431/c

ID ABL79431 standard; cDNA; 349 BP.

XX AC ABL79431;

DT 17-MAY-2002 (first entry)
 DE Human ovarian cancer related cDNA clone SEQ ID NO:2409.
 DE Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
 OS Homo sapiens.
 XX WO200192581-A2.
 XX 06-DEC-2001.
 XX 29-MAY-2001; 2001WO-US17756.
 XX 26-MAY-2000; 2000US-207484P.
 XX (CORI-) CORIXA CORP.
 XX Algate PA, Harlocker SL, Jones R;
 XX WPI: 2002-122075/16.
 XX
 PT Composition for therapy and diagnosis of ovarian cancer comprising
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
 PT polypeptide, antibody specific to polypeptide or T cell expressing
 PT polypeptide
 PS Claim 1; SEQ ID 2409; 489pp; English.
 XX
 CC The present invention describes a composition (I) comprising: carriers
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumor
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
 CC (SI) from the 10912 nucleotide sequences as given in ABL77023 to
 CC ABL87934, (II) encoding (II) having a sequence (S2), a T cell
 CC population of (II), or antigen presenting cells that express (II).
 CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridizes to
 CC (SI) can be used for detecting ovarian cancer in a patient's biological
 CC sample preferably serum or ovarian tissue. The method comprises
 CC contacting a biological sample from a patient with (IV), detecting the
 CC amount of polynucleotide hybridizing to (IV) and comparing the amount to
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the
 CC patient, where the amount of polynucleotide hybridizing to (IV) is
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells
 CC specific for an ovarian tumor protein comprising contacting T cells
 CC with (III) or (II). (III) is useful in design and preparation of
 CC ribozyme molecules for inhibiting expression of the tumor polypeptides
 CC and proteins in tumor cells; and to isolate a full length gene from a
 CC suitable library e.g., a tumor cDNA library using well known
 CC techniques.
 CC
 SQ Sequence 349 BP; 79 A; 84 C; 78 G; 108 T; 0 other;
 Query Match 16.2%; Score 307; DB 24; Length 349;
 Best Local Similarity 100.0%; Pred. No. 9.5e-114;
 Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1570 CCATGATCTCCGAATCTGTGGGATCCAGCATCGGCCAATGTCAACAATCAATCACC 1629
 Db 310 CCATATCTCTCCGAATCTGTGGGATCCAGCATCGGCCAATGTCAACAATCAATCACC 251
 Oy 1630 CTGGGACAGACGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1689
 Db 250 CTGGGACAGACGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191
 Oy 1690 GTAAATGATAAAACCATTAATATTTAGCCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1749
 Db 190 GTAAATGATAAAACCATTAATATTTAGCCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 131
 Oy 1750 TGTGTACCAATTTTTCAGTGTGGAGCTTGAACAGCTTCTTTTGGCCACAGAGAGAGATT 1809
 Db 130 TGTGTACCAATTTTTCAGTGTGGAGCTTGAACAGCTTCTTTTGGCCACAGAGAGAGATT 71

Oy 1810 TAACAGTGTTCAAACCCGGGGAGTGGCTGTGTAAAGAAACCATTAATGCTTTA 1869
 Db 70 TAACAGTGTTCAAACCCGGGGAGTGGCTGTGTAAAGAAACCATTAATGCTTTA 11
 Oy 1870 GACAGCTG 1876
 Db 10 GACAGCTG 4
 RESULT 31
 ABL703282
 ID ABL703282 standard; cDNA; 1010 BP.
 XX
 AC ABL703282;
 XX
 DT 05-SEP-2002 (first entry)
 XX
 DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 212.
 XX
 KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
 KW cytostatic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200239885-A2.
 XX
 PD 23-MAY-2002.
 XX
 PF 13-NOV-2001; 2001WO-US45395.
 XX
 PR 14-NOV-2000; 2000US-0713550.
 PR 03-APR-2001; 2001US-0825294.
 PR 02-OCT-2001; 2001US-0970966.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;
 XX WPI: 2002-500186/53.
 XX
 DR Novel ovarian cancer polypeptide and polynucleotide, useful for
 DR detecting the presence of ovarian cancer in a patient, and in
 DR pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
 PT
 PT
 PS Claim 2; Page 195; 197pp; English.
 XX
 CC The present invention provides human ovarian cancer associated proteins
 CC and coding sequences. The sequences can be used in the diagnosis and
 CC treatment of ovarian cancers. The present sequence is a coding sequence
 CC of the invention.
 CC
 SQ Sequence 1010 BP; 266 A; 344 C; 254 G; 146 T; 0 other;
 Query Match 14.3%; Score 271; DB 24; Length 1010;
 Best Local Similarity 100.0%; Pred. No. 2.5e-99;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 310 AGGCTTGGCGGTGAATCCAGTCTACGATGTAAGAAATTCAGCTGAACAACGACTG 369
 Db 258 AGGCTTGGCGGTGAATCCAGTCTACGATGTAAGAAATTCAGCTGAACAACGACTG 317
 Oy 370 CTCTCTCCCGAGTTCATTGTGAATTCAGAGGTAACGTTCAAGACATGTGTGAGAAAGA 429
 Db 318 CTCTCTCCCGAGTTCATTGTGAATTCAGAGGTAACGTTCAAGACATGTGTGAGAAAGA 377
 Oy 430 AGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGCTG 489
 Db 378 AGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGCTG 437
 Oy 490 TCTATGCGCGTGGCGGGTACAGTCTCTGTCTCTCCCGAGGAAACTGAACATCACTTGG 549
 Db 438 TCTATGCGCGTGGCGGGTACAGTCTCTCTCTCCCGAGGAAACTGAACATCACTTGG 497

OY 550 CATCAGCTGCTGCAACACCCCTTTTGTAAAC 580
 DB 498 CATCAGCTGCTGCAACACCCCTTTTGTAAAC 528

RESULT 32

ABL40350
 ID ABL40350 standard; cDNA: 1010 BP.

AC ABL40350;

DT 28-JUN-2002 (first entry)

DE Ovarian carcinoma BF345141 nucleotide sequence.

KM Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
 ss.

OS Homo sapiens.

PN US2002004491-A1.

PD 10-JAN-2002.

PF 03-APR-2001; 2001US-0825294.

PR 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.

PR 15-AUG-2000; 2000US-0640173.

PR 07-SEP-2000; 2000US-0656668.

PR 14-NOV-2000; 2000US-0713550.

PA (XUJ/) XU J.

PA (STOL/) STOLK J A.

PA (ALGA/) ALGATE P A.

PA (FLIN/) FLING S P.

PI XU J, Stolk JA, Algate PA, Fling SP;

DR WPI: 2002-171027/22.

PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,

PT prevention and/or treatment of cancer, especially ovarian cancer -

PS Claim 1a: Page 126-127; 131pp; English.

XX The invention relates to ovarian tumour polynucleotides and polypeptides
 CC that may be utilised in cancer therapy, for example in a vaccine or
 CC gene therapy. Polypeptides and polynucleotides of the invention are
 CC useful for detecting a cancer in a patient, for stimulating and/or
 CC expanding T-cells specific for a tumour protein, and for inhibiting the
 CC development of a cancer in a patient. They are also useful for
 CC stimulating an immune response in a patient, and for treating a cancer in
 CC a patient and for determining the presence of a cancer in a patient.
 CC The isolated polynucleotides of the invention are useful for their
 CC ability to selectively form duplex molecules with complementary stretches
 CC of the entire desired gene or gene fragments, and for designing and
 CC preparing ribozyme molecules for inhibiting expression of tumour and
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
 CC invention are also useful in recombinant DNA molecules to direct
 CC expression of a polypeptide in appropriate host cells. The current
 CC sequence represents the ovarian carcinoma BF345141 nucleotide
 CC sequence.

XX Sequence 1010 BP; 266 A; 344 C; 254 G; 146 T; 0 other;

XX Query Match 14.3%; Score 271; DB 24; Length 1010;

XX Best Local Similarity 100.0%; Pred. No. 2,5e-99;

OY Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

310 AGGCTTTGGCGTGCATTCAGTGTACAGTGTGAAGAATTCCAGTGAACACGACTG 369
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 258 AGGCTTTGGCGTGCATTCAGTGTACAGTGTGAAGAATTCCAGTGAACACGACTG 317

OY 370 CTCTCTCCCCGAGTTCATTTGTGAATTCACAGGTTCAAGACATGTGTCAAGAA 429

DB 318 CTCTCTCCCCGAGTTCATTTGTGAATTCACAGGTTCAAGACATGTGTCAAGAA 377

OY 430 AGTGATGAGCAAGTGCAGGATTCATGACGCAAGTCTTGATCAGCGGCTG 489

DB 378 AGTGATGAGCAAGTGCAGGATTCATGACGCAAGTCTTGATCAGCGGCTG 437

OY 490 TCTCATGCGCTTCGCGGGTACCAAGTCTTGCTCCCGAGGAACTCACTCACTTGG 549

DB 438 TCTCATGCGCTTCGCGGGTACCAAGTCTTGCTCCCGAGGAACTCACTCACTTGG 497

OY 550 CATCAGCTGCTGCAACACCCCTTTTGTAAAC 580

DB 498 CATCAGCTGCTGCAACACCCCTTTTGTAAAC 528

RESULT 33

ABL81262/C
 ID ABL81262 standard; cDNA: 409 BP.

AC ABL81262;

DT 17-MAY-2002 (first entry)

DE Human ovarian cancer related cDNA clone SEQ ID NO:4240.

KM Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

OS Homo sapiens.

PN WO200192581-A2.

PD 06-DEC-2001.

PF 29-MAY-2001; 2001WO-0517756.

PR 26-MAY-2000; 2000US-207484P.

PA (CORI-) CORIXA CORP.

PI Algate PA, Harlocker SL, Jones R;

DR WPI: 2002-122075/16.

PT Composition for therapy and diagnosis of ovarian cancer comprising

PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding

PT polypeptide, antibody specific to polypeptide or T cell expressing

PS Claim 1; SEQ ID 4240; 489pp; English.

XX The present invention describes a composition (I) comprising: carriers
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
 CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
 CC population of (II), or antigen presenting cells that express (II).
 CC (1) has cytostatic activity. An oligonucleotide (IV) that hybridises to
 CC (S1) can be used for detecting ovarian cancer in a patient's biological
 CC sample preferably serum or ovarian tissue. The method comprises
 CC contacting a biological sample from a patient with (IV), detecting the
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the
 CC patient, where the amount of polynucleotide hybridising to (IV) is
 CC detected preferably by polymerase chain reaction (PCR). (1) comprising
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells
 CC specific for an ovarian tumour protein comprising contacting T cells
 CC with (III) or (II). (III) is useful in design and preparation of
 CC ribozyme molecules for inhibiting expression of the tumour polypeptides
 CC and proteins in tumour cells; and to isolate a full length gene from a

PT polypeptide, antibody specific to polypeptide or T cell expressing
PT polypeptide -
PS Claim 1; SEQ ID 4251; 489pp; English.
XX
XX
The present invention describes a composition (I) comprising: carriers
CC and immunostimulants; and a polypeptide (II) of an ovarian tumour
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to
CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
CC population of (II), or antigen presenting cells that express (II).
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC (S1) can be used for detecting ovarian cancer in a patient's biological
CC sample preferably serum or ovarian tissue. The method comprises
CC contacting a biological sample from a patient with (IV), detecting the
CC amount of polynucleotide hybridising to (IV) and comparing the amount to
CC a predetermined cutoff value and thereby detecting ovarian cancer in the
CC patient, where the amount of polynucleotide hybridising to (IV) is
CC detected preferably by polymerase chain reaction (PCR). (I) comprising
CC (III) and/or (II) is useful for stimulating and/or expanding T cells
CC specific for an ovarian tumour protein comprising contacting T cells
CC with (III) or (II). (II) is useful in design and preparation of
CC ribozyme molecules for inhibiting expression of the tumour polypeptides
CC and proteins in tumour cells; and to isolate a full length gene from a
CC suitable library e.g., a tumour cDNA library using well known
CC techniques.
XX
SQ Sequence 430 BP; 92 A; 121 C; 108 G; 109 T; 0 other;
XX
Query Match 6.3%; Score 120; DB 24; Length 430;
Best Local Similarity 100.0%; Pred. No. 1.4e-38;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 710 CCGCATGTTGTTCCAGCCGCTGCCCCCAACCCACCTCCCTGAGTGAAGTTCTTCG 769
DB 182 CCGCATGTTGTTCCAGCCGCTGCCCCCAACCCACCTCCCTGAGTGAAGTTCTTCG 241
OY 770 GGTGTCCTTTTATTCGGGTAGGAGCGGAGTCCGTCTCTTTTGTCTCTGCAAA 829
DB 242 GGTGTCCTTTTATTCGGGTAGGAGCGGAGTCCGTCTCTTTTGTCTCTGCAAA 301
RESULT 38
ABL79397
ID ABL79397 standard; cDNA; 558 BP.
XX
XX ABL79397;
AC
XX
DT 17-MAY-2002 (first entry)
XX
DE Human ovarian cancer related cDNA clone SEQ ID NO:2375.
XX
KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200192581-A2.
XX
PD 06-DEC-2001.
XX
PE 29-MAY-2001; 2001WO-US17756.
XX
PR 26-MAY-2000; 2000US-207484P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA, Harlocker SL, Jones R;
XX
DR WPI: 2002-122075/16.
XX
PT Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing

PT polypeptide -
PS Claim 1; SEQ ID 2375; 489pp; English.
XX
XX
The present invention describes a composition (I) comprising: carriers
CC and immunostimulants; and a polypeptide (II) of an ovarian tumour
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to
CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
CC population of (II), or antigen presenting cells that express (II).
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC (S1) can be used for detecting ovarian cancer in a patient's biological
CC sample preferably serum or ovarian tissue. The method comprises
CC contacting a biological sample from a patient with (IV), detecting the
CC amount of polynucleotide hybridising to (IV) and comparing the amount to
CC a predetermined cutoff value and thereby detecting ovarian cancer in the
CC patient, where the amount of polynucleotide hybridising to (IV) is
CC detected preferably by polymerase chain reaction (PCR). (I) comprising
CC (III) and/or (II) is useful for stimulating and/or expanding T cells
CC specific for an ovarian tumour protein comprising contacting T cells
CC with (III) or (II). (III) is useful in design and preparation of
CC ribozyme molecules for inhibiting expression of the tumour polypeptides
CC and proteins in tumour cells; and to isolate a full length gene from a
CC suitable library e.g., a tumour cDNA library using well known
CC techniques.
XX
SQ Sequence 558 BP; 147 A; 133 C; 166 G; 106 T; 6 other;
XX
Query Match 6.3%; Score 120; DB 24; Length 558;
Best Local Similarity 100.0%; Pred. No. 1.4e-38;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1408 ACAGACCTGACGACAAACCGCCGCAAACTGCTCGAGACACCGTGATACAGAGCGG 1467
DB 134 ACAGACCTGACGACAAACCGCCGCAAACTGCTCGAGACACCGTGATACAGAGCGG 193
OY 1468 TGATGACCGAGCTGAGTGAAGAAACGCTCTCGAAGAGGAGGAGATCATGTACGCC 1527
DB 194 TGATGACCGAGCTGAGTGAAGAAACGCTCTCGAAGAGGAGGAGATCATGTACGCC 253
RESULT 39
ABN41977/c
ID ABN41977 standard; DNA; 60 BP.
XX
XX ABN41977;
AC
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:14725.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PE 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
XX
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPTGEN INC.
XX
PI Shoshan A, Wassefman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI: 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of

PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes -

XX Example 1; SEQ ID 14725; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises
 CC several oligonucleotides, each capable of hybridizing selectively to a
 CC set of messenger RNAs transcribed from a given transcription unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition; to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering
 CC from a particular disorder. ABN27253 to ABN29589 represent
 CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC XX

SO Sequence 60 BP; 17 A; 17 C; 15 G; 11 T; 0 other;

Query Match 3.2%; Score 60; DB 24; Length 60;
 Best Local Similarity 100.0%; Pred. No. 2.4e-14;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1143 AACCATTCTGACAGCAATTTGGTGTTCGCGCCTGAGTGGGCTCTAGTACTCG 1202
 ID AAS60824 standard; CDNA; 1368 BP.
 XX AAS60824;
 AC AAS60824;
 XX 29-JAN-2002 (first entry)
 DE Human cancer agent-sensitive marker #326.
 XX Human cancer agent-sensitive marker #326.
 DE Human cancer agent-sensitive marker #326.
 XX Human; cancer cell marker; TAXOL; cytosolic; tumour; carcinoma;
 KW squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
 KW lymphocytic leukaemia; lymphoma; plasmocytoma; reticulom cell sarcoma;
 KW Hodgkin's disease; glioma; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200179556-A2.
 PN WO200179556-A2.
 XX 25-OCT-2001.
 PD 13-APR-2001; 2001WO-US12132.
 PF 14-APR-2000; 2000US-197538P.
 PR 14-APR-2000; 2000US-197538P.
 XX (MIL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA Lillie J, Brown JL, Bolt A, Van Huffel C;
 PI WPI: 2001-602933/68.
 DR Novel nucleic acid, used as a marker to determine the effectiveness of
 XX

PT using TAXOL to treat cancer cell growth in individuals -
 XX Claim 1; Page 339-340; 527pp; English.

XX The invention relates to 1046 novel nucleic acids which are used as
 CC markers for determining the sensitivity of a cancer cell to the
 CC anticancer agent TAXOL. Cancer cells can be treated with TAXOL when
 CC they are shown to express one of the 242 sensitivity markers or the
 CC cells are shown not to express one of the 804 resistance markers.
 CC The methods can be used to determine the effectiveness of TAXOL
 CC in the treatment of cancer cell growth in an individual. The markers
 CC can be used as targets in developing anti-cancer agents such as
 CC chemotherapeutic compounds. The markers can also be used as targets in
 CC developing treatments for cancer, particularly those cancers which
 CC display resistance to agents and exhibit expression of the markers. The
 CC anticancer agents developed by the novel method can be used to treat
 CC cancer. Probes based on the markers can be used to detect transcripts or
 CC genomic sequences corresponding to the markers, in the identification of
 CC cells or tissues which mis-express the protein. Cancers which may
 CC be targeted include carcinoma (e.g. squamous cell carcinoma),
 CC sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic leukaemia),
 CC lymphoma, plasmocytoma, reticulom cell sarcoma, Hodgkin's disease and
 CC tumours (e.g. glioma). The present sequence is one of the 1046
 CC novel cancer cell markers.
 CC XX

SO Sequence 1368 BP; 517 A; 312 C; 321 G; 213 T; 5 other;

Query Match 1.4%; Score 27; DB 22; Length 1368;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1871 ACGCTGTAAATAAAAAAAAAAAAAA 1897
 ID AAL33984 standard; DNA; 50 BP.
 XX AAL33984;
 AC AAL33984;
 XX 24-JAN-2002 (first entry)
 DE Human SNP oligonucleotide #7192.
 XX Human SNP oligonucleotide #7192.
 DE Human SNP oligonucleotide #7192.
 XX Immunosuppressive; immunostimulatory; antiinflammatory; cytosolic;
 KW neutroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200147944-A2.
 PN WO200147944-A2.
 XX 05-JUL-2001.
 PD 28-DEC-2000; 2000WO-US35498.
 PF 28-DEC-1999; 99US-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 XX (CURA-) CURAGEN CORP.
 PA Shinkets RA, Leach M;
 PI WPI: 2001-465210/50.
 DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 XX

PT Oncogenes and histones, useful for diagnosing and treating, e.g.
 cancer, autoimmune diseases and infections -
 PS Claim 1, Page 3450; 4143pp; English.
 CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinases, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 SQ Sequence 50 BP; 11 A; 16 C; 10 G; 13 T; 0 other;
 Query Match 1.4%; Score 26; DB 22; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1212 GACTGGAGCTAGACTGAGGCTCGGC 1237
 DB 50 GACTGGAGCTAGACTGAGGCTCGGC 25
 RESULT 42
 ID AAL33985/c
 AC AAL33985 standard; DNA; 50 BP.
 XX AAL33985;
 DT 24-JAN-2002 (first entry)
 DE Human SNP oligonucleotide #7193.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinase; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 OS Homo sapiens.
 XX
 PN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US35498.
 XX
 PR 28-DEC-1999; 99US-0173419.
 XX
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX
 DR WPI; 2001-465210/50.
 XX
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 PS Claim 1, Page 3451; 4143pp; English.

PS Claim 1, Page 3451; 4143pp; English.
 CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinases, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 SQ Sequence 50 BP; 14 A; 13 C; 17 G; 6 T; 0 other;
 Query Match 1.4%; Score 26; DB 22; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1563 GCCCGAGCCAGTACCTCCGATCTCG 1588
 DB 26 GCCCGAGCCAGTACCTCCGATCTCG 1
 RESULT 43
 ID AAL33986/c
 AC AAL33986 standard; DNA; 50 BP.
 XX AAL33986;
 DT 24-JAN-2002 (first entry)
 DE Human SNP oligonucleotide #7194.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinase; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 OS Homo sapiens.
 XX
 PN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US35498.
 XX
 PR 28-DEC-1999; 99US-0173419.
 XX
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX
 DR WPI; 2001-465210/50.
 XX
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 PS Claim 1, Page 3451; 4143pp; English.
 CC The present invention relates to oligonucleotides encoding polymorphic

CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.

XX
 SQ Sequence 51 BP; 9 A; 5 C; 10 G; 27 T; 0 other:

Query Match

Best Local Similarity 1.3%; Score 25; DB 22; Length 51;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1671 AACACAGCATGAGACACAGTAAT 1695

DB 51 AACACAGCATGAGACACAGTAAT 27

Search completed: November 7, 2002, 18:16:25
 Job time : 399.511 secs

430

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:00:33 ; Search time 71.0849 Seconds
(without alignments)
8184.096 Million cell updates/sec

Title: US-09-970-966-214

Perfect score: 1897
Sequence: 1 gccaaactccgagagctctg.....aaaaaaaaaaaaaaaaaa 1897

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 10

Total number of hits satisfying chosen parameters: 162838

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents, NA:*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCRTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	1.3	967	3	US-09-248-335-59
2	24	1.3	1046	4	US-09-068-140A-5
3	24	1.3	1522	4	US-09-413-574-1
4	24	1.3	2671	6	5168051-9
5	24	1.3	3073	1	US-07-688-352C-31
6	24	1.3	3073	2	US-08-474-379C-31
7	24	1.3	3073	3	US-09-146-249A-31
8	24	1.3	3073	3	US-08-206-188B-31
9	24	1.3	3073	5	PCT-US91-02714-30
10	24	1.3	3375	4	US-09-511-625B-67
11	24	1.3	4184	2	US-08-785-310A-4
12	24	1.3	176373	3	US-09-128-155-17
13	24	1.2	40	4	US-09-306-290-11
14	24	1.2	40	4	US-09-306-290-16
15	24	1.2	321	1	US-08-171-385-22
16	24	1.2	321	1	US-08-361-441B-22
17	24	1.2	340	1	US-08-171-385-27
18	24	1.2	340	1	US-08-361-441B-27
19	24	1.2	345	3	US-08-171-385-20
20	24	1.2	345	3	US-08-361-441B-20
21	24	1.2	347	1	US-08-104-072B-2
22	24	1.2	350	1	US-08-171-385-14
23	24	1.2	350	3	US-08-361-441B-14
24	24	1.2	393	4	US-09-605-785-357
25	24	1.2	393	4	US-09-439-313-357
26	24	1.2	393	4	US-09-352-616A-357
27	24	1.2	413	2	US-09-014-969-5

c	28	23	1.2	436	4	US-09-605-785-353	Sequence 353, App
c	29	23	1.2	436	4	US-09-439-313-353	Sequence 353, App
c	30	23	1.2	436	4	US-09-352-616A-353	Sequence 353, App
c	31	23	1.2	442	4	US-09-372-422A-7	Sequence 29, App
c	32	23	1.2	502	4	US-09-186-276B-29	Sequence 29, App
c	33	23	1.2	502	4	US-08-842-445-29	Sequence 29, App
c	34	23	1.2	502	4	US-09-186-188B-29	Sequence 29, App
c	35	23	1.2	530	1	US-08-462-894-5	Sequence 5, App
c	36	23	1.2	530	1	US-08-206-185-5	Sequence 5, App
c	37	23	1.2	588	4	US-09-433-248A-7	Sequence 7, App
c	38	23	1.2	593	4	US-09-385-982-262	Sequence 262, App
c	39	23	1.2	752	6	5212073-1	Sequence 1, App
c	40	23	1.2	772	4	US-09-575-602-1	Sequence 5, App
c	41	23	1.2	933	1	US-08-032-393-5	Sequence 15, App
c	42	23	1.2	1008	1	US-08-252-966B-15	Sequence 21, App
c	43	23	1.2	1162	4	US-09-173-300-21	Sequence 10, App
c	44	23	1.2	1174	1	US-07-869-933-10	Sequence 10, App
c	45	23	1.2	1174	4	US-09-103-663-10	Sequence 10, App

ALIGNMENTS

RESULT 1
US-09-248-335-59
; Sequence 59, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEF, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1128-A
; CURRENT APPLICATION NUMBER: US/09/248, 335
; EARLIER FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 08/924, 759
; EARLIER FILING DATE: 1997-September-05
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 59
; LENGTH: 967
; TYPE: DNA
; ORGANISM: maize
US-09-248-335-59
Query Match 1.3%; Score 24; Length 967;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1874 GTGTAAGAAAAA 1897
943 GTGTAAGAAAAA 966
RESULT 2
US-09-068-140A-5
; Sequence 5, Application US/09068140A
; Patent No. 6281409
; GENERAL INFORMATION:
; APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor
; APPLICANT: and Rex Michael Brennan
; TITLE OF INVENTION: Blackcurrant Promoters and Genes
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,140A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCP/EP96/04807
FILING DATE: NO.6281409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Diner, Dara L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C70237
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5017
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1046 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Ribes nigrum
STRAIN: Ben Alder
US-09-068-140A-5
Query Match 1.3%; Score 24; DB 4; Length 1046;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1874 GTGTAAAAAAAAAAAAAAAA 1897
|||||
Db 1015 GTGTAAAAAAAAAAAAAAAA 1038
RESULT 3
US-09-413-574-1
Sequence 1, Application US/09413574
Patent No. 6235972
GENERAL INFORMATION:
APPLICANT: Mahajan, Pramod B.
TITLE OF INVENTION: Maize Rad23 Genes and Uses Thereof
FILE REFERENCE: 0964
CURRENT APPLICATION NUMBER: US/09/413,574
CURRENT FILING DATE: 1999-10-06
EARLIER APPLICATION NUMBER: 60/109,728
EARLIER FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1522
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (58)...(1272)
US-09-413-574-1
Query Match 1.3%; Score 24; DB 4; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1874 GTGTAAAAAAAAAAAAAAAA 1897
|||||
Db 1456 GTGTAAAAAAAAAAAAAAAA 1479
RESULT 4

5168051-9
Patent No. 5168051
APPLICANT: DERYNCK, RIK M.A.; GOEDEL, DAVID V.
TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B IIS USES
NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/389,929
FILING DATE: 04-AUG-1989
SEQ ID NO: 9
LENGTH: 2671
5168051-9
Query Match 1.3%; Score 24; DB 6; Length 2671;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1874 GTGTAAAAAAAAAAAAAAAA 1897
|||||
Db 2577 GTGTAAAAAAAAAAAAAAAA 2600
RESULT 5
US-07-688-352C-31
Sequence 31, Application US/07688352C
Patent No. 5527896
GENERAL INFORMATION:
APPLICANT: Wiegler, Michael H.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/688,352C
FILING DATE: 19910419
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 27805/30197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 3073 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1111
US-07-688-352C-31
Query Match 1.3%; Score 24; DB 1; Length 3073;

Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAAAAAAAAAAAAAAAAA 1897
|||||
DB 1520 GTGTAAAAAAAAAAAAAAAAAAAA 1543

RESULT 6

US-08-474-379C-31
; Sequence 31, Application US/08474379C
; Patent No. 5977305
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
; TITLE OF INVENTION: PROCESSES
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,379C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/206,188
; FILING DATE: 01-MAR-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,352
; FILING DATE: 19-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 27866/32771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3073 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..1109
; US-08-474-379C-31

Query Match 1.3%; Score 24; DB 2; Length 3073;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAAAAAAAAAAAAAAAAA 1897
|||||
DB 1520 GTGTAAAAAAAAAAAAAAAAAAAA 1543

RESULT 7

US-09-146-249A-31

; Sequence 31, Application US/09146249A
; Patent No. 6069240
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,249A
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3073 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..1111
; US-09-146-249A-31

Query Match 1.3%; Score 24; DB 3; Length 3073;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAAAAAAAAAAAAAAAAA 1897
|||||
DB 1520 GTGTAAAAAAAAAAAAAAAAAAAA 1543

RESULT 8

US-08-206-188B-31
; Sequence 31, Application US/08206188B
; Patent No. 6100025
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:

Query Match 1.3%; Score 24; DB 3; Length 3073;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,1888
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3073 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..1111
; US-08-206-188B-31

Query Match 1.3%; Score 24; DB 3; Length 3073;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAACAAAAA 1897
DB 1520 GTGTAACAAAAA 1543

RESULT 9
PCT-US91-02714-30
; Sequence 30, Application PC/TUS9102714
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning By Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02714
; FILING DATE: 19910419
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 27805/30197

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3073 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..1111
; PCT-US91-02714-30

Query Match 1.3%; Score 24; DB 5; Length 3073;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAACAAAAA 1897
DB 1520 GTGTAACAAAAA 1543

RESULT 10
US-09-511-625B-67
; Sequence 67, Application US/09511625B
; Patent No. 6368828
; GENERAL INFORMATION:
; APPLICANT: Larochelle, William J.
; APPLICANT: Patel, Bhavin
; APPLICANT: Pierce, Jacalyn H.
; TITLE OF INVENTION: ATTENUATED AND DOMINANT NEGATIVEVARIANT
; TITLE OF INVENTION: CDNAS OF STAT6: STAT6b AND STAT6c
; FILE REFERENCE: 14014.0300u1
; CURRENT APPLICATION NUMBER: US/09/511,625B
; CURRENT FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: PCT/US98/17821
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/070,397
; PRIOR FILING DATE: 1998-01-05
; PRIOR APPLICATION NUMBER: 60/056,075
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 67
; LENGTH: 3375
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial Sequence: /No. 6368828e -
; OTHER INFORMATION: synthetic construct
; NAME/KEY: CDS
; LOCATION: (115)...(2655)
; US-09-511-625B-67

Query Match 1.3%; Score 24; DB 4; Length 3375;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAACAAAAA 1897
DB 3321 GTGTAACAAAAA 3344

RESULT 11
US-08-785-310A-4
; Sequence 4, Application US/08785310A
; Patent No. 5840532
; GENERAL INFORMATION:
; APPLICANT: McKnight, Steven L.
; APPLICANT: Russell, David W.

```


TITLE OF INVENTION: Neuronal PAS Domain Protein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,310A
FILING DATE: 21-JAN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UTSD:1226
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4184 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-785-310A-4

Query Match 1.3%: Score 24; DB 2; Length 4184;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1874 GTGTAAAAAAAAAAAAAAAAAAAA 1897
Db 4138 GTGTAAAAAAAAAAAAAAAAAAAA 4161

RESULT 12
US-09-128-155-17/c
Sequence 17, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
EARLIER FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 176373
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: m1sc_feature
LOCATION: (1)...(176373)
OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

Query Match 1.3%: Score 24; DB 3; Length 176373;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAAAAAAAAAAAAAAAAA 1897
Db 68491 GTGTAAAAAAAAAAAAAAAAAAAA 68468

RESULT 13
US-09-306-290-11/c
Sequence 11, Application US/09306290
Patent No. 6221635
GENERAL INFORMATION:
APPLICANT: Rovera, Giovanni
TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE
FILE REFERENCE: 09924-10
CURRENT APPLICATION NUMBER: US/09/306,290
CURRENT FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer RCP
US-09-306-290-11

Query Match 1.2%: Score 23; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
Db 23 TGTAAAAAAAAAAAAAAAAAAAA 1

RESULT 14
US-09-306-290-16/c
Sequence 16, Application US/09306290
Patent No. 6221635
GENERAL INFORMATION:
APPLICANT: Rovera, Giovanni
TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE
FILE REFERENCE: 09924-10
CURRENT APPLICATION NUMBER: US/09/306,290
CURRENT FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PrimerRCP
US-09-306-290-16

Query Match 1.2%: Score 23; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
Db 23 TGTAAAAAAAAAAAAAAAAAAAA 1

RESULT 15
US-08-171-385-22/c
Sequence 22, Application US/08171385

Patent No. 5527884
GENERAL INFORMATION:
APPLICANT: Mary E. Russell
TITLE OF INVENTION: Mediators of Chronic Allograft
TITLE OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,385
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/006001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 321
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-171-385-22
Query Match 1.2%; Score 23; DB 1; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1875 TGTAAAAAAAAAAAAAAAAA 1897
DB 24 TGTAAAAAAAAAAAAAAAAA 2
RESULT 16
US-08-361-441B-22/C
Sequence 22, Application US/08361441B
GENERAL INFORMATION:
PATENT No. 6077948
APPLICANT: Russell, Mary E.
APPLICANT: Utans, Ulrike
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/361,441B
FILING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/171,385
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-361-441B-22
Query Match 1.2%; Score 23; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1875 TGTAAAAAAAAAAAAAAAAA 1897
DB 24 TGTAAAAAAAAAAAAAAAAA 2
RESULT 17
US-08-171-385-27/C
Sequence 27, Application US/08171385
PATENT No. 5527884
GENERAL INFORMATION:
APPLICANT: Mary E. Russell
APPLICANT: Ulrike Utans
TITLE OF INVENTION: Mediators of Chronic Allograft
TITLE OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,385
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/006001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 340
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-171-385-27

Query Match 1.2%; Score 23; DB 1; Length 340;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
|||||
DB 40 TGTAAAAAAAAAAAAAAAAAAAA 18

RESULT 18

US-08-361-441B-27/C
Sequence 27, Application US/08361441B
Patent No. 6077948
GENERAL INFORMATION:
APPLICANT: Russell, Mary E.
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,441B
FILING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/171,385
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-361-441B-27

Query Match 1.2%; Score 23; DB 3; Length 340;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
|||||
DB 40 TGTAAAAAAAAAAAAAAAAAAAA 18

RESULT 19

US-08-171-385-20/C
Sequence 20, Application US/08171385
Patent No. 5527884
GENERAL INFORMATION:
APPLICANT: Mary E. Russell
TITLE OF INVENTION: Mediators of Chronic Allograft
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 555X

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/171,385

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 05433/006001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 345

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear
US-08-171-385-20

Query Match 1.2%; Score 23; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
|||||
DB 23 TGTAAAAAAAAAAAAAAAAAAAA 1

RESULT 20

US-08-361-441B-20/C
Sequence 20, Application US/08361441B
Patent No. 6077948
GENERAL INFORMATION:
APPLICANT: Russell, Mary E.
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,441B
FILING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/171,385
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-361-441B-20

Query Match
Best Local Similarity 100.0%; Score 23; DB 3; Length 345;
Pred. No. 0.91;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
DB 23 TGTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 21
US-08-104-072B-2
Sequence 2, Application US/08104072B
Patent No. 5639948
GENERAL INFORMATION:
APPLICANT: Michiels, Frank
APPLICANT: Morloka, Sinjl
APPLICANT: Scheirlinck, Trees
APPLICANT: Komari, Toshiko
TITLE OF INVENTION: Stramen-specific Promoters from Rice
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5639948west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/104,072B
FILING DATE: 05-AUG-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 9200272
FILING DATE: 06-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91403352.7
FILING DATE: 10-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91402590.3
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91400318.1
FILING DATE: 08-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchuk, Katherine M.
REFERENCE/DOCKET NUMBER: 8076, 93USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-9081
TELEFAX: 612-332-5300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: rice
TISSUE TYPE: anther
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..322
OTHER INFORMATION: /product= "cDNA T23"
FEATURE:
NAME/KEY: misc.feature
LOCATION: 333..347
OTHER INFORMATION: /product= "cloning adaptor"
US-08-104-072B-2

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 347;
Pred. No. 0.91;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
DB 284 TGTAAAAAAAAAAAAAAAAAAAAA 306

RESULT 22
US-08-171-385-14/C
Sequence 14, Application US/08171385
Patent No. 5527884
GENERAL INFORMATION:
APPLICANT: Mary E. Russell
APPLICANT: Ulrike Utans
TITLE OF INVENTION: Mediators of Chronic Allograft
TITLE OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,385
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/006001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 350
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-171-385-14

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 350;
Pred. No. 0.91;

	Matches	23;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0
OY	1875	TGTA	AAAAAAAAAAAAAAAAAAAA	1897						
Db	43	TGTA	AAAAAAAAAAAAAAAAAAAA	21						

```

RESULT 23
US-08-361-441B-14/c
: Sequence 14, Application US/08361441B
: Patent No. 6077948
: GENERAL INFORMATION:
: APPLICANT: Russell, Mary E.
: APPLICANT: Utans, Utrike
: TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
: NUMBER OF SEQUENCES: 43
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows 95
: SOFTWARE: FASTSEO for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/361,441B
: FILING DATE: 21-DEC-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/171,385
: FILING DATE: 21-DEC-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Fraser, Janis K.
: REGISTRATION NUMBER: 34,819
: REFERENCE/DOCKET NUMBER: 05433/014001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617/542-5070
: TELEFAX: 617/542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 350 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: US-08-361-441B-14

Query Match 1.2%; Score 23; DB 3; Length 350;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 23; Conservative 0; Mismatches 0; Indels 0

QY 1875 TGTAAATAAAAAAAAAAAAAA 1897
Db 43 TGTAAATAAAAAAAAAAAAAA 21

RESULT 24
US-09-605-785-357/c
: Sequence 357, Application US/09605785
: Patent No. 6321716
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Devin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kaios, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.

```

RESULT 24
US-09-605-785-357/c
: Sequence 357, Application US/0960578-
: Patent No. 6321716
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Devin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Hatlocke, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.

```

1  APPLICANT: Stolk, John A.
2  APPLICANT: Day, Craig H.
3  APPLICANT: Vedvick, Thomas S.
4  APPLICANT: Carter, Darrell
5  APPLICANT: Li, Samuel
6  APPLICANT: Wang, Aljun
7  APPLICANT: Skeiky, Isidr A.W.
8  APPLICANT: Hepler, William
9  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
10 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
11 FILE REFERENCE: 210121.42YC16
12 CURRENT APPLICATION NUMBER: US/09/605,785
13 CURRENT FILING DATE: 2000-06-27
14 NUMBER OF SEQ ID NOS: 835
15 SOFTWARE: FastSeq for Windows Version 3.0
16 SEQ ID NO 357
17 LENGTH: 393
18 TYPE: DNA
19 ORGANISM: Homo sapien
20 US-09-605-785-357

```

```

RESULT 25:
US-09-439-313-357/c
Sequence 357, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michel
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42709
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ. ID NOS: 575
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 357
LENGTH: 393
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-357

```

RESULT 26
US-09-352-616A-357/c
; Sequence 357, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:

APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqi
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 357
LENGTH: 393
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-357

Query Match 1.2%; Score 23; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
|||||
DB 34 TGTAAAAAAAAAAAAAAAAAAAA 12

RESULT 27
US-09-014-969-5
Sequence 5, Application US/09014969
Patent No. 5965397

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Racle, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 413 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-014-969-5

Query Match 1.2%; Score 23; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
|||||
DB 387 TGTAAAAAAAAAAAAAAAAAAAA 409

RESULT 28
US-09-605-785-353/C
Sequence 353, Application US/09605785
Patent No. 6321716

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 353
LENGTH: 436
TYPE: DNA
ORGANISM: Homo sapien
US-09-605-785-353

Query Match 1.2%; Score 23; DB 4; Length 436;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
|||||
DB 29 TGTAAAAAAAAAAAAAAAAAAAA 7

RESULT 29
US-09-439-313-353/C
Sequence 353, Application US/09439313
Patent No. 6329505

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9

```

; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 353
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-353

Query Match
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
DB 29 TGTAAAAAAAAAAAAAAAAAAAAA 7

RESULT 30
US-09-352-616A-353/C
; Sequence 353, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiaochun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 353
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-353

Query Match
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
DB 29 TGTAAAAAAAAAAAAAAAAAAAAA 7

RESULT 31
US-09-372-422A-35
; Sequence 35, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Barrieu
; TITLE OF INVENTION: Matre Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)...(257)
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US-09-372-422A-35

Query Match
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
DB 406 TGTAAAAAAAAAAAAAAAAAAAAA 428

RESULT 32
US-09-186-276B-29/C
; Sequence 29, Application US/09186276B
; Patent No. 6388173
; GENERAL INFORMATION:
; APPLICANT: Benfey, Philip
; APPLICANT: Dilaurenzio, Laura
; APPLICANT: Wysocka-Diller, Joanna
; APPLICANT: Malamy, Jocelyn E.
; APPLICANT: Pysh, Leonard
; APPLICANT: Helariutta, Yrjo
; TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses Thereof
; FILE REFERENCE: 5914-075-999
; CURRENT APPLICATION NUMBER: US/09/186,276B
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 08/842,445
; PRIOR FILING DATE: 1997-04-24
; PRIOR APPLICATION NUMBER: 08/638,617
; PRIOR FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Oryza sp.
US-09-186-276B-29

Query Match
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
DB 34 TGTAAAAAAAAAAAAAAAAAAAAA 12

RESULT 33
US-08-842-445-29/C
; Sequence 29, Application US/08842445A
; Patent No. 6441270
; GENERAL INFORMATION:
; APPLICANT: Benfey et al.
; TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses
; FILE REFERENCE: 5914-056-999
; CURRENT APPLICATION NUMBER: US/08/842,445A
; CURRENT FILING DATE: 1997-04-24
; EARLIER APPLICATION NUMBER: 08/638,617
; EARLIER FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Plant
US-08-842-445-29

Query Match
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
```


DB 34 TGTAAAAAAAAAAAAAAAAAAAA 12

RESULT 34

US-09-186-188B-29/C
Sequence 29, Application US/09186188B
Patent No. 6455672
GENERAL INFORMATION:
APPLICANT: Benfey et al.
TITLE OF INVENTION: Scatterrow Gene, Promoter and Uses
FILE REFERENCE: 5914-074-999
CURRENT APPLICATION NUMBER: US/09/186,188B
CURRENT FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 08/842,445
PRIOR FILING DATE: 1997-04-24
PRIOR APPLICATION NUMBER: 08/638,617
PRIOR FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 79
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 502
TYPE: DNA
ORGANISM: Plant
US-09-186-188B-29

Query Match 1.2%; Score 23; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
DB 34 TGTAAAAAAAAAAAAAAAAAAAA 12

RESULT 35

US-08-462-894-5
Sequence 5, Application US/08462894
Patent No. 5723312
GENERAL INFORMATION:
APPLICANT: NOESKE-JUNGBLUT, CHRISTIANE
APPLICANT: HAENDLER, BERNHARD
APPLICANT: KRAETZSCHMAR, JOERN
APPLICANT: SCHLEUNING, WOLF-DIETER
APPLICANT: ALAGON, ALEJANDRO
APPLICANT: POSSANI, LOURIVAL
APPLICANT: CUEVAS-AGUIRRE, DELIA
TITLE OF INVENTION: COLLAGEN-INDUCED PLATELET AGGREGATION
TITLE OF INVENTION: INHIBITOR
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,894
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,185
FILING DATE: 07-MAR-1994
APPLICATION NUMBER: US 08/116,889
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/EP92/02052
FILING DATE: 04-SEP-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,383
FILING DATE: 17-JUL-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,884
FILING DATE: 31-DEC-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/756,211
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: SCH 1359
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-462-894-5

Query Match 1.2%; Score 23; DB 1; Length 530;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
DB 508 TGTAAAAAAAAAAAAAAAAAAAA 530

RESULT 36

US-08-206-185-5
Sequence 5, Application US/08206185
Patent No. 5756454
GENERAL INFORMATION:
APPLICANT: NOESKE-JUNGBLUT, CHRISTIANE
APPLICANT: HAENDLER, BERNHARD
APPLICANT: KRAETZSCHMAR, JOERN
APPLICANT: SCHLEUNING, WOLF-DIETER
APPLICANT: ALAGON, ALEJANDRO
APPLICANT: POSSANI, LOURIVAL
APPLICANT: CUEVAS-AGUIRRE, DELIA
TITLE OF INVENTION: COLLAGEN-INDUCED PLATELET AGGREGATION
TITLE OF INVENTION: INHIBITOR
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,185
FILING DATE: 07-MAR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,889
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP92/02052
FILING DATE: 04-SEP-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,383
FILING DATE: 17-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,884
FILING DATE: 31-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/756,211
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: SCH 1359
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-206-185-5

Query Match 1.2%: Score 23; DB 1; Length 530;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
|||||
DB 508 TGTAAAAAAAAAAAAAAAAAAAAA 530

RESULT 37
US-09-433-248A-7
Sequence 7, Application US/09433248A
Patent No. 6355462
GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omolayo O.
APPLICANT: Han, Feng
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Disease Resistance Factors
FILE REFERENCE: B1252 US NA
CURRENT APPLICATION NUMBER: US/09/433,248A
CURRENT FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107,242
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Microsoft Office 97
SEQ ID NO 7
LENGTH: 588
TYPE: DNA
ORGANISM: Trilicium aestivum
US-09-433-248A-7

Query Match 1.2%: Score 23; DB 4; Length 588;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
|||||
DB 563 TGTAAAAAAAAAAAAAAAAAAAAA 565

RESULT 38
US-09-385-982-262/C
Sequence 262, Application US/09385982
Patent No. 626234
GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 262
LENGTH: 593
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(593)
OTHER INFORMATION: n = A,T,C or G
US-09-385-982-262

Query Match 1.2%: Score 23; DB 4; Length 593;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
|||||
DB 75 TGTAAAAAAAAAAAAAAAAAAAAA 53

RESULT 39
5212073-1
PATENT NO. 5212073
APPLICANT: ROLLINS, BARRETT,STILES, CHARLES;MONG, GORDON G.
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
NUMBER OF SEQUENCES: 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/351,008
FILING DATE: 12-MAY-1989
SEQ ID NO:1:
LENGTH: 752
5212073-1

Query Match 1.2%: Score 23; DB 6; Length 752;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
|||||
DB 730 TGTAAAAAAAAAAAAAAAAAAAAA 752

RESULT 40
US-09-575-602-1
Sequence 1, Application US/09575602
Patent No. 6392123
GENERAL INFORMATION:
APPLICANT: Crossland, Lyle D
APPLICANT: Harper, Stacy M
TITLE OF INVENTION: Method of Hybrid Seed Production Using
TITLE OF INVENTION: Conditional Female Sterility
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6392123artis Corporation - Patent & Trademark
ADDRESSER: Dept.
STREET: P.O. Box 12257
CITY: Research Triangle Park
STATE: NCNY
COUNTRY: USA
ZIP: 22057
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/575,602
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/032,086
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M
REGISTRATION NUMBER: 40,403
REFERENCE/DOCKET NUMBER: CGC 1915/Reg
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "cDNA sequence for
DESCRIPTION: female-preferential transcript designated B20014-2"
HYPOTHETICAL: NO
US-09-575-602-1

Query Match 1.2%; Score 23; DB 4; Length 772;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1875 TGTAAAAAAAAAAAAAAAAA 1897
Db 747 TGTAAAAAAAAAAAAAAAAA 769

RESULT 41
US-08-032-393-5
Sequence 5, Application US/08032393
Patent No. 5332660
GENERAL INFORMATION:
APPLICANT: Osamu TAKEDA et al.
TITLE OF INVENTION: Gene of Candida Yeast
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Displaywrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/032,393
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/729,414
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 933 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Candida albicans
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

US-08-032-393-5

Query Match 1.2%; Score 23; DB 1; Length 933;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1875 TGTAAAAAAAAAAAAAAAAA 1897
Db 911 TGTAAAAAAAAAAAAAAAAA 933

RESULT 42
US-08-252-966B-15
Sequence 15, Application US/08252966B
Patent No. 562818
GENERAL INFORMATION:
APPLICANT: Eisenman, Robert N.
APPLICANT: Hurlin, Peter J.
TITLE OF INVENTION: Regulatory Proteins that Dimerize with
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Christensen, O'Connor, Johnson, and KindnessP/LC
STREET: 1420 Fifth Ave., Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,966B
FILING DATE: 01-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
REFERENCE/DOCKET NUMBER: FHCRI7694
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1008 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: clone 19; see Figure 26
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus

US-08-252-966B-15

Query Match
Best Local Similarity 1.2%; Score 23; DB 1; Length 1008;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1875 TGTAAAAA 1897
975 TGTAAAAA 997

RESULT 43
US-09-173-300-21
Sequence 21, Application US/09173300
Patent No. 6451581
GENERAL INFORMATION:
APPLICANT: Falco, Saverio Carl
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BB-1126
CURRENT APPLICATION NUMBER: US/09/173,300
CURRENT FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 60/063,423
EARLIER FILING DATE: 1997 October 28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 21
LENGTH: 1162
TYPE: DNA
ORGANISM: Glycine max
US-09-173-300-21

Query Match
Best Local Similarity 1.2%; Score 23; DB 4; Length 1162;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1875 TGTAAAAA 1897
1132 TGTAAAAA 1154

RESULT 44
US-07-869-933-10
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Sequence 10, Application US/07869933
Patent No. 5770396
GENERAL INFORMATION:
APPLICANT: KINET, Jean-Pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1174 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..880
US-07-869-933-10

Query Match
Best Local Similarity 1.2%; Score 23; DB 1; Length 1174;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1875 TGTAAAAA 1897
1150 TGTAAAAA 1172

RESULT 45
US-09-103-663-10
Sequence 10, Application US/09103663D
Patent No. 6171803
GENERAL INFORMATION:
APPLICANT: Kinet et al.
TITLE OF INVENTION: Isolation, characterization, and use of the human beta
TITLE OF INVENTION: subunit of the high affinity receptor for
FILE REFERENCE: 50490
CURRENT APPLICATION NUMBER: US/09/103,663D
CURRENT FILING DATE: 1998-06-23
EARLIER APPLICATION NUMBER: 07/869,933
EARLIER FILING DATE: 1992-04-16
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 1174
TYPE: DNA
ORGANISM: Homo sapiens
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FEATURE:
NAME/KEY: CDS
LOCATION: (107)..(880)
US-09-103-663-10

867

Query Match 1.2%; Score 23; DB 4; Length 1174;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
|||||
DB 1150 TGTAAAAAAAAAAAAAAAAAAAA 1172

Search completed: November 7, 2002, 23:21:20
Job time : 366.085 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 23:08:43 ; Search time 82.4417 Seconds
(without alignments)
8163.686 Million cell updates/sec

Title: US-09-970-966-214

Perfect score: 1897

Sequence: 1 gccactccgagagctctg.....aaaaaaaaaaaaaaaa 1897

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 320260 seqs, 177392727 residues

Word size: 10

Total number of hits satisfying chosen parameters: 274654

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Published Applications_NA:*

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2: /cgn2_6/ptodata/2/pubpna/PC1_NEM_PUB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1897	100.0	1897	US-09-825-294-214	Sequence 214, App
2	1396	73.6	1619	US-09-825-294-205	Sequence 205, App
3	1396	73.6	1619	US-09-825-294-211	Sequence 211, App
4	606	31.9	625	US-09-825-294-210	Sequence 210, App
5	606	31.9	625	US-09-867-701-10876	Sequence 10876, A
6	506	26.7	1362	US-09-825-294-208	Sequence 208, App
7	425	22.4	480	US-09-825-294-213	Sequence 213, App
8	316	16.7	396	US-09-825-294-9	Sequence 9, App1
9	315	16.6	396	US-09-825-294-199	Sequence 199, App
10	315	16.6	396	US-09-867-701-1516	Sequence 1516, App
11	307	16.2	349	US-09-867-701-2409	Sequence 2409, App
12	271	14.3	1010	US-09-825-294-212	Sequence 212, App
13	264	13.9	409	US-09-867-701-4240	Sequence 4240, App
14	166	8.8	201	US-09-867-701-8894	Sequence 8894, App
15	154	8.1	390	US-09-867-701-1532	Sequence 1532, App
16	125	6.6	381	US-09-867-701-7826	Sequence 7826, App
17	120	6.3	430	US-09-867-701-4251	Sequence 4251, App
18	120	6.3	558	US-09-867-701-2375	Sequence 2375, App
19	27	1.4	1368	US-09-834-975-825	Sequence 825, App

c 20	25	1.3	152	10	US-09-960-352-9079	Sequence 9079, App
c 21	25	1.3	363	10	US-09-867-701-4911	Sequence 4911, App
c 22	25	1.3	395	10	US-09-867-701-5174	Sequence 5174, App
c 23	25	1.3	568	10	US-09-919-580-143	Sequence 143, App
c 24	25	1.3	2968	10	US-09-925-301-584	Sequence 584, App
c 25	25	1.3	208	10	US-09-770-696-104	Sequence 104, App
c 26	24	1.3	258	10	US-09-920-300A-58	Sequence 58, App1
c 27	24	1.3	258	12	US-10-033-528-58	Sequence 58, App1
c 28	24	1.3	373	10	US-09-770-791-315	Sequence 315, App
c 29	24	1.3	419	10	US-09-824-035A-439	Sequence 439, App
c 30	24	1.3	766	12	US-10-062-234-125	Sequence 125, App
c 31	24	1.3	871	10	US-09-925-300-627	Sequence 627, App
c 32	24	1.3	939	12	US-10-078-929-89	Sequence 89, App1
c 33	24	1.3	1029	10	US-09-925-300-384	Sequence 384, App
c 34	24	1.3	1046	10	US-09-800-528-5	Sequence 5, App1
c 35	24	1.3	1066	10	US-09-764-870-15	Sequence 15, App1
c 36	24	1.3	1190	10	US-09-410-194-14	Sequence 14, App1
c 37	24	1.3	1337	9	US-09-992-598-286	Sequence 286, App
c 38	24	1.3	1337	10	US-09-989-722-286	Sequence 286, App
c 39	24	1.3	1337	10	US-09-989-723-286	Sequence 286, App
c 40	24	1.3	1337	10	US-09-989-729-286	Sequence 286, App
c 41	24	1.3	1337	10	US-09-989-727-286	Sequence 286, App
c 42	24	1.3	1337	10	US-09-989-731-286	Sequence 286, App
c 43	24	1.3	1337	10	US-09-989-732-286	Sequence 286, App
c 44	24	1.3	1337	10	US-09-991-073-286	Sequence 286, App
c 45	24	1.3	1337	10	US-09-990-442-286	Sequence 286, App

ALIGNMENTS

RESULT 1
US-09-825-294-214
Sequence 214, Application US/09825294
Patent No. US20020004491A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Filing, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C5
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 214
LENGTH: 1897
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1)...(1897)
OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214

Query Match 100.0%; Score 1897; DB 10; Length 1897;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAAGTCGAGAGCTGTCGTCGCGCGGAGCGAGCGGAGAGACAGACCG 60
DB 1 GCCAAGTCGAGAGCTGTCGTCGCGCGGAGCGAGCGGAGAGACAGACCG 60
QY 61 CAGCCGGAGCGCGAGCGCGGCGATCGAGCGCGGAGCGGAGCGGAGCGGCTCTCTA 120
DB 61 CAGCCGGAGCGCGAGCGCGGCGATCGAGCGCGGAGCGGAGCGGAGCGGCTCTCTA 120
QY 121 AGTACGACGCTGTCGTCGCGGAGCGAGCGCGGCGCGGAGCGGAGCGGAGCGGCTCTCTA 180
DB 121 AGTACGACGCTGTCGTCGCGGAGCGAGCGCGGCGCGGAGCGGAGCGGAGCGGCTCTCTA 180

Oy	181	CGGCGAGCCGGGGGACGCTCCGCTGCTGCGCTCTGATGAGCGCTGCGCTCCG	240
Db	181	CGGTGACGCGGGGACCGCCGCTGCTGCGCTCTGATGAGCGCTGCGCTCCG	240
Oy	241	GCCCCGGGACCTCGGGAGAAATGTGGGTCCTAGGCATCCGGGCAACTTTTTCGGGATTT	300
Db	241	GCCCCGGGACCTCGGGAGAAATGTGGGTCCTAGGCATCCGGGCAACTTTTTCGGGATTT	300
Oy	301	CTTGCTTCACAGGCTTTTCCGCTGCAAAATTCAGATGCTACAGTGTGAAGAATTCACGCTGAA	360
Db	301	CTTGCTTCACAGGCTTTTCCGCTGCAAAATTCAGATGCTACAGTGTGAAGAATTCAGCTGAA	360
Oy	361	CAAGAGCGCTCCCGCCCGAGTTCAATTGGAAATTGCACGAGGAAAGTTCAAGACATGTG	420
Db	361	CAAGAGCGCTCCCGCCCGAGTTCAATTGGAAATTGCACGAGGAAAGTTCAAGACATGTG	420
Oy	421	TCAGAAAGAAATGATGAGGAGCAAAATCCCGGATCATGTACCCCAAGTCTGTGCAATC	480
Db	421	TCAGAAAGAAATGATGAGGAGCAAAATCCCGGATCATGTACCCCAAGTCTGTGCAATC	480
Oy	481	AGCGGCGTGTCTCATGCGCTCTGCGGGATACAGTCTTTCTGCCAGGAAATGAA	540
Db	481	AGCGGCGTGTCTCATGCGCTCTGCGGGATACAGTCTTTCTGCCAGGAAATGAA	540
Oy	541	CTCAGTTTGCATCGAGTGTGCAACACCCCTCTTTGTATACGGGGCCAAAGGCCAAGAAAG	600
Db	541	CTCAGTTTGCATCGAGTGTGCAACACCCCTCTTTGTATACGGGGCCAAAGGCCAAGAAAG	600
Oy	601	GGAAGTTTCTCTCCGCGCCCTCAGAGGCGAGGGCTCCGACACACATCTGTTCTCAATT	660
Db	601	GGAAGTTTCTCTCCGCGCCCTCAGAGGCGAGGGCTCCGACACACATCTGTTCTCAATT	660
Oy	661	AGCCCTTTCTCGGCGACATGCTGAAGCTGAAGAGATGCCACCCCTCTGCAATTGTT	720
Db	661	AGCCCTTTCTCGGCGACATGCTGAAGCTGAAGAGATGCCACCCCTCTGCAATTGTT	720
Oy	721	TTTCAGGCGCTGCGCCCAACCCGACGCTGAGTGAATTTCTTGGGGTGCCTTT	780
Db	721	TTTCAGGCGCTGCGCCCAACCCGACGCTGAGTGAATTTCTTGGGGTGCCTTT	780
Oy	781	ATTCTGGGTAGGAGCGGAGTCCGTTCTCTTTGTCTCGTGCATAATAATGAAGAG	840
Db	781	ATTCTGGGTAGGAGCGGAGTCCGTTCTCTTTGTCTCGTGCATAATAATGAAGAG	840
Oy	841	CTCGGTAAGCATTTCTGAATTAATTACGCTGACTGAATTTTACGTAATGTAAGGA	900
Db	841	CTCGGTAAGCATTTCTGAATTAATTACGCTGACTGAATTTTACGTAATGTAAGGA	900
Oy	901	AGGAGGTGAGTGAAGATTCACCCCACTGCTGTGAACCGGAGTCAGAGCCAGGCTGCG	960
Db	901	AGGAGGTGAGTGAAGATTCACCCCACTGCTGTGTGAACCGGAGTCAGAGCCAGGCTGCG	960
Oy	961	AGAGTCMGTCCTGTGAAGTCACTGAGGTGGGCAATCGCTTTTGTGAAGCCTCACGTGC	1020
Db	961	AGAGTCMGTCCTGTGAAGTCACTGAGGTGGGCAATCGCTTTTGTGAAGCCTCACGTGC	1020
Oy	1021	CATTTCATCCCTGATGGGGGCAATGTTGAGCTGCAAGTGAAGATGACGTTTTCTTAG	1080
Db	1021	CATTTCATCCCTGATGGGGGCAATGTTTGAAGTCAAGTGAAGTGAAGTTCGTTCTTAG	1080
Oy	1081	GGCTGGAGGGCACTTCCCACTCAAGGCTCCCGGTTTACATTCAAATTCATCTCT	1140
Db	1081	GGCTGGAGGGCACTTCCCACTCAAGGCTCCCGGTTTACATTCAAATTCATCTCT	1140
Oy	1141	GAAACCAATTCCTGACAGCAAAATTTGGCTGTTTCCGCGCTGAGTTGGGCTCTAGTACT	1200
Db	1141	GAAACCAATTCCTGACAGCAAAATTTGGCTGTTTCCGCGCTGAGTTGGGCTCTAGTACT	1200
Oy	1201	CGAGACTCAATGACTGGGACTTTAGACTGGGGCTCGGCTCTGCTGAAAAGTCTTAAAGA	1260
Db	1201	CGAGACTCAATGACTGGGACTTTAGACTGGGGCTCGGCTCTGCTGAAAAGTCTTAAAGA	1260
Oy	1261	AAATTTCTCAGTTCTCTTGACAGAGACTGGCGCGGAGCGGAAGACAAAGGGCGCT	1320

[illegible]

```

RESULT 2
; US-09-825-294-205
; Sequence 205, Application US/09825294
; Patent No. US2002000491A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITILE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484CS
CURRENT APPLICATION NUMBER: US/09/825, 294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 205
; LENGTH: 1619
; TYPE: DNA
ORGANISM: Homo sapiens
US-09-825-294-205

Query Match          73.6%; Score 1396; DB 10; Length 1619;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1616; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      280  GGCAACTTTTGCGGATGGTCTTCCTCCAGGCTTTGGCGGTGAANAACAGTGCATCCA 339
        |||               |||||                |||||                |||
DB       1   GCGCACTTTTTCGGGATTCTTCCTGCCAGGCTTTGGCGGTGAANAATCAAGTGTACCA 60

```


QY 340 GTGTGAATAATTCAGCTGAACAAACGACTGCTCTCCGCCAGTTCATTGTGAATTGAC 399
 DB 61 GTGTGAATAATTCAGCTGAACAAACGACTGCTCTCCGCCAGTTCATTGTGAATTGAC 120
 QY 400 GGTGAACGTTCAAGCATGTGTCAAGAAAGAGTGTGAGCAAAAGTGTCCGGGATCATGTA 459
 DB 121 GGTGAACGTTCAAGCATGTGTCAAGAAAGAGTGTGAGCAAAAGTGTCCGGGATCATGTA 180
 QY 460 CCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCTCTGCGGGTACAGTCTT 519
 DB 181 CCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCTCTGCGGGTACAGTCTT 240
 QY 520 CTGCTCCCAAGGAAACTGAACTGATTTGCATGCTGCTGCAACACCCCTTTTGTAA 579
 DB 241 CTGCTCCCAAGGAAACTGAACTGATTTGCATGCTGCTGCAACACCCCTTTTGTAA 300
 QY 580 CGGGCCCAAGGAAAGGAAAGGAAAGTTCGCTCGGCTCGGCTCGGCAAGGCTCGGAC 639
 DB 301 CGGGCCCAAGGAAAGGAAAGGAAAGTTCGCTCGGCTCGGCTCGGCAAGGCTCGGAC 360
 QY 640 CACCATCTCTTCTCTCAAAATTAAGCCCTTCTCGGCACTGCTGAAAGTGAAGAGATG 699
 DB 361 CACCATCTCTTCTCTCAAAATTAAGCCCTTCTCGGCACTGCTGAAAGTGAAGAGATG 420
 QY 700 CCACCCCTCTCTGATTTGTTCTTCCAGCCCTCGCCCAACCCCAACCCCTCTGAGTGA 759
 DB 421 CCACCCCTCTCTGATTTGTTCTTCCAGCCCTCGCCCAACCCCAACCCCTCTGAGTGA 480
 QY 760 GTTTCCTCTGCTGCTCTTCTTATCTGCTGAGGAGCGGAGTCCGCTCTTCTTGT 819
 DB 481 GTTTCCTCTGCTGCTCTTCTTATCTGCTGAGGAGCGGAGTCCGCTCTTCTTGT 540
 QY 820 CCTGTGCAAAATTAATGAAGAGCTGCTGTAAGCAATTCGAATAATTCAGCTGATGAAT 879
 DB 541 CCTGTGCAAAATTAATGAAGAGCTGCTGTAAGCAATTCGAATAATTCAGCTGATGAAT 600
 QY 880 TTTCAGTATGATGTAAGAGAGAGTGTGAGTGAAGTTCACCCCATCTCTGCTGTAAC 939
 DB 601 TTTCAGTATGATGTAAGAGAGAGTGTGAGTGAAGTTCACCCCATCTCTGCTGTAAC 660
 QY 940 CGGAGTCAAGGAGGCTGAGAGTCTGCTGTAAGAGTCACTGAGTGGGATCGGCTG 999
 DB 661 CGGAGTCAAGGAGGCTGAGAGTCTGCTGTAAGAGTCACTGAGTGGGATCGGCTG 720
 QY 1000 TTTTGTAAACCTTCAAGTCTGCTTCCATCCCTGATGAGGAGTGTGAGACTGACA 1059
 DB 721 TTTTGTAAACCTTCAAGTCTGCTTCCATCCCTGATGAGGAGTGTGAGACTGACA 780
 QY 1060 GTGAGATGAGCTTTTCTTGTAGGCTGAGGAGGAGTCCCACTCAAGGCTCGCTG 1119
 DB 781 GTGAGATGAGCTTTTCTTGTAGGCTGAGGAGGAGTCCCACTCAAGGCTCGCTG 840
 QY 1120 ACATTTCAAACTTCACTCTCTGAAACCAATTCCTGACAGAGATTTGGCTGTGCGGC 1179
 DB 841 ACATTTCAAACTTCACTCTCTGAAACCAATTCCTGACAGAGATTTGGCTGTGCGGC 900
 QY 1180 CTGAGTTGGGCTGTAGTGAAGTCAAGTCAATGACTGAGACTTAACTGAGGCTG 1239
 DB 901 CTGAGTTGGGCTGTAGTGAAGTCAAGTCAATGACTGAGACTTAACTGAGGCTG 960
 QY 1240 CCGCTGTAAAGTGTCTTAAGAAATTTCTCTGAGTTCCTGAGAGGAGTGGCGGCGG 1299
 DB 961 CCGCTGTAAAGTGTCTTAAGAAATTTCTCTGAGTTCCTGAGAGGAGTGGCGGCGG 1020
 QY 1300 AGCCGAAGAGCAACGCGGCTGCAAAAGCGGCTGTGCTGCTGAGTGTGAGTGTGATTA 1359
 DB 1021 AGCCGAAGAGCAACGCGGCTGCAAAAGCGGCTGTGCTGCTGAGTGTGAGTGTGATTA 1080
 QY 1360 CCGGAGGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1418
 DB 1081 CCGGAGGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140

QY 1419 ACGAACACCCCGGAAACCTGCTGAGAGACACGCTGTACAGAGCGGGTGTGATGACCGAG 1478
 DB 1141 ACGAACACCCCGGAAACCTGCTGAGAGACACGCTGTACAGAGCGGGTGTGATGACCGAG 1200
 QY 1479 CTGAGGTAGAAAAACGCTCTCGAAGAGGAGAGGATCATGTACGCGCGGAAGTAGAGAC 1538
 DB 1201 CTGAGGTAGAAAAACGCTCTCGAAGAGGAGAGGATCATGTACGCGCGGAAGTAGAGAC 1260
 QY 1539 CTGCTCAGTCTGCTGCTTGGGTTGGCCGACCCATGATCCTCCGAATCTGTTGGGATC 1598
 DB 1261 CTGCTCAGTCTGCTGCTTGGGTTGGCCGACCCATGATCCTCCGAATCTGTTGGGATC 1320
 QY 1599 CAGCATACGGCCATGTCACAAATCAGCCCTGGGCAACACAGAGAGAGAGAGAC 1658
 DB 1321 CAGCATACGGCCATGTCACAAATCAGCCCTGGGCAACACAGAGAGAGAGAGAC 1380
 QY 1659 AGAGAAAAAGAAAAACACAGATGAGAACACAGTAATTAATTAACATTAATTAATTA 1718
 DB 1381 AGAGAAAAAGAAAAACACAGATGAGAACACAGTAATTAATTAATTAATTAATTA 1440
 QY 1719 CCCCCTGCTGCTGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1778
 DB 1441 CCCCCTGCTGCTGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
 QY 1779 CAGCTTCTTTGCAACAGAGAGAGAAATTAACATGTTTCAACCCGGGGAGATTG 1838
 DB 1501 CAGCTTCTTTGCAACAGAGAGAGAAATTAACATGTTTCAACCCGGGGAGATTG 1560
 QY 1839 CTGTGTTAAAGAAACCAATTAATGCTTTAGACAGTGTAAACAAAAA 1897
 DB 1561 CTGTGTTAAAGAAACCAATTAATGCTTTAGACAGTGTGTAAACAAAAA 1619

RESULT 3

US-09-825-294-211
 ; Sequence 211, Application US/09825294
 ; Patent No. US20020004491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Algate, Paul A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.4845
 ; CURRENT FILING DATE: 2001-04-03
 ; NUMBER OF SEQ ID NOS: 215
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 211
 ; LENGTH: 1619
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-825-294-211

Query Match 73.6%; Score 1396; DB 10; Length 1619;

Best Local Similarity 99.8%; Pred. No. 0; Matches 1616; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 280 GGCACCTTTTGGCGATTTGTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 339
 DB 1 GGCACCTTTTGGCGATTTGTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
 QY 340 GTGTGAATAATTCAGCTGAACAAACGACTGCTCTCCGCCAGTTCATTGTGAATTGAC 399
 DB 61 GTGTGAATAATTCAGCTGAACAAACGACTGCTCTCCGCCAGTTCATTGTGAATTGAC 120
 QY 400 GGTGAACGTTCAAGCATGTGTCAAGAAAGAGTGTGAGCAAAAGTGTCCGGGATCATGTA 459
 DB 121 GGTGAACGTTCAAGCATGTGTCAAGAAAGAGTGTGAGCAAAAGTGTCCGGGATCATGTA 180
 QY 460 CCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCTCTGCGGGTACAGTCTT 519

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Db 181 CCGCAGTCTGTGATCATCAGCGGCTGTCTCATGCTCTCCGGGTACCACTCTT 240
QY 520 CTGCTCCCAAGGGAAGTGAACCTGATTTGCATCAGCTGCTGCAACACCCCTTTGTAA 579
    |||||
Db 241 CTGCTCCCAAGGGAAGTGAACCTGATTTGCATCAGCTGCTGCAACACCCCTTTGTAA 300
QY 580 CGGCGCAAGGCGCCAAAGAAAGGGAAGTGTGCTCGGCGCTCAGGCGCAGGCTCCGCGAC 639
    |||||
Db 301 CGGCGCAAGGCGCCAAAGAAAGGGAAGTGTGCTCGGCGCTCAGGCGCAGGCTCCGCGAC 360
QY 640 CACCATCCTGTTCTCTCAAAATTAAGCCCTCTTCTCGGCACTGCTGAAGCTGAAGAGATG 699
    |||||
Db 361 CACCATCCTGTTCTCTCAAAATTAAGCCCTCTTCTCGGCACTGCTGAAGAGATG 420
QY 700 CCACCCCTCTCTGATGTTCTTCCAGCCCTCGCCCAACCCCGCACTCTCTGATGA 759
    |||||
Db 421 CCACCCCTCTCTGATGTTCTTCCAGCCCTCGCCCAACCCCGCACTCTCTGATGA 480
QY 760 GTTCTCTGCTGCTGCTCTTATCTGCTGAGGAGGCGGAGTCCGTTCTCTTTGTT 819
    |||||
Db 481 GTTCTCTGCTGCTGCTCTTATCTGCTGAGGAGGCGGAGTCCGTTCTCTTTGTT 540
QY 820 CCTGTCAAAATATGAAAGAGCTCGGTAAAGCATTTCTGAATAAATGACCTGATGAT 879
    |||||
Db 541 CCTGTCAAAATATGAAAGAGCTCGGTAAAGCATTTCTGAATAAATGACCTGATGAT 600
QY 880 TTTTCAGTATGTAAGTGAAGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 939
    |||||
Db 601 TTTTCAGTATGTAAGTGAAGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 660
QY 940 CGGAGTCAAGGCGCAGGCTGCGAGAGTCTGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 999
    |||||
Db 661 CGGAGTCAAGGCGCAGGCTGCGAGAGTCTGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 720
QY 1000 TTTTGTAAAGCTCCAGTGTCCATTCATCCCTGATGCGGCGATAGTTGAGACTGCAGA 1059
    |||||
Db 721 TTTTGTAAAGCTCCAGTGTCCATTCATCCCTGATGCGGCGATAGTTGAGACTGCAGA 780
QY 1060 GTGAGAGTGAAGTCTTCTTAAGGCGTGAAGGCGAGTCCCACTCAAGGCTCCCTGCTG 1119
    |||||
Db 781 GTGAGAGTGAAGTCTTCTTAAGGCGTGAAGGCGAGTCCCACTCAAGGCTCCCTGCTG 840
QY 1120 ACATTTCAAACTTCATGCTCTCTGAAAACCATTTCTGACAGAGAAATTTGGCTTGGCGC 1179
    |||||
Db 841 ACATTTCAAACTTCATGCTCTCTGAAAACCATTTCTGACAGAGAAATTTGGCTTGGCGC 900
QY 1180 CTGAGTGGGCTCTAGTGAATCTGAACTCAATGACTGGGACTTGAAGTGGGCTGGGCT 1239
    |||||
Db 901 CTGAGTGGGCTCTAGTGAATCTGAACTCAATGACTGGGACTTGAAGTGGGCTGGGCT 960
QY 1240 CGCTCTGAAGAAAGTGTAAAGAAATCTTCTCAGTTCTCTCTGCAAGAGACTGGCGCGG 1299
    |||||
Db 961 CGCTCTGAAGAAAGTGTAAAGAAATCTTCTCAGTTCTCTCTGCAAGAGACTGGCGCGG 1020
QY 1300 ACGCGAAGAGCAAGGCGGCTGCACAAAGCGGCGCTGTGGTGTGAAGTGGCATGTA 1359
    |||||
Db 1021 ACGCGAAGAGCAAGGCGGCTGCACAAAGCGGCGCTGTGGTGTGAAGTGGCATGTA 1080
QY 1360 CGGCGAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1418
    |||||
Db 1081 CGGCGAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 1419 ACGAATACCCCGCGAAGTCTGCTGCGAGACACCGTGAAGAGAGGAGTGAAGTGAAGAG 1478
    |||||
Db 1141 ACGAATACCCCGCGAAGTCTGCTGCGAGACACCGTGAAGAGAGGAGTGAAGTGAAGAG 1200
QY 1479 CTGAGGTAGAAAAAGTCTCTCGAAGAGAGGAGAGGAGTGAAGTGAAGTGAAGAGAG 1538
    |||||
Db 1201 CTGAGGTAGAAAAAGTCTCTCGAAGAGAGGAGAGGAGTGAAGTGAAGTGAAGAGAG 1260
QY 1539 CTGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1598
    |||||
Db 1261 CTGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320

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QY 1599 CAGCATAGCGGCAATGTGCAACAAATTCAGCCCTGGGCGAGACGAGAGAGAGAGAC 1658
    |||||
Db 1321 CAGCATAGCGGCAATGTGCAACAAATTCAGCCCTGGGCGAGACGAGAGAGAGAGAC 1380
QY 1659 AGAGAAAGAAAAAACACACATGAGAAACACAGTAAATGAATAAACATTAATATTTAG 1718
    |||||
Db 1381 AGAGAAAGAAAAAACACACATGAGAAACACAGTAAATGAATAAACATTAATATTTAG 1440
QY 1719 CCCCTGTGTTGCTGCTTACTGCGCAGAAATGTACCAATTTTCAGTTGAGTGA 1778
    |||||
Db 1441 CCCCTGTGTTGCTGCTTACTGCGCAGAAATGTACCAATTTTCAGTTGAGTGA 1500
QY 1779 CAGCTCTTTTGGCAACAGAGAGAGAAATTTAACACTGTTTCAAAACCGGGGAGTTGG 1838
    |||||
Db 1501 CAGCTCTTTTGGCAACAGAGAGAGAAATTTAACACTGTTTCAAAACCGGGGAGTTGG 1560
QY 1839 CTGTGTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAATTTAAAAA 1897
    |||||
Db 1561 CTGTGTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAATTTAAAAA 1619

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RESULT 4
US-09-825-294-210
; Sequence 210, Application US/09825294
; Patent No. US2002004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(625)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-210

```

```

Query Match          31.9%; Score 606; DB 10; Length 625;
Best Local Similarity 100.0%; Pred. No. 8.6e-241;
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1271 AGTTCCTCTTGCAGAGAGTGGCGCGCGGAGCGGAAAGAGCAAGCGGCTGCACAAAGCG 1330
    |||||
Db 1 AGTTCCTCTTGCAGAGAGTGGCGCGCGGAGCGGAAAGAGCAAGCGGCTGCACAAAGCG 60
QY 1331 GGCCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1390
    |||||
Db 61 GGCCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 120
QY 1391 CAGGACAGGCGGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1450
    |||||
Db 121 CAGGACAGGCGGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 180
QY 1451 CGTGTACAGAGAGCGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1510
    |||||
Db 181 CGTGTACAGAGAGCGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 1511 GAGATCATGTAGCCCGCGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1570
    |||||
Db 241 GAGATCATGTAGCCCGCGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300
QY 1571 CATGATCTCCGAATCTGTGTTGGGCAATCCAGCAATAGGCCCAATGTCACAAATACACCC 1630

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|||||
Db 301 CATGATCCTCCGAAATCTGGTGGGCATCCAGCATACGGCCAAATGTCAACAAATCAGCCC 360
Oy 1631 TGGGCACACGACGAGGAGGAGAGACAGAAAAAGAAAAACACAGCATGAGAACACAG 1690
Db 361 TGGGCACACGACGAGGAGGAGAGACAGAAAAAGAAAAACACAGCATGAGAACACAG 420
Oy 1691 TAAATGAATAAACCATAAATATTTAGCCCCCTGTGTCTGTCTTACTGTGGCAGGAAT 1750
Db 421 TAAATGAATAAACCATAAATATTTAGCCCCCTGTGTCTGTCTTACTGTGGCAGGAAT 480
Oy 1751 GGTACCAATTTTTCAGTGTGGTGTGACTGTGACAGCTTCTTTTGCACAAAGAGAAATTT 1810
Db 481 GGTACCAATTTTTCAGTGTGGTGTGACTGTGACAGCTTCTTTTGCACAAAGAGAAATTT 540
Oy 1811 AACACTGTTTCAAAACCGGGGAGTGGTGTGTTAAAGAAACCATTAATGCTTTAG 1870
Db 541 AACACTGTTTCAAAACCGGGGAGTGGTGTGTTAAAGAAACCATTAATGCTTTAG 600
Oy 1871 ACAGTG 1876
Db 601 ACAGTG 606

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RESULT 5
US-09-867-701-10876

```

/ Sequence 10876, Application US/09867701
/ Patent No. US2002013237A1
/ GENERAL INFORMATION:
/ APPLICANT: Aglate, Paul A.
/ APPLICANT: Jones, Robert
/ APPLICANT: Harlocker, Susan L.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.497
/ CURRENT APPLICATION NUMBER: US/09/867,701
/ NUMBER OF SEQ ID NOS: 10912
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10876
/ LENGTH: 625
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 607
/ OTHER INFORMATION: n = A,T,C or G
US-09-867-701-10876

```

Query Match 31.9%; Score 606; DB 10; Length 625;
Best Local Similarity 100.0%; Pred. No. 8.6e-241;
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1271 AGTTCTCTTGCAGAGACTGGGGCGGGAGCGGAAGCAACAGGGCGCTGCACAAAGG 1330
Db 1 AGTTCTCTTGCAGAGAGATGGGCGGGAGCGGAAGCAACAGGGCGCTGCACAAAGG 60
Oy 1331 GGGCGTGTGCTGTGAGTGGCATGTACGGCGAGGCGCTTCTGTGTGGTGGCTGTG 1390
Db 61 GGGCGTGTGCTGTGAGTGGCATGTACGGCGAGGCGCTTCTGTGTGGTGGCTGTG 120
Oy 1391 CAGCGACAGCGGCGGACAGACACCTGCGAGAACACCCCGAAACTGCTGCAGAGAC 1450
Db 121 CAGCGACAGCGGCGGACAGACACCTGCGAGAACACCCCGAAACTGCTGCAGAGAC 180
Oy 1451 CGTGTACAGAGACGGGTTGATGACGAGCTGAGTGAAGAAACGTTCTCGAGAAAGGAG 1510
Db 181 CGTGTACAGAGACGGGTTGATGACGAGCTGAGTGAAGAAACGTTCTCGAGAAAGGAG 240
Oy 1511 GAGGATCATGTACGCCGGAAGTAGAGACTGTCAGTGTGCTTGGGTTGGCCGAGC 1570
Db 241 GAGGATCATGTACGCCGGAAGTAGAGACTGTCAGTGTGCTTGGGTTGGCCGAGC 300

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Oy 1571 CATGATCCTCCGAAATCTGGTGGGCATCCAGCATACGGCCAAATGTCAACAAATCAGCCC 1630
Db 301 CATGATCCTCCGAAATCTGGTGGGCATCCAGCATACGGCCAAATGTCAACAAATCAGCCC 360
Oy 1631 TGGGCACACGACGAGGAGGAGAGACAGAAAAAGAAAAACACAGCATGAGAACACAG 1690
Db 361 TGGGCACACGACGAGGAGGAGAGACAGAAAAAGAAAAACACAGCATGAGAACACAG 420
Oy 1691 TAAATGAATAAACCATAAATATTTAGCCCCCTGTGTCTGTCTTACTGTGGCAGGAAT 1750
Db 421 TAAATGAATAAACCATAAATATTTAGCCCCCTGTGTCTGTCTTACTGTGGCAGGAAT 480
Oy 1751 GGTACCAATTTTTCAGTGTGGTGTGACTGTGACAGCTTCTTTTGCACAAAGAGAAATTT 1810
Db 481 GGTACCAATTTTTCAGTGTGGTGTGACTGTGACAGCTTCTTTTGCACAAAGAGAAATTT 540
Oy 1811 AACACTGTTTCAAAACCGGGGAGTGGTGTGTTAAAGAAACCATTAATGCTTTAG 1870
Db 541 AACACTGTTTCAAAACCGGGGAGTGGTGTGTTAAAGAAACCATTAATGCTTTAG 600
Oy 1871 ACAGTG 1876
Db 601 ACAGTG 606

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RESULT 6
US-09-825-294-208/C

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/ Sequence 208, Application US/09825294
/ Patent No. US2002004491A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Stolk, John A.
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Fling, Steven P.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
/ FILE REFERENCE: 210121.4845
/ CURRENT APPLICATION NUMBER: US/09/825,294
/ NUMBER OF SEQ ID NOS: 215
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 208
/ LENGTH: 1362
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-825-294-208

```

Query Match 26.7%; Score 506; DB 10; Length 1362;
Best Local Similarity 100.0%; Pred. No. 1.4e-199;
Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1124 TCAAACTTCATGCTCTCTAAACCATTTCTGTCAGACAGAAATGGCTGGTGGCGCTGA 1183
Db 1362 TCAAACTTCATGCTCTCTAAACCATTTCTGTCAGACAGAAATGGCTGGTGGCGCTGA 1303
Oy 1184 GTTGGGCTCTAGTGAATGATGATGAGTGGGACTTAACTGAGGCTGGCTGGCT 1243
Db 1302 GTTGGGCTCTAGTGAATGATGATGAGTGGGACTTAACTGAGGCTGGCTGGCT 1243
Oy 1244 CTGAAGAGTCTTAAAGAAATCTTCTAGTTCCTTTCAGAGAGACTGGCCGGGAGC 1303
Db 1242 CTGAAGAGTCTTAAAGAAATCTTCTAGTTCCTTTCAGAGAGACTGGCCGGGAGC 1183
Oy 1304 GAAAGGCAAGGGGCTGTCAAAAGCGGGCGCTGTGGTGTGAGTGGCATTTACGG 1363
Db 1182 GAAAGGCAAGGGGCTGTCAAAAGCGGGCGCTGTGGTGTGAGTGGCATTTACGG 1123
Oy 1364 CAGGCGCTTCTGCTGTGGTGGCTGTGAGGAGCGGAGGAGGAGGAGGAGGAGGAGG 1423
Db 1122 CAGGCGCTTCTGCTGTGGTGGCTGTGAGGAGCGGAGGAGGAGGAGGAGGAGGAGG 1063
Oy 1424 CAGGCGGGAAGTGTGCGAGGAGACCGGTGTACAGAGGCGGCTTGTATGACGAGCTGAG 1483

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Db 1062 CACCGCGCAACTGCTGCGAGACACCGTGTACAGAGCGGGTGTGATGACCGAGCTGAG 1003
Oy 1484 GTAGAAAAACCTCTCCGAGAGGGAGAGATCATGTACCCCGGAAGTAGACCTCGT 1543
Db 1002 GTAGAAAAACCTCTCCGAGAGGGAGAGATCATGTACCGCCGGAAGTAGACCTCGT 943
Oy 1544 CCAGTCGCTGGTGGTGGCGGAGCAGCATGATCTCCGAATGTGTTGGGATCCAGCA 1603
Db 942 CCAGTCGCTGGTGGTGGCGGAGCAGCATGATCTCCGAATGTGTTGGGATCCAGCA 883
Oy 1604 TACGGCCAATGTACACACATCAGCC 1629
Db 882 TACGGCCAATGTACACACATCAGCC 857

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RESULT 7

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US-09-825-294-213
; Sequence 213, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 213
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-213

```

```

Query Match 22.4%; Score 425; DB 10; Length 480;
Best Local Similarity 99.8%; Pred. No. 3,7e-166;
Matches 475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 GCCAACTCCGAGGCTGTGTGCTCGGCCCGGAGCGCGAGCGGGAGGAGCAGAGACCCG 60
Db 1 GCCAACTCCGAGGCTGTGTGCTCGGCCCGGAGCGCGAGCGGGAGGAGCAGAGACCCG 60
Oy 61 CAGCCGGGAGCGCGGCGGCGATGCAAGCTCCGAGCGGCGCCAGAGAGCTCGGCTCTCTA 120
Db 61 CAGCCGGGAGCGCGGCGGCGATGCAAGCTCCGAGCGGCGCCAGAGAGCTCGGCTCTCTA 120
Oy 121 AGCTACGACCGTCTCTCGCGGAGCAGCGCGGCGCCAGCAGAGCTCGGCGAGCAGC 180
Db 121 AGCTACGACCGTCTCTCGCGGAGCAGCGCGGCGCCAGCAGAGCTCGGCGAGCAGC 180
Oy 181 CGCTGACGCGGGGAGCGCTCCGCTGTGTGCTCTGTGATGGCTTGGCTCTCCG 240
Db 181 CGCTGACGCGGGGAGCGCTCCGCTGTGTGCTCTGTGATGGCTTGGCTCTCCG 240
Oy 241 GCCCGGGAGCTCGGGAGAAATGTGGTCTAGCATCGGGCAATTTTGGGATTTGT 300
Db 241 GCCCGGGAGCTCGGGAGAAATGTGGTCTAGCATCGGGCAATTTTGGGATTTGT 300
Oy 301 CTGTGCTTCAGGCTTGGCGCTGCAAAATCGATGTACAGATGTGAAGATTCACAGTGA 360
Db 301 CTGTGCTTCAGGCTTGGCGCTGCAAAATCGATGTACAGATGTGAAGATTCACAGTGA 360
Oy 361 CAACAGCTCTCTCCCGAGTTGATGTGAATTCAGCGGTGAAGCTTCAAGATATG 420
Db 361 CAACAGCTCTCTCCCGAGTTGATGTGAATTCAGCGGTGAAGCTTCAAGATATG 420
Oy 421 TGAGAAAGAGTGAAGAGCAAGTCCGGATCATGTACCCAGTCTCTGTGAT 476
Db 421 TGAGAAAGAGTGAAGAGCAAGTCCGGATCATGTACCCAGTCTCTGTGAT 476

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RESULT 8

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US-09-825-294-9
; Sequence 9, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-9

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Query Match 16.7%; Score 316; DB 10; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.2e-121;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 274 CATCGCGCAACTTTTTCGATGTGCTTCAGCGCTTTCGCTCAATTCAGTG 333
Db 5 CATCGCGCAACTTTTTCGATGTGCTTCAGCGCTTTCGCTCAATTCAGTG 64
Oy 334 CTACCAATGTGAAGATTCAGCTGAACAGACTCTCTCCCGGATTCATTTGAA 393
Db 65 CTACCAATGTGAAGATTCAGCTGAACAGACTCTCTCCCGGATTCATTTGAA 124
Oy 394 TTGACGCTGAAGCTTCAAGATGTGTGAGAAAGATGTGAGCAAAAGTCCGGAT 453
Db 125 TTGACGCTGAAGCTTCAAGATGTGTGAGAAAGATGTGAGCAAAAGTCCGGAT 184
Oy 454 CATGTACCGAAGTCTGTGCATCATCAGCGGCTGTTCATGCTCTGCGGGTACA 513
Db 185 CATGTACCGAAGTCTGTGCATCATCAGCGGCTGTTCATGCTCTGCGGGTACA 244
Oy 514 GTCTTTGTCTCCCGAGGAACTGAATCAATGATGATGATGATGATGATGATGAT 573
Db 245 GTCTTTGTCTCCCGAGGAACTGAATCAATGATGATGATGATGATGATGATGAT 304
Oy 574 TTGTACGGGCCAAG 589
Db 305 TTGTACGGGCCAAG 320

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RESULT 9

```

US-09-825-294-199
; Sequence 199, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 199

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LENGTH: 369
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)-(369)
OTHER INFORMATION: n = A,T,C or G
US-09-825-294-199

Query Match
Best Local Similarity 100.0%; Score 315; DB 10; Length 369;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 CAGGCTTGGCGTCAATCCAGTGTACCAAGTGAAGATTCCAGTGAACAGACT 368
DB 30 CAGGCTTGGCGTCAATCCAGTGTACCAAGTGAAGATTCCAGTGAACAGACT 89
QY 369 GCTCTCCCCGAGTTCATTTGTAATTCAGCGGTGAACGTTCAAGCATGTGCAGAAAG 428
DB 90 GCTCTCCCCGAGTTCATTTGTAATTCAGCGGTGAACGTTCAAGCATGTGCAGAAAG 149
QY 429 AAGTGTAGAGCAAGTCCGCGGATCATGTACCGCAAGTCTGTGATCATCAGCGCT 488
DB 150 AAGTGTAGAGCAAGTCCGCGGATCATGTACCGCAAGTCTGTGATCATCAGCGCT 209
QY 489 GTCTCATCCCTTCCCGGTTACCACTCTTCTGCTCCCGAGGAACTGAATCAGTTT 548
DB 210 GTCTCATCCCTTCCCGGTTACCACTCTTCTGCTCCCGAGGAACTGAATCAGTTT 269
QY 549 GCATCAGCTGCTCAACACCCCTTTGTAACGGGCAAGCCCAAGAAAGGGAGTT 608
DB 270 GCATCAGCTGCTCAACACCCCTTTGTAACGGGCAAGCCCAAGAAAGGGAGTT 329
QY 609 CTGCTCTGGGCTCA 623
DB 330 CTGCTCTGGGCTCA 344

RESULT 10
US-09-867-701-1516/c
Sequence 1516, Application US/09867701
Patent No. US2002013237A1
GENERAL INFORMATION:

APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1516
LENGTH: 373
TYPE: DNA
ORGANISM: Homo sapien
US-09-867-701-1516

Query Match
Best Local Similarity 100.0%; Score 315; DB 10; Length 373;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1563 GCCGAGCCATGATCTCGAATCTGTTGGCATCCAGCATACGGCCAAATGTCAACA 1622
DB 315 GCCGAGCCATGATCTCGAATCTGTTGGCATCCAGCATACGGCCAAATGTCAACA 256
QY 1623 ATCAGCCCTGGGCAAGACAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1682
DB 255 ATCAGCCCTGGGCAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 196
QY 1683 GAACACAGTAATGAATAAACCATAAATATTTAGCCCTGTGTTCTGTCTCTGCTG 1742

DB 195 GAACACAGTAATGAATAAACCATAAATATTTAGCCCTGTGTTCTGTCTCTGCTG 136
QY 1743 CAGGAATGGTACCAATTTTTCAGTGTGGACTTACAGCTTCTTTGCCACAGACA 1802
DB 135 CAGGAATGGTACCAATTTTTCAGTGTGGACTTACAGCTTCTTTGCCACAGACA 76
QY 1803 GAGAAATTTACACTGTTTCAACACCGGGGAGTGTGCTGTAAAGAAAGCAATTAA 1862
DB 75 GAGAAATTTACACTGTTTCAACACCGGGGAGTGTGCTGTAAAGAAAGCAATTAA 16
QY 1863 TCGTTTACAGCTGT 1877
DB 15 TCGTTTACAGCTGT 1

RESULT 11
US-09-867-701-2409/c
Sequence 2409, Application US/09867701
Patent No. US2002013237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2409
LENGTH: 349
TYPE: DNA
ORGANISM: Homo sapien
US-09-867-701-2409

Query Match
Best Local Similarity 100.0%; Score 307; DB 10; Length 349;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1570 CCATATCTCTCGAATCTGTTGGCATCCAGCATACGGCCAAATGTCAACAATCAGCC 1629
DB 310 CCATATCTCTCGAATCTGTTGGCATCCAGCATACGGCCAAATGTCAACAATCAGCC 251
QY 1630 CTGGGCAAGACAG 1689
DB 250 CTGGGCAAGACAG 191
QY 1690 GTAAATGAATAAACCATAAATATTTAGCCCTGTGTTCTGTCTTACTGTGCGCAGAAA 1749
DB 190 GTAAATGAATAAACCATAAATATTTAGCCCTGTGTTCTGTCTTACTGTGCGCAGAAA 131
QY 1750 TGGTACCAATTTTTCAGTGTGGACTTACAGCTTCTTTGCCAAGAGAGAGAAAT 1809
DB 130 TGGTACCAATTTTTCAGTGTGGACTTACAGCTTCTTTGCCAAGAGAGAGAAAT 71
QY 1810 TAACACTGTTTCAACACCGGGGAGTGTGCTGTAAAGAAAGCAATTAAATGCTTTA 1869
DB 70 TAACACTGTTTCAACACCGGGGAGTGTGCTGTAAAGAAAGCAATTAAATGCTTTA 11
QY 1870 GACAGTG 1876
DB 10 GACAGTG 4

RESULT 12
US-09-825-294-212
Sequence 212, Application US/09825294
Patent No. US20020004491A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.

APPLICANT: Filing, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.4845
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 212
LENGTH: 1010
TYPE: DNA
ORGANISM: Homo sapiens
US-09-825-294-212

Query Match 14.3%; Score 271; DB 10; Length 1010;
Best Local Similarity 100.0%; Pred. No. 1.1e-102;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 310 AGGCTTGGCTGCAAAATCCAGTGTACAGTGAAGATTCAGTGAACAAGCACTG 369
DB 258 AGGCTTGGCTGCAAAATCCAGTGTACAGTGAAGATTCAGTGAACAAGCACTG 317
QY 370 CTCCTCCCGGAGTTGATTTGATTCAGCGGTGAACGTTCAAGCATGTGTCAAGAA 429
DB 318 CTCCTCCCGGAGTTGATTTGATTCAGCGGTGAACGTTCAAGCATGTGTCAAGAA 377
QY 430 ACTGATGAGCAAAATCCCGGATCATGTACCGCAAGTCTGTGATCATGACGGCGCTG 489
DB 378 ACTGATGAGCAAAATCCCGGATCATGTACCGCAAGTCTGTGATCATGACGGCGCTG 437
QY 490 TCTCATCCGCTTGGCGGGGTACAGTCTTGTCTCCCGAGGAATGAATCAGTTTG 549
DB 438 TCTCATCCGCTTGGCGGGGTACAGTCTTGTCTCCCGAGGAATGAATCAGTTTG 497
QY 550 CATCAGCTCTCTCAACACCCCTCTTTGTAC 580
DB 498 CATCAGCTCTCTCAACACCCCTCTTTGTAC 528

RESULT 13

US-09-867-701-4240/c
Sequence 4240, Application US/09867701
Patent No. US20020132237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4240
LENGTH: 409
TYPE: DNA
ORGANISM: Homo sapiens
US-09-867-701-4240

Query Match 13.9%; Score 264; DB 10; Length 409;
Best Local Similarity 99.7%; Pred. No. 8.7e-100;
Matches 314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1563 GCCGCGCATGATCTCTCGAATCTGTGGCATTCACGATACGCCCAATGTCAACA 1622
DB 315 GCCGCGCATGATCTCTCGAATCTGTGGCATTCACGATACGCCCAATGTCAACA 256
QY 1623 ATCAGCCCTGGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1682
DB 255 ATCAGCCCTGGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 196
QY 1683 GAACACGTAATGAATAAACCATTAATATTAGCCCTCTGTGTGCTTACTGGC 1742

DB 195 GAACACGTAATGAATAAACCATTAATATTAGCCCTCTGTGTGCTTACTGGC 136
QY 1743 CAGGAATGTGATCCATTTTTCAGTGTGGACTTGCACAGTCTTTTGGCAGAGAA 1802
DB 135 CAGGAATGTGATCCATTTTTCAGTGTGGACTTGCACAGTCTTTTGGCAGAGAA 76
QY 1803 GAGATTTTACACTGTTTCAAAACCGGGAGTGGCTGTGTTAAAGAAACCATTA 1862
DB 75 GAGATTTTACACTGTTTCAAAACCGGGAGTGGCTGTGTTAAAGAAACCATTA 16
QY 1863 TCGTTTACAGTGT 1877
DB 15 TCGTTTACAGTGT 1

RESULT 14
US-09-867-701-8894/c
Sequence 8894, Application US/09867701
Patent No. US20020132237A1
GENERAL INFORMATION:

APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8894
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-09-867-701-8894

Query Match 8.8%; Score 166; DB 10; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.3e-59;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1501 AGAAGGAGAGAGATATGATGACCCCGGAAGTAGACCTCTGCTGCTTGGGTT 1560
DB 181 AGAAGGAGAGAGATATGATGACCCCGGAAGTAGACCTCTGCTGCTTGGGTT 122
QY 1561 TGGCGGAGCATGATCTCTCGAATCTGTGGCATTCACGATACGCCCAATGTCA 1620
DB 121 TGGCGGAGCATGATCTCTCGAATCTGTGGCATTCACGATACGCCCAATGTCA 62
QY 1621 CAATCAGCCCTGGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 1666
DB 61 CAATCAGCCCTGGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 16

RESULT 15

US-09-867-701-1532
Sequence 1532, Application US/09867701
Patent No. US20020132237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1532
LENGTH: 390
TYPE: DNA
ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(390)
; OTHER INFORMATION: n = A,T,C OR G
US-09-867-701-1532

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Query Match	8.1%;	Score 154;	DB 10;	Length 390;
Best Local Similarity	100.0%;	Pred. No. 2e-54;		
Matches 154;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy 1636 AGACACGAGCAGGAGGGAGAGACAGAGAAGAAAAACACAGCATGAGAACACAGTAAT 1695
|||||
Dd 147 AGACACGAGCAGGAGGGAGAGACAGAGAAGAAAAACACAGCATGAGAAACACAGTAAT 206
|||||

1596 GAATGAAACCAATTAATATTAGCCCTCTGCTCTGCTTACTGGCAGGAAATGGTAC 1555
 |||||
 207 GAATGAAACCAATTAATATTAGCCCTCTGCTCTGCTTACTGGCAGGAAATGGTAC 266

1/56	CAATTTTTCAGGCTGTGGACATTCAGAGCTTCTTTT	1/89
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RESULT 16
US-09-867-701-7826
: Sequence 7826, Application US/09867701

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; Patent NO: 032002010223/01
;
; GENERAL INFORMATION:
;
; APPLICANT: Aglate, Paul A.
;
; APPLICANT: Jones, Robert

```

FILE REFERENCE: 210121.497

```

; CURRENT FILING DATE: 2001-05-29
;
; NUMBER OF SEQ ID NOS: 10912
;
; SOFTWARE: FastSeq for Windows Version 4.0

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; LENGTH: 381
; TYPE: DNA
; ORGANISM: Homo sapien

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Query Match	6.6%	Score 125	DB 10	Length 381
Best Local Similarity	100.0%	Pred. No.	1.8e-42	
Matches 125	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Oy 1238 CTGGCTCTGAAAGTGCCTTAGAATACTTCACGTTCCTTGACAGAGACTGGGCCG 1297
Dd 116 CTCGCTCTGAAGAAGTCTTAAGAAATCTTCACGTTCCTTGACAAGACTGGGCCG 175			

Dy 1298 GGACCGCAAGAGCAACGGGCGCTGCACAACGCCGCGTGTGGTGAGAGCCGATG 1357

Db 176 GCACGCCAAGAGCAACGGGCGCTGCACAACGCCGCGTGTGGTGAGAGCCGATG 235

Qy	1358	TACGC	1362
Db	236	TACGC	240

RESULT 17
US-09-867

US-09-867-701-4251
; Sequence 4251, Application US/09867701
; Patent No. US20020132237A1

```

; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L

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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;
; FILE REFERENCE: 210121.497

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839
840
84

```

; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4251
; LENGTH: 430

```

ORGANISM: Homo sapiens
US-09-867-701-4251

Best Local Similarity	100.0%	Pred. No. 2e-40:	
Matches 120; Conservative	0;	Mismatches	0; Indels
			0; Gaps

Db 182 CTGCATTGTTCTTCCAGCCCTGCCCCAACCCGCCACCTCCCTGAGTGAGTTCTTCTG 241

Db 242 GGTCCTTTATTCGTGGTAAGGACGGAGTCCGTGTTCTCTTTTGTTCTCTGTGCAA 301

US-09-867-701-2375
; Sequence 2375, Application US/09867701
; Patent No. US20020132237A1

```

; GENERAL INFORMATION:
;
; APPLICANT: Aglate, Paul A.
;
; APPLICANT: Jones, Robert
;
; APPLICANT: Harlocker, Susan L.

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; OF OVARIAN CANCER
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.497
 ; CURRENT APPLICATION NUMBER: US/09/8657 701

```

; COMMENT FILLING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2375

```

```

;
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

```

OTHER INFORMATION: n = A, T, C or G
US-09-867-701-2375

Best Local Similarity 100.0%; Pred. No. 2e+40;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 134 ACAGCACCTGCAGCAACCCGCCAAATCTCTGGAGGACACCGTGTACAGAGCGGGT 193

Db 194 TGAATGACCGAGCTGAGGTTGAAAAACGTCTCCGAGAGGGGAGAGGATCATGTACGCC 253

US-09-834

Sequence 825, Application US/09834975
Patent No. US20020110815A1
GENERAL INFORMATION:

;	APPLICANT:	Brown, Jeffrey
;	APPLICANT:	Bolt, Andrew
;	APPLICANT:	Van Huffel, Christophe

: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
 : TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
 : TITLE OF INVENTION: OF HUMAN CANCERS

FILE REFERENCE: MRI-016E

Db 35 AGTGTAAAAA 11

RESULT 24

US-09-925-301-584

; Sequence 584, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 584
; LENGTH: 2968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (454)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1437)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2961)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2964)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-584

Query Match 1.3%; Score 25; DB 10; Length 2968;

Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1873 AGTGTAAAAA 1897
Db 2886 AGTGTAAAAA 2910

RESULT 25

US-09-770-696-104

; Sequence 104, Application US/09770696
; Patent No. US20010044940A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maia
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurdan, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis

; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2031US (PARA-020PRV)
; CURRENT APPLICATION NUMBER: US/09/770,696
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,278
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 911
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 208
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-696-104

Query Match 1.3%; Score 24; DB 10; Length 208;

Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAA 1897
Db 169 GTGTAAAAA 192

RESULT 26

US-09-920-300A-58

; Sequence 58, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jianshun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121,547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 258
; OTHER INFORMATION: n = A,T,C or G
US-09-920-300A-58

Query Match 1.3%; Score 24; DB 10; Length 258;

Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAA 1897
Db 228 GTGTAAAAA 251

RESULT 27

US-10-033-528-58

; Sequence 58, Application US/10033528
; Patent No. US2002013971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jianshun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121,547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 258
; OTHER INFORMATION: n = A,T,C or G
; US-10-033-528-58
```

```
Query Match 1.3%; Score 24; DB 12; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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OY 1874 GTGTAACAAAAA 1897
DB 228 GTGTAACAAAAA 251
```

```
RESULT 28
US-09-770-791-315/C
```

```
; Sequence 315, Application US/09770791
; Patent No. US2002062014A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Olang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hufman, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2029 (PARA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770,791
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,480
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 315
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-770-791-315
```

```
Query Match 1.3%; Score 24; DB 10; Length 373;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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OY 1874 GTGTAACAAAAA 1897
DB 24 GTGTAACAAAAA 1
```

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RESULT 29
US-09-924-035A-439/C
; Sequence 439, Application US/09924035A
; Patent No. US20020142319A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Gilach, Jiri
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2011US
; CURRENT APPLICATION NUMBER: US/09/924,035A
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,784
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 439
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-924-035A-439
```

```
Query Match 1.3%; Score 24; DB 10; Length 419;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1874 GTGTAACAAAAA 1897
DB 45 GTGTAACAAAAA 22
```

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RESULT 30
US-10-062-254-125
```

```
; Sequence 125, Application US/10062254
; Patent No. US2002013882A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Fang, Yixen
; APPLICANT: Hanke, Sabine S.
; APPLICANT: Lee, Jian-Ming
; APPLICANT: Li, Zhongsen
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Morgante, Michele
; APPLICANT: Niu, Xiping
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Zheng, Peizhong
; APPLICANT: Zhu, Qun
; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/630,346
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146511
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/156006
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/157287
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/169767
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/171054
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/172958
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/171515
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/173535
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 125
; LENGTH: 766
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; TYPE: DNA
; ORGANISM: Picramnia pentandra
; US-10-062-254-125

Query Match
Best Local Similarity 1.3%; Score 24; DB 12; Length 766;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAA 1897
DB 734 GTGTAAAAA 757

RESULT 31
US-09-925-300-627
; Sequence 627, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 627
; LENGTH: 871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (863)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-300-627

Query Match
Best Local Similarity 1.3%; Score 24; DB 10; Length 871;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAA 1897
DB 836 GTGTAAAAA 859

RESULT 32
US-10-078-929-89
; Sequence 89, Application US/10078929
; Patent No. US20020152497A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; TITLE OF INVENTION: Stress Response
; FILE REFERENCE: BB1357 US NA
; CURRENT APPLICATION NUMBER: US/10/078,929
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/566,394
; PRIOR FILING DATE: 2000-05-05
```

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; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 89
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Glycine max
; US-10-078-929-89

Query Match
Best Local Similarity 1.3%; Score 24; DB 12; Length 939;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAA 1897
DB 886 GTGTAAAAA 909

RESULT 33
US-09-925-300-384
; Sequence 384, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 384
; LENGTH: 1029
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1014)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1015)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1026)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-300-384

Query Match
Best Local Similarity 1.3%; Score 24; DB 10; Length 1029;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAA 1897
DB 978 GTGTAAAAA 1001
```

RESULT 34
US-09-800-528-5
; Sequence 5, Application US/09800528
; Patent No. US20010016955A1
; GENERAL INFORMATION:
; APPLICANT: Woodhead, Mary Rose
; APPLICANT: Taylor, Mark Andrew
; APPLICANT: Brennan, Rex Michael
; TITLE OF INVENTION: BLACKCURRANT PROMOTERS AND GENES
; FILE REFERENCE: C70237D1
; CURRENT APPLICATION NUMBER: US/09/800.528
; CURRENT FILING DATE: 2001-03-07
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/EP/9604807
; PRIOR FILING DATE: 1996-11-04
; PRIOR APPLICATION NUMBER: GE9522558.7
; PRIOR FILING DATE: 1995-11-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1046
; TYPE: DNA
; ORGANISM: Ribes nigrum
US-09-800-528-5

Query Match 1.3%; Score 24; DB 10; Length 1046;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAATAAAAAAAAAAAAAA 1897
|||||
DB 1015 GTGTAATAAAAAAAAAAAAAA 1038

RESULT 35
US-09-764-870-15
; Sequence 15, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764.870
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1066
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-870-15

Query Match 1.3%; Score 24; DB 10; Length 1066;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAATAAAAAAAAAAAAAA 1897
|||||
DB 1043 GTGTAATAAAAAAAAAAAAAA 1066

RESULT 36
US-09-410-194-14
; Sequence 14, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly

; APPLICANT: Irmier, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroeter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410.194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1190
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (394)...(1056)
US-09-410-194-14

Query Match 1.3%; Score 24; DB 10; Length 1190;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAATAAAAAAAAAAAAAA 1897
|||||
DB 1121 GTGTAATAAAAAAAAAAAAAA 1144

RESULT 37
US-09-992-598-286
; Sequence 286, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Bacon, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paonli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992.598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092162
PRIOR FILING DATE: 1998-07-09

Query Match

Best Local Similarity 1.3%; Score 24; DB 9; Length 1337;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1874 GTGTAAAAA 1897
Db 1298 GTGTAAAAA 1321

RESULT 38
US-09-989-722-286

Sequence 286, Application US/09989722
Patent No. US20020072067A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlesen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.3%; Score 24; DB 10; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1874 GTGTAAAAAAAAAAAAAAAA 1897
Db 1298 GTGTAAAAAAAAAAAAAAAA 1321

RESULT 39
US-09-989-723-286
Sequence 286, Application US/09989723
Patent No. US2002072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: KJavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Steward, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C62
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
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Query Match 1.38; Score 24; DB 10; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAA 1897
Db 1298 GTGTAAAAA 1321

RESULT 40
US-09-989-279-286
Sequence 286, Application US/09989279
Patent No. US20020072496A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC56
CURRENT APPLICATION NUMBER: US/09/989, 279
PRIOR APPLICATION NUMBER: 2001-11-19
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PRIOR FILING DATE: 1998-07-09

Query Match 1.3%; Score 24; DB 10; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 41
US-09-989-727-286
; Sequence 286, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C65
; CURRENT APPLICATION NUMBER: US/09/989,727
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.3%; Score 24; DB 10; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0.72;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1874 GGTGTAATAAAAAAAAAAAAAA 1897
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Db 1298 GTGTAAAAAAAAAAAAAAAA 1321

RESULT 42
US-09-989-731-286
Sequence 286, Application US/09989731
Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1C70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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 PRIOR FILING DATE: 1998-07-09

Query Match 1.3%; Score 24; DB 10; Length 1337;
 Best Local Similarity 100.0%; Pred. No. 0.72;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAAAAAAAAAAAAA 1897
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 Db 1298 GTGTAAAAAAAAAAAAAAAA 1321

RESULT 43
 US-09-989-732-286
 : Sequence 286, Application US/09989732
 : Patent No. US20020123463A1
 : GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Geriltsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730PIC57
 CURRENT APPLICATION NUMBER: US/09/989,732
 CURRENT FILING DATE: 2001-11-19
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Query Match 1.3%; Score 24; DB 10; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAAAAAAAAAAAAA 1897
Db 1298 GTGTAAAAAAAAAAAAAAAA 1321

RESULT 44
US-09-991-073-286
Sequence 286, Application US/09991073
Patent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C15
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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; APPLICANT: Ashkenazi, Avi J.
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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
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Query Match 1.3%: Score 24; DB 10; Length 1337;
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 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.3
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6	1714	90.4	1918	17 US-09-397-022-4454	Sequence 4454, App
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: GENERAL INFORMATION:			
: APPLICANT: Chenault, Ruth A.			
: APPLICANT: Xu, Jlangchun			
: APPLICANT: Fanger, Gary R.			
: APPLICANT: Harlocke, Susan L.			
: APPLICANT: McNeill, Patricia D.			
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
: FILE REFERENCE: 210121.48AC7			
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: CURRENT FILING DATE: 2002-08-02			

[illegible]

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Db 1741 GCCAGGAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800
Qy 1801 GAGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
Db 1801 GAGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
Qy 1861 AATGCTTTAGACAGTGTAAAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1897
Db 1861 AATGCTTTAGACAGTGTAAAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1897

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RESULT 5
 PCT-US02-29964-16
 ; Sequence 16, Application PC/TUS0229964
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom

```

; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Dunrui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Asundi, Vinod
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle W.
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: PCT/US02/29964
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,739
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 992
; SOFTWARE: PCT-FL-Genes Version 6.0
; SEQ ID NO 16
; LENGTH: 1967
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (338)..(763)
; PCT-US02-29964-16

Query Match 90.6%; Score 1718; DB 1; Length 1967;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1866; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 19 GGTGCTGGCCGCGGAGCGGAGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 78
Db 97 GGTGCTGGCCGCGGAGCGGAGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 156
Qy 79 GGGGCGATGAGAGCTCCGCGAGGGGCACTGCGGCTCTTAAGCTAAGCAGCGTGCTC 138
Db 157 GGGGCGATGAGAGCTCCGCGAGGGGCACTGCGGCTCTTAAGCTAAGCAGCGTGCTC 216
Qy 139 GCGGCGAGCGAGCGGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 198
Db 217 GCGGCGAGCGAGCGGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 276
Qy 199 CTCGCTGTGTGCTGCTCTGTATGCGCTTCCCTCTCCCGGCGCGGAGACTCGGGAG 258
Db 277 CTCGCTGTGTGCTGCTCTGTATGCGCTTCCCTCTCCCGGCGCGGAGACTCGGGAG 336
Qy 259 AATGTTGGTCTTATGAGCATCGCGGCACTTTTTCGGAATGTTCTTCTTCCAGGCTTTC 318

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Db 337 AATGTGGCTCTAGGCATCGGGCAACTTTTGGGATTTGTTCTGCTCCAGGCTTTGC 396
Qy 319 GCTGCAAAATCCAGTGTCTACAGTGTGAAGAAATTCAGCTGAACAACAGATGCTCTCC 378
Db 397 GCTGCAAAATCCAGTGTCTACAGTGTGAAGAAATTCAGCTGAACAACAGATGCTCTCC 456
Qy 379 CGAGTTCAATTTGGAATTTGCACAGGTGAACGTTCAAGACATGTGTGAGAAGAGTATGA 438
Db 457 CGAGTTCAATTTGGAATTTGCACAGGTGAACGTTCAAGACATGTGTGAGAAGAGTATGA 516
Qy 439 GCAAAGTCCCGGATCATGTATCCGCAAGTCTGTGCAATCATCAGGCGCTGTCTATGCC 498
Db 517 GCAAAGTCCCGGATCATGTATCCGCAAGTCTGTGCAATCATCAGGCGCTGTCTATGCC 576
Qy 499 CTGTGCGGGGTACCAAGTCTTCTGCTCCCGAGGGAATCACTAGTTGATCAGCTG 558
Db 577 CTGTGCGGGGTACCAAGTCTTCTGCTCCCGAGGGAATCACTAGTTGATCAGCTG 636
Qy 559 CTGCAACACCCCTCTTGTAAACGGGCCCAAGGCCAAGAAAAGGGAAGTTCTGCTCGG 618
Db 637 CTGCAACACCCCTCTTGTAAACGGGCCCAAGGCCAAGAAAAGGGAAGTTCTGCTCGG 696
Qy 619 CCTCAGGCGAGGCTCCGCAACCATCTGTTCCCTCAATATGAGCCCTCTCTCGGCA 678
Db 697 CCTCAGGCGAGGCTCCGCAACCATCTGTTCCCTCAATATGAGCCCTCTCTCGGCA 756
Qy 679 CTGCTGAAGCTGAAGAGATGCCACCCCTCTGCAATGTTCTTCCAGCCCTCGGCCA 738
Db 757 CTGCTGAAGCTGAAGAGATGCCACCCCTCTGCAATGTTCTTCCAGCCCTCGGCCA 816
Qy 739 ACCCCACACCTCCCTGATGATGTTCTTGGGTCCTTTTCTGGGTAGGAGCGG 798
Db 817 ACCCCACACCTCCCTGATGATGTTCTTGGGTCCTTTTCTGGGTAGGAGCGG 876
Qy 799 GAGTCCGTGTTCTTTTGTCTGTGCAAAATATGAAAGAGCTCGTAACATCTGA 858
Db 877 GAGTCCGTGTTCTTTTGTCTGTGCAAAATATGAAAGAGCTCGTAACATCTGA 936
Qy 859 ATAAATTCACGTCGATGATTTTCAATATGATCTGAAGAGAGAGGTGAGTGAAGT 918
Db 937 ATAAATTCACGTCGATGATTTTCAATATGATCTGAAGAGAGAGGTGAGTGAAGT 996
Qy 919 TCACCCCATGCTGTGTAAACGAGTCAAGCCAGGTGCGAGATCGTCTTGAAG 978
Db 997 TCACCCCATGCTGTGTAAACGAGTCAAGCCAGGTGCGAGATCGTCTTGAAG 1056
Qy 979 TCACGAGGTGGGATCTGCTTTTAAAGCTCCAGTGTCCATTCATCCCTGATGG 1038
Db 1057 TCACGAGGTGGGATCTGCTTTTAAAGCTCCAGTGTCCATTCATCCCTGATGG 1116
Qy 1039 GGCATAGTTGAGACTGCAAGAGTGAAGTGTCTTAAAGGCTGAGAGCCAGTTCC 1098
Db 1117 GGCATAGTTGAGACTGCAAGAGTGAAGTGTCTTAAAGGCTGAGAGCCAGTTCC 1176
Qy 1099 CACTCAAGGCTCCCTGCTTGAACATTCATGCTCTGAAAGACATTTCTGTGAG 1158
Db 1177 CACTCAAGGCTCCCTGCTTGAACATTCATGCTCTGAAAGACATTTCTGTGAG 1236
Qy 1159 CAGAATTTGCTGTTCCGGGCTGAGTTGGGCTGAGTACGAGATCAATGATGGG 1218
Db 1237 CAGAATTTGCTGTTCCGGGCTGAGTTGGGCTGAGTACGAGATCAATGATGGG 1296
Qy 1219 ACTTAGACTGGGCTCGGCTGCTGTAAGATGCTTAAAGAAATCTTCAATTTCC 1278
Db 1297 ACTTAGACTGGGCTCGGCTGCTGTAAGATGCTTAAAGAAATCTTCAATTTCC 1356
Qy 1279 TTGCAAGAGCAGGCGGCGGAGAGAGAGACAGGCGCTGCACAAAGGCGGCTGT 1338
Db 1357 TTGCAAGAGCAGGCGGCGGAGAGAGAGACAGGCGCTGCACAAAGGCGGCTGT 1416
Qy 1339 CGGTGTGAGTGTGCATGTAGCGCAGGCGCTTCTGTGTGGCGGTGCGAGCGACA 1398
Db 1417 CGGTGTGAGTGTGCATGTAGCGCAGGCGCTTCTGTGTGGCGGTGCGAGCGACA 1476

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Qy 1399 GCGGCGACAGCAGCCTGCAAGAACCCGCCGAACCTGCTCGAGACACCGTGA 1458
Db 1477 GCGGCGACAGCAGCCTGCAAGAACCCGCCGAACCTGCTCGAGACACCGTGA 1536
Qy 1459 GGAGCGGGTTGATGACCGAGCTGAGGTAGAAAACGTTCTCCGAGAGGAGAGATCA 1518
Db 1537 GGAGCGGGTTGATGACCGAGCTGAGGTAGAAAACGTTCTCCGAGAGGAGAGATCA 1596
Qy 1519 TGTACGCCCGGAAGTAGAGCTCTGCAAGTGTGCTTGGGTTGGCGGAGCATATCC 1578
Db 1597 TGTACGCCCGGAAGTAGAGCTCTGCAAGTGTGCTTGGGTTGGCGGAGCATATCC 1656
Qy 1579 TCCGATCTGTTGGGCAATCCAGCATACGGCAATGTACACAAATCAGCCCTGGCAGA 1638
Db 1657 TCCGATCTGTTGGGCAATCCAGCATACGGCAATGTACACAAATCAGCCCTGGCAGA 1716
Qy 1639 CACGAGCAGGAGGAGAGACAGAGAAAAGAAAACACAGATGAGAACAGTAATGAA 1698
Db 1717 CACGAGCAGGAGGAGAGACAGAGAAAAGAAAACACAGATGAGAACAGTAATGAA 1776
Qy 1699 TAAACCATTAATATTTAGCCCTCTGTTCTGCTTACTGCGCAGGAATGATACAA 1758
Db 1777 TAAACCATTAATATTTAGCCCTCTGTTCTGCTTACTGCGCAGGAATGATACAA 1836
Qy 1759 TTTTCAAGTGTGACTTGTGACAGCTTTTGGCACAGCAAGAGAGAAATTAACACTGT 1818
Db 1837 TTTTCAAGTGTGACTTGTGACAGCTTTTGGCACAGCAAGAGAGAAATTAACACTGT 1896
Qy 1819 TTCAACCCGAGGAGTGTGCTGTGTTAAGAAAGACATTAATGCTTTACAGCTGA 1878
Db 1897 TTCAACCCGAGGAGTGTGCTGTGTTAAGAAAGACATTAATGCTTTACAGCTGA 1956
Qy 1879 AAAAAAAAAA 1889
Db 1957 AAAAAAAAAA 1967

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RESULT 6
US-09-397-022-4454
: Sequence 4454, Application US/09397022
: GENERAL INFORMATION:
: APPLICANT: Gearing, David P.
: APPLICANT: Holtzman, Douglas A.
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
: FILE REFERENCE: HUMAN FETAL SKIN LIBRARY
: CURRENT APPLICATION NUMBER: US/09/397,022
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: 60/100,465
: PRIOR FILING DATE: 1998-09-15
: PRIOR APPLICATION NUMBER: 60/106,443
: PRIOR FILING DATE: 1998-10-30
: PRIOR APPLICATION NUMBER: 60/107,257
: PRIOR FILING DATE: 1998-11-05
: PRIOR APPLICATION NUMBER: 60/126,906
: PRIOR FILING DATE: 1999-03-30
: PRIOR APPLICATION NUMBER: 60/132,099
: PRIOR FILING DATE: 1999-04-30
: NUMBER OF SEQ ID NOS: 5775
: SOFTWARE: Pasted for Windows Version 3.0
: SEQ ID NO 4454
: LENGTH: 1918
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-397-022-4454

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```

Query Match 90.4% Score 1714 DB 17 Length 1918;
Best Local Similarity 99.8% Pred. No. 0;
Matches 1864; Conservative 3; Indels 0; Gaps 0;
Qy 19 GGTGTGCGCCGAGGAGGCGAGAGAGAGAGACCCGACGCGGAGCCGACGC 78
|||||

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[illegible]

QY	1159	CAGAAATTGGCTGTTTCGGCCCTGAGTTGGCTCTAGAGACTCCAGAGCTCAATGACTGGG	1218
Db	1175	CAGAAATTGGCTGTTTCGGCCCTGAGTTGGCTCTAGAGACTCCAGAGCTCAATGACTGGG	1234
QY	1219	ACTTAAGACTGGGGCTGGGCGCTCGCTCTGAAAGTGGCTTAAGAAATCTTCTCACTTCC	1278
Db	1235	ACTTAAGACTGGGGCTGGGCGCTCGCTCTGAAAGTGGCTTAAGAAATCTTCTCACTTCC	1294
QY	1279	TTTGAGAGACTGGCGCCGGGACGCGAAGACGACAGGGCCCTGCGCAAAAGCGGCGCTGT	1338
Db	1295	TTTGAGAGAGACTGGCGCCGGGACGCGAAGACGAGGGCGCTGCGCAAAAGCGGCGCTGT	1354
QY	1339	CGGTGTGGAGTGGGCGCATTTAGCGCGAGCGCTTCTCGGTGGTGGCGTGTGACGACGA	1398
Db	1355	CGGTGTGGAGTGGGCGCATTTAGCGCGAGCGCTTCTCGGTGGTGGCGTGTGACGACGA	1414
QY	1399	GAGCGGACGACAGCAGCTTCGACGACACCCTCGGAAATGCTGTGCGAGACACCTGTACA	1458
Db	1415	GAGCGGACGACAGCAGCTTCGACGACACCCTCGGAAATGCTGTGCGAGAGACACCTGTACA	1474
QY	1459	GGAGCGGCTTGATATACCGAGCTGAGGTAAAGAAACGTCGCGAGAGGGGAGAGATCA	1518
Db	1475	GGAGCGGCTTGATATACCGAGCTGAGGTAAAGAAACGTCGCGAGAGGGGAGAGATCA	1534
QY	1519	TGTACGCCCGGAGATGAGACCTGTCAGTCTGCTTGGGTTTGGCCCGCAGCATGATCC	1578
Db	1533	TGTACGCCCGGAGATGAGACCTGTCAGTCTGCTTGGGTTTGGCCCGCAGCATGATCC	1594
QY	1579	TCCGAATCTGGTTGGGCTCCAGCATACGGCCCAATGTCAACATCATCCCTGGGCGAGA	1638
Db	1595	TCCGAATCTGGTTGGGCTCCAGCATACGGCCCAATGTCAACATCATCCCTGGGCGAGA	1654
QY	1639	CACGAGCAGGAGGGAGAGACAGCAAGAAAGAAACACAGATGAGAACACAGTAATGAA	1698
Db	1655	CACGAGCAGGAGGGAGAGACAGCAAGAAAGAAACACAGATGAGAACACAGTAATGAA	1714
QY	1699	TAAACCCATTAATAATTTTAGCCCCCTGTGTTCTGTCTTACTGGCCAGGAATGTACCA	1758
Db	1715	TAAACCCATTAATAATTTTAGCCCCCTGTGTTCTGTCTTACTGGCCAGGAATGTACCA	1774
QY	1759	TTTTTCAGTGTGACCTTGACAGCTTCTTTTGGCCACAGCAAGAGATTTTAACAGT	1818
Db	1775	TTTTTCAGTGTGACCTTGACAGCTTCTTTTGGCCACAGCAAGAGATTTTAACAGT	1834
QY	1819	TTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACCATTAATGCTTTAGCAGGTGA	1878
Db	1835	TTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACCATTAATGCTTTAGCAGGTGA	1894
QY	1879	AAAAAAA 1885	
Db	1895	AAAAAAA 1901	
RESULT 7			
US-09-808-383-4454			
: Sequence 4454, Application US/09808383			
: GENERAL INFORMATION:			
: APPLICANT: Geilzman, David P.			
: APPLICANT: Holtzman, Douglas A.			
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A			
: TITLE OF INVENTION: HUMAN FETAL SKIN LIBRARY			
: FILE REFERENCE: 1600.1046-002			
: CURRENT APPLICATION NUMBER: US/09/808.383			
: CURRENT FILING DATE: 2001-03-13			
: PRIOR APPLICATION NUMBER: US 09/397,022			
: PRIOR FILING DATE: 1999-09-15			
: PRIOR APPLICATION NUMBER: US 60/100,465			
: PRIOR FILING DATE: 1998-09-15			
: PRIOR APPLICATION NUMBER: US 60/106,443			
: PRIOR FILING DATE: 1998-10-30			
: PRIOR APPLICATION NUMBER: US 60/107,257			
: PRIOR FILING DATE: 1998-11-15			

```

RESULT 7
US-09-808-383-4454
Sequence 4454, Application US/09808383
GENERAL INFORMATION:
APPLICANT: Geating, David P.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
TITLE OF INVENTION: HUMAN FEET SKIN LIBRARY
FILE REFERENCE: 1600, 1046-002
CURRENT APPLICATION NUMBER: US/09/808, 383
CURRENT FILING DATE: 2001-03-13
PRIORITY APPLICATION NUMBER: US 09/397, 022
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: US 60/100,465
PRIORITY FILING DATE: 1998-09-15
PRIORITY APPLICATION NUMBER: US 60/106,443
PRIORITY FILING DATE: 1998-10-30
PRIORITY APPLICATION NUMBER: US 60/107,257
PRIORITY FILING DATE: 1998-11-15

```



```

RESULT 9
US-09-652-128-9375/c
; Sequence 9375, Application US/09652128
; GENERAL INFORMATION:
; APPLICANT: Shytan, Andrew W.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1171-001
; CURRENT APPLICATION NUMBER: US/09/652.128
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,133
; NUMBER OF SEQ ID NOS: 10265
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9375
; LENGTH: 1925
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-652-128-9375

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Query Match	90.0%;	Score 1707;	DB 25;	Length 1925;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1857; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

OY	19	GGTCTCGGCCGGGAGCCGAGCAGTGGGAGAGACAGAGACCGGCACCGGAGACCAGC	78
Db	1888	GGTGCTGGCCCCGGGABCCGGAGCCGGAGGAGACAGAGACCGGCACCGGAGACCAGC	1829
OY	79	CGGGCATGCAAGGCTCCGGCAGCGGACACTGGCGCTCTTAAGCTACAGCGTGTCTC	138
Db	1828	CGGGCATGCAAGGCTCCGGCAGCGGACACTGGCGCTCTTAAGCTACAGCGTGTCTC	1766
OY	139	CGGGGAGAGAGCCGGGCCCCCACACCTTCGGCAGCACAGCCGCTGCAGCCGGGACG	198
Db	1768	CGGGGAGAGAGCCGGGCCCCCACACCTTCGGCAGCACAGCCGCTGCAGCCGGGACG	1709
OY	199	CTCCGCTGTGTGGCTCCCTCTATGTCAGCTGGCTCTCCGGCCC GGGAATCCGGGAG	258
Db	1708	CTCCGCTGTGTGGCTCCCTCTATGTCAGCTGGCTCTCCGGCCC GGGAATCCGGGAG	1649
OY	259	AATGGGCTCTTAGCATTGCGGCAACTTTTTCGGGATTGTCTTGCTTCAGGCTTTGC	318
Db	1648	AATGGGCTCTTAGGATCGCGGCAACTTTTTCGGGATTGTCTTGCTTCAGGCTTTGC	1589
OY	319	GCTGCAAATCCATGCTTACCAGTGTAAAGAATTTCCAGCTGAACAACGACTGCTCTCCC	378
Db	1588	GCTGCAAATCCATGCTTACCAGTGTAAAGAATTTCCAGCTGAACAACGACTGCTCTCCC	1529
OY	379	CGAGTTCATTGTAAATTGCGACGGTGAAGCTTCAAGCATGTGTCAAGAAAGATGATGA	438
Db	1528	CGAGTTCATTGTAAATTGCGACGGTGAAGCTTCAAGCATGTGTCAAGAAAGATGATGA	1459
OY	439	GCAAAGTCCGGGATCATGTACC GCAAGTCTGTGCATCATCAGCGGCTGTCTATGC	498
Db	1468	GCAAAGTCCGGGATCATGTACC GCAAGTCTGTGCATCATCAGCGGCTGTCTATGC	1409
OY	499	CTGCGCGGGTACCACTCCCTTGCGCCCAAGGAAAGTGAATCAGTTTCATCATGTC	558
Db	1408	CTGCGCGGGTACCACTCCCTTGCGCCCAAGGAAAGTGAATCAGTTTCATCATGTC	1349
OY	559	CTGCAACACCCCTTTTGTAAAGGGCCAAGGCCCAAGAAAAGGAGATTTGCTCGGC	618
Db	1348	CTGCAACACCCCTTTTGTAAAGGGCCAAGGCCCAAGAAAAGGAGATTTGCTCGGC	1289
OY	619	CCTCAGGCCAGGGCTCCGACACCACTCTGTTCTCAATAATTAGCCCTTCTCGGACA	678
Db	1288	CCTCAGGCCAGGGCTCCGACACCACTCTGTTCTCAATAATTAGCCCTTCTCGGACA	1229
OY	679	CTGCTGAAGTGAAGAGATGCAACCCCTCTGGAATGTTCTTCACGCTCCGCCACA	738

Dh	1228	CTGCTGAGCTGGAAGGAGATGCCACCCCTTCGCAATGTGTTCTTCACGCCCTCGGCCCA	1165
Qy	739	ACCCCCACCTCCCTGAGTGAAGTTCTCTTCGGGTGTCCTTTATTTGGGTAGGACGG	798
Dh	1168	ACCCCCACCTCCCTGAGTGAAGTTCTCTTCGGGTGTCCTTTATTTGGGTAGGACGG	1105
Qy	799	GAGTCCGTCTCTCTTTGTCTCCGTGCAATATATGAAGAGCTGGTAACCATTTCTGA	858
Dh	1108	GAGTCCGTCTCTCTTTGTCTCCGTGCAATATATGAAGAGCTGGTAACCATTTCTGA	1049
Qy	859	ATAATTCAGCTGACGTGAATTTTCACTATGTACTTGAAGAGAGGTGAGTGAAGT	918
Dh	1048	ATAATTCAGCTGACGTGAATTTTCACTATGTACTTGAAGAGAGGTGAGTGAAGT	989
Qy	919	TCACCCCATCTCTGTGTAAACCGGAGCAAGGCGAGGCGAGAGTCTGCTTATGAG	978
Dh	988	TCACCCCATCTCTGTGTAAACCGGAGCAAGGCGAGGCGAGAGTCTGCTTATGAG	929
Qy	979	TCACAGAGTGGGCAATCGCTTTTGTAAAGCCCTCCAGTGTCCATTCATCCCTATGG	1038
Dh	928	TCACAGAGTGGGCAATCGCTTTTGTAAAGCCCTCCAGTGTCCATTCATCCCTATGG	869
Qy	1039	GGCATAGTTTAAGACTGCAGAGTGAAGTACGTTTTTTTAGGGCTGAGGGCCAGTTCC	1098
Dh	868	GGCATAGTTTAAAGACTGCAGAGTGAAGTACGTTTTTTTAGGGCTGAGGGCCAGTTCC	809
Qy	1099	CACCTAAGGCTCCCTCGCTTGACATTTAAACCTTCATGCTCTCGAAACCATCTCTGAG	1158
Dh	808	CACCTAAGGCTCCCTCGCTTGACATTTAAACCTTCATGCTCTCGAAACCATCTCTGAG	749
Qy	1159	CAGAAATGGCTGTTTTCGCGCTGAGTTGGGCTCTGTAGTACCTCGACATCAATGATGG	1218
Dh	748	CAGAAATGGCTGTTTTCGCGCTGAGTTGGGCTCTGTAGTACCTCGACATCAATGATGG	689
Qy	1219	ACTTGAAGTGGGGGTGGGCGTCGCTGAAAGTGTGTTAAAGAAATCTTCTACAGTTTCC	1278
Dh	688	ACTTGAAGTGGGGGTGGGCGTCGCTGAAAGTGTGTTAAAGAAATCTTCTACAGTTTCC	629
Qy	1279	TTGCAAGAGACTGGCGCGGGGAGCGCAAGAGCAACGGCGCTGCACAAAGCGGGCGTGT	1338
Dh	628	TTGCAAGAGACTGGCGCGGGGAGCGCAAGAGCAACGGCGCTGCACAAAGCGGGCGTGT	569
Qy	1339	CGGTGTGTGAGATGGGCAATGTACGGCGCAAGCGGCTTCTCTGTGTTGGCGCTGTCAAGCA	1398
Dh	568	CGGTGTGTGAGATGGGCAATGTACGGCGCAAGCGGCTTCTCTGTGTTGGCGCTGTCAAGCA	509
Qy	1399	GGCGGCAAGACAGACACTGTGACAGCAACCGCGCGAAATGCTGCGAGGACACCGTGTACA	1458
Dh	508	GGCGGCAAGCAAGCACTGTGACAGCAACCGCGCGAAATGCTGCGAGGACACCGTGTACA	449
Qy	1459	GGAGCGGGTTGTATGACCGAGCTGAAGGTAGAAAAAGTCTTCGAGAAAGGGAGGAGATCA	1518
Dh	448	GGAGCGGGTTGTATGACCGAGCTGAAGGTAGAAAAAGTCTTCGAGAAAGGGAGGAGATCA	389
Qy	1519	TGTACGCGCCGGAATATAGACCTGTCGACAGTCGTGTGGGTTTGGCGCCAGCATGATCC	1578
Dh	388	TGTACGCGCCGGAATATAGACCTGTCGACAGTCGTGTGGGTTTGGCGCCAGCATGATCC	329
Qy	1579	TCCGAATCTGTGTGGGCAATCGACATACGGCCATGTCAACCAATCAAGCCTTGGGCGAGA	1638
Dh	328	TCCGAATCTGTGTGGGCAATCGACATACGGCCATGTCAACCAATCAAGCCTTGGGCGAGA	269
Qy	1639	CACGAGCGAGGGGAGAGACAGAGAAAAAACAACACACATGAGAACACAGTAAATGAA	1698
Dh	268	CACGAGCGAGGGGAGAGACAGAGAAAAAACAACACACATGAGAACACAGTAAATGAA	209
Qy	1699	TAAACCATTAATATTTTACCCCTCTGTCTGTGCTTACTGGCCAGAGAAATGTATACCA	1758
Dh	208	TAAACCATTAATATTTTACCCCTCTGTCTGTGCTTACTGGCCAGAGAAATGTATACCA	149
Qy	1759	TTTTTTCAGTGTGGACTTGACACGCTTTCTTTGGCACAGCAAGAGAGATTTAAACCTGT	1818
Dh	148	TTTTTTCAGTGTGGACTTGACACGCTTTCTTTGGCACAGCAAGAGAGATTTAAACCTGT	89

Qy 1519 TGTACCCCGGAGTAAGACCTGTCAGTCTGCTTGGGTTTGGCCGACCATGATCC 1578
Db TGTACCCCGGAGTAAGACCTGTCAGTCTGCTTGGGTTTGGCCGACCATGATCC 329
Qy 1579 TCGAATCTGTGGGATCCAGCATACGCCAATGTCAACATCAGCCCTGGGACA 1638
Db TCGAATCTGTGGGATCCAGCATACGCCAATGTCAACATCAGCCCTGGGACA 269
Qy 1639 CACGACGAGGAGAGAGACAGAGAAAGAAACACAGCATGAGACAGCACTAATGAA 1698
Db CACGACGAGGAGAGAGACAGAGAAAGAAACACAGCATGAGACAGCACTAATGAA 209
Qy 1699 TAAACCATATAATATTAGCCCTCTGCTGCTTACTGCGAGAAATGTACCAA 1758
Db TAAACCATATAATATTAGCCCTCTGCTGCTTACTGCGAGAAATGTACCAA 149
Qy 1759 TTTTTCAGTGTGAGACTTACAGCTTCTTTGCCACAGAGAGAAATTAACACTGT 1818
Db TTTTTCAGTGTGAGACTTACAGCTTCTTTGCCACAGAGAGAAATTAACACTGT 89
Qy 1819 TTCAAACCCGGGAGTGTGCTGTATAAGAAAGACATTAAATGCTTTAGACAGTGA 1878
Db TTCAAACCCGGGAGTGTGCTGTATAAGAAAGACATTAAATGCTTTAGACAGTGA 29

RESULT 14
US-09-371-168-7188
; Sequence 7188, Application US/09371168
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, M. Alexandra
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: MLN98-37PA
; CURRENT APPLICATION NUMBER: US/09/371,168
; EARLIER FILING DATE: 1999-08-10
; EARLIER APPLICATION NUMBER: 60/095,907
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/103,145
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 8285
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 7188
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-168-7188

Query Match 83.7%; Score 1587; DB 17; Length 1917;
Best Local Similarity 99.8%; Pred. No. 1.2e-298;
Matches 1857; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 19 GGTGCTCGGCGCGGAGCGGAGGAGAGAGACCCGCGGAGCGCGAGG 78
Db 33 GGTGCTCGGCGCGGAGCGGAGGAGAGAGACCCGCGGAGCGCGAGG 92
Qy 79 CGGCGATGACAGCTCCGAGAGCGGACCTGCGCTCTCTAAGTACAGCGTGTCTC 138
Db 93 CGGCGATGACAGCTCCGAGAGCGGACCTGCGCTCTCTAAGTACAGCGTGTCTC 152
Qy 139 CGGCGAGAGCGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGC 198
Db 153 CGGCGAGAGCGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGC 212
Qy 199 CTCCTGCTGTGCTCTCTCTCTGATGCGCTTCCGCGCGGAGATCCGGGAG 258
Db 213 CTCCTGCTGTGCTCTCTCTCTGATGCGCTTCCGCGCGGAGATCCGGGAG 272
Qy 259 AATGTGGTCTAGGATCGGCAACTTTTGGGATTTGTTCTTCCAGGCTTTGC 318
Db 273 AATGTGGTCTAGGATCGGCAACTTTTGGGATTTGTTCTTCCAGGCTTTGC 332
Qy 319 GCTGCAATTCAGTGTCTACAGTGTGAAGATTCAGCT -GAACAAGACTGCTCTCC 377
|||||

Db 333 GCTGCATATTCAGTGTCTACAGTGTGAAGATTCAGCTAGAACACACTGCTCTCC 392
Qy 378 CCGAGTTCATTTGATATTCAGCGGTGAACGTTCAAGACATGTGTCAAGAAAGATGAG 437
Db 393 CCGAGTTCATTTGATATTCAGCGGTGAACGTTCAAGACATGTGTCAAGAAAGATGAG 452
Qy 438 AGCAAGTCCGCGGATCATATGATCCGCAAGCTCTGTGATCATCAGCGGCTGTCTACG 497
Db 453 AGCAAGTCCGCGGATCATATGATCCGCAAGCTCTGTGATCATCAGCGGCTGTCTACG 512
Qy 498 CCTCTGCGGATTCAGTCT 557
Db 513 CCTCTGCGGATTCAGTCT 572
Qy 558 GCTGCATATTCAGTGTCTACAGTGTGAAGATTCAGCTAGAACACACTGCTCTCC 617
Db 573 GCTGCATATTCAGTGTCTACAGTGTGAAGATTCAGCTAGAACACACTGCTCTCC 632
Qy 618 CCTCTGCGGATTCAGTCT 677
Db 633 CCTCTGCGGATTCAGTCT 692
Qy 678 ACTGCTGAAGTGAAGAGATGCCACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 737
Db 693 ACTGCTGAAGTGAAGAGATGCCACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 752
Qy 738 AACCCCGACCT 797
Db 753 AACCCCGACCT 812
Qy 798 GAGTCCGCT 857
Db 813 GAGTCCGCT 872
Qy 858 AATAATTCACCTGACCTGATTTTTCAGTGTGAAGAGATTCAGCTAGAACACACTG 917
Db 873 AATAATTCACCTGACCTGATTTTTCAGTGTGAAGAGATTCAGCTAGAACACACTG 932
Qy 918 TTCAACCCCGACCT 977
Db 933 TTCAACCCCGACCT 992
Qy 978 GTCACTGAGTGGGATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1037
Db 993 GTCACTGAGTGGGATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1052
Qy 1038 GGCATATTTGACATCTGAGAGTGAAGATGAGCTTTTCTTAGGCTGAGGCGCACTTC 1097
Db 1053 GGCATATTTGACATCTGAGAGTGAAGATGAGCTTTTCTTAGGCTGAGGCGCACTTC 1112
Qy 1098 CCACGCAAGGCT 1157
Db 1113 CCACGCAAGGCT 1172
Qy 1158 GCAGATTTGCTGCT 1217
Db 1173 GCAGATTTGCTGCT 1232
Qy 1218 GACTTGAAGTGGGCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1277
Db 1233 GACTTGAAGTGGGCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1292
Qy 1278 CTTGCAAGAGCTGCGGCGGAGAGCAAGCAAGCGGCGGAGCGGAGCGGAGC 1337
Db 1293 CTTGCAAGAGCTGCGGCGGAGAGCAAGCAAGCGGCGGAGCGGAGCGGAGC 1352
Qy 1338 TCGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1397
Db 1353 TCGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1412
Qy 1398 AGGCGGAGCAGACACCTGACGAGAACACCGCGGAAATGCTGCGAGAGACCGTGTAC 1457
Db 1413 AGGCGGAGCAGACACCTGACGAGAACACCGCGGAAATGCTGCGAGAGACCGTGTAC 1472
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Db 1113 CCACTCAAGGCTCCCTGCTTGAATTCATCAACTTCATGCTCTGAAACCAATTCCTGCA 1172
1158 GCAGATATGGCTGGTTTCGCGCTAGATTGGGCTCTAGTACTGAGACTCAATGACTGG 1217
1173 GCAGATATGGCTGGTTTCGCGCTAGATTGGGCTCTAGTACTGAGACTCAATGACTGG 1232
1218 GACTTGAATGGGCTGGGCTGGCTCTGTAAGAAAGTCTTAAGAAATCTTCTCAGTTCTC 1277
1233 GACTTGAATGGGCTGGGCTGGCTCTGTAAGAAAGTCTTAAAGAAATCTTCTCAGTTCTC 1292
1278 CTTCGAGAGGACTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTG 1337
1293 CTTCGAGAGGACTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTG 1352
1338 TCGGTGTGTGAGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTG 1397
1353 TCGGTGTGTGAGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTG 1412
1398 AGCGGCGACAGCAGTCTGACGAAACCCGCGGAAATCTGCGAGAGACCGGTGAC 1457
1413 AGCGGCGACAGCAGTCTGACGAAACCCGCGGAAATCTGCGAGAGACCGGTGAC 1472
1458 AGGAGCGGCTGATGACGAGCTGAGTAAAGAAACGTCCTCGAGAGAGGAGGAGATC 1517
1473 AGGAGCGGCTGATGACGAGCTGAGTAAAGAAACGTCCTCGAGAGAGGAGGAGATC 1532
1518 ATGTACGCGCGGAGTACGAGCTGCTCCAGTCTGCTTGGGCTTGGCCGACAGCATATC 1577
1533 ATGTACGCGCGGAGTACGAGCTGCTCCAGTCTGCTTGGGCTTGGCCGACAGCATATC 1592
1578 CTCCCAATCTGTTGGGCTATCCAGTATCGGCGAATGTCACAAATACAGCCCTGGGAG 1637
1593 CTCCCAATCTGTTGGGCTATCCAGTATCGGCGAATGTCACAAATACAGCCCTGGGAG 1652
1638 ACACGAGCAGAGGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1697
1653 ACACGAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1712
1698 ATAAACCATTAATATTATGACCCCTCTGTTCTGTTCTTACTGCGCAGAGAAATGGTACCA 1757
1713 ATAAACCATTAATATTATGACCCCTCTGTTCTGTTCTTACTGCGCAGAGAAATGGTACCA 1772
1758 ATTTTCAAGTGTGGACTGTGACAGCTCTTTTGCACAAGCAGAGAAATTTTACACTG 1817
1773 ATTTTCAAGTGTGGACTGTGACAGCTCTTTTGCACAAGCAGAGAAATTTTACACTG 1832
1818 TTTCAAAACCCGGGAGGAGTGGCTGTAAAGAAAGACCAATTAATGCTTTAGACAGTGT 1877
1833 TTTCAAAACCCGGGAGGAGTGGCTGTAAAGAAAGACCAATTAATGCTTTAGACAGTGT 1892
1878 A 1878
1893 A 1893

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RESULT 18
US-09-652-128-7518
Sequence 7518, Application US/09652128

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GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600.1171-001
CURRENT APPLICATION NUMBER: US/09/652.128
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,133
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 10265
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7518
LENGTH: 1917

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-128-7518
Query Match 83.7%; Score 1587; DB 25; Length 1917;
Best Local Similarity 99.8%; Pred. No. 1.2e-298;
Matches 1857; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

19 GGTGCTGCGCCCGGAGGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 78
33 GGTGCTGCGCCCGGAGGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 92
79 GCGGCGATGAGAGCTCGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 138
93 GCGGCGATGAGAGCTCGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 152
139 GCGGCGAGAGGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 198
153 GCGGCGAGAGGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 212
199 CTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 258
213 CTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 272
259 AATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 318
273 AATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 332
319 GGTGCAATTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 377
333 GGTGCAATTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 392
378 CCGAGTTCATTTGAAATTTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAG 437
393 CCGAGTTCATTTGAAATTTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAG 452
438 AGCAAAATGCGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 497
453 AGCAAAATGCGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 512
498 CTTCTGCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 557
513 CTTCTGCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 572
558 GCTGCAACACCCCTCTTGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 617
573 GCTGCAACACCCCTCTTGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 632
618 CCGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 677
633 CCGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 692
678 ACTGCTGAAGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 737
693 ACTGCTGAAGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
738 AACCCCGACCTCCCTAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 797
753 AACCCCGACCTCCCTAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 812
798 GGAATCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 857
813 GGAATCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 872
858 AATAAATTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 917
873 AATAAATTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 932
918 TTTACCCCATGCTGTGTAACCGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 977
933 TTTACCCCATGCTGTGTAACCGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 992
978 GTCACTGAGTGGGAGTGTGCTTTTGTAAAGGCTCCAGTGTGATTCATTCATTCCTGATGG 1037

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Db 873 AATAAATTCAGCTTGAATTTTACATATGCTACTTGAAGGAAGAGGTGAGTGAAG 932

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Db 933 TTACACCCCATCTCTGTGTAAACCGAGTCAAGGCCAGGCTGGCAGAGTCTGCTTAGAA 992

QY 978 GTCACTGAGGTGGGATATGCTTTTGTAAAGCCTCCAGTGTCCATTCATCCCTGATGG 1037

Db 993 GTCACTGAGGTGGGATATGCTTTTGTAAAGCCTCCAGTGTCCATTCATCCCTGATGG 1052

QY 1038 GGGCATATTTGAGACTCAGAGTGAAGTACGTTTTCTTAGGGCTGAGAGGCCAGTTC 1097

Db 1053 GGGCATATTTGAGACTCAGAGTGAAGTACGTTTTCTTAGGGCTGAGAGGCCAGTTC 1112

QY 1098 CCACATCAAGGCTCCCTCCCTTGAACATTCATTCATTCCTGATAAATCCATTCCTGCA 1157

Db 1113 CCACATCAAGGCTCCCTCCCTTGAACATTCATTCATTCCTGATAAATCCATTCCTGCA 1172

QY 1158 GCAGAAATGGGCTGGTGGGCTGAGTGGGCTGCTAGTACTGAGAGCTCAATGACTGG 1217

Db 1173 GCAGAAATGGGCTGGTGGGCTGAGTGGGCTGCTAGTACTGAGAGCTCAATGACTGG 1232

QY 1218 GACTTAGACTGGGGCTCGGCTCGCTGTGAAGAGTGTAGAAATCTTCTCAGTTCTC 1277

Db 1233 GACTTAGACTGGGGCTCGGCTCGCTGTGAAGAGTGTAGAAATCTTCTCAGTTCTC 1292

QY 1278 CTTCGAGAGAGACTGGCGCCGGGAGCGGAAGCAACGGGGCTGCACAAAGCGGGCTG 1337

Db 1293 CTTCGAGAGAGACTGGCGCCGGGAGCGGAAGCAACGGGGCTGCACAAAGCGGGCTG 1352

QY 1338 TCGGGTGGGAGTGGGCTGATGACGGGAGGGGCTCTGCTGGTGGGCTGGTGGAGCAG 1397

Db 1353 TCGGGTGGGAGTGGGCTGATGACGGGAGGGGCTCTGCTGGTGGGCTGGTGGAGCAG 1412

QY 1398 AGCGGCGAGCAGACAGCTGACGAGAACCCGCGAAACTGCTGCGAGAGACCGTGTAC 1457

Db 1413 AGCGGCGAGCAGACAGCTGACGAGAACCCGCGAAACTGCTGCGAGAGACCGTGTAC 1472

QY 1458 AGGACCGGTTATGATCCGAGTGAAGTGAAGAAACGTCCTCCGANAAGGGAGGAGATC 1517

Db 1473 AGGACCGGTTATGATCCGAGTGAAGTGAAGAAACGTCCTCCGANAAGGGAGGAGATC 1532

QY 1518 ATGTACGCCCGGAGATAGGAGCTCTCCAGTCTGCTGGTGGTGGGCGCAGCCATGATC 1577

Db 1533 ATGTACGCCCGGAGATAGGAGCTCTCCAGTCTGCTGGTGGTGGGCGCAGCCATGATC 1592

QY 1578 CTCCGATCTGCTGGGCTCCAGATACGGCAATGTCACAAATACAGCCCTGGCAG 1637

Db 1593 CTCCGATCTGCTGGGCTCCAGATACGGCAATGTCACAAATACAGCCCTGGCAG 1652

QY 1638 ACACGAGCAGGAGGAGAGACAGAGAAAGAAACACAGCATGTGAACACAGTAATGA 1697

Db 1653 ACACGAGCAGGAGGAGAGACAGAGAAAGAAACACAGCATGTGAACACAGTAATGA 1712

QY 1698 AATAAAACATAAATATTTAGCCCTCTGTTCTGTCTTACTGTGCGCAGAGAAATGATACA 1757

Db 1713 AATAAAACATAAATATTTAGCCCTCTGTTCTGTCTTACTGTGCGCAGAGAAATGATACA 1772

QY 1758 ATTTTCACTGTGGTGAATGACAGCTTCTTTGCCACAAGAGAGAGATTTAATCACTG 1817

Db 1773 ATTTTCACTGTGGTGAATGACAGCTTCTTTGCCACAAGAGAGAGATTTAATCACTG 1832

QY 1818 TTTCAAACCCGGGAGTGGCTGTGTAAAGAAAGACCATTAATGCTTTAGACAGTGT 1877

Db 1833 TTTCAAACCCGGGAGTGGCTGTGTAAAGAAAGACCATTAATGCTTTAGACAGTGT 1892

QY 1878 A 1878

Db 1893 A 1893

RESULT 20
US-09-652-914-8473

; Sequence 8473, Application US/09652914

; GENERAL INFORMATION:

; APPLICANT: Shyjan, Andrew W.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

; FILE REFERENCE: 1600.1193-001

; CURRENT APPLICATION NUMBER: US/09/652,914

; PRIOR FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 60/152,112

; NUMBER OF SEQ ID NOS: 9677

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8473

; LENGTH: 1917

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-652-914-8473

Query Match 83.7%; Score 1587; DB 25; Length 1917;

Best Local Similarity 99.8%; Pred. No. 1.2e-298;

Matches 1857; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 19 GGTGCTGGCCCGGAGCGGAGCGGAGCGAGAGAGACCCGAGCGGAGCGGAGCG 78

Db 33 GGTGCTGGCCCGGAGCGGAGCGGAGCGGAGCGAGAGACCCGAGCGGAGCGGAGCG 92

QY 79 CGGGGATGAGGCTCCGCGAGGCGGACCTGGGGCTCTTAAAGCTAAGACGGTGTCTC 138

Db 93 CGGGGATGAGGCTCCGCGAGGCGGACCTGGGGCTCTTAAAGCTAAGACGGTGTCTC 152

QY 139 CGGGGAGCAGCGGCGGCGCCAGCAGCTCGCAGCAGCAGCCGCTGCAAGCCGGGAGC 198

Db 153 CGGGGAGCAGCGGCGGCGCCAGCAGCTCGCAGCAGCAGCCGCTGCAAGCCGGGAGC 212

QY 199 CTCGCTGCTGTGGCTCTCTCTATGATGGCTTGGCTTCCCGGCGGCGGAG 258

Db 213 CTCGCTGCTGTGGCTCTCTCTATGATGGCTTGGCTTCCCGGCGGCGGAG 272

QY 259 AATGTGGTCTTGAAGCAATTCGCGCACTTTTGGGATTTGTTCTTCTTCAAGCTTTGC 318

Db 273 AATGTGGTCTTGAAGCAATTCGCGCACTTTTGGGATTTGTTCTTCTTCAAGCTTTGC 332

QY 319 GCTGCAATCCAGTCTACGAGTGTGAAGATTCAGCT- GAACAAAGACTGCTCTCC 377

Db 333 GCTGCAATCCAGTCTACGAGTGTGAAGATTCAGCT- GAACAAAGACTGCTCTCC 392

QY 378 CCGAGTCAATTTGAATTCAGGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 437

Db 393 CCGAGTCAATTTGAATTCAGGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 452

QY 438 AGCAAAATGCGGGATCATGTACCGCAAGTCTGTGATCATGAGGAGGCTGTCTATCG 497

Db 453 AGCAAAATGCGGGATCATGTACCGCAAGTCTGTGATCATGAGGAGGCTGTCTATCG 512

QY 498 CTTTGGCGGGTACAGTCTTCTGCTTCCAGGGAATCTGAATCTAGTTGATCAGCT 557

Db 513 CTTTGGCGGGTACAGTCTTCTGCTTCCAGGGAATCTGAATCTAGTTGATCAGCT 572

QY 558 GCTGCAACACCCCTTTTGAAGGGGCAAGGCCCAAGAAAGGGAGTTCGCTCGG 617

Db 573 GCTGCAACACCCCTTTTGAAGGGGCAAGGCCCAAGAAAGGGAGTTCGCTCGG 632

QY 618 CCGTCAGGCGAGGCTCCGAGCAGCATCTGTTCTCAATTAAGCCCTTCTCGGAC 677

Db 633 CCGTCAGGCGAGGCTCCGAGCAGCATCTGTTCTCAATTAAGCCCTTCTCGGAC 692

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Db 693 ACTGCTGAAGTGAAGAGATGCCACCCCTCTGCAATTTCTTCAGAGCCCTCGCC 752

QY 738 AACGCCACCTCCCTGAGTGTGTTCTTGGGTGCTTTTATTTGAGGAGCG 797

Db 753 AACGCCACCTCCCTGAGTGTGTTCTTGGGTGCTTTTATTTGAGGAGCG 812

Db 633 CCTCAGGCGCAGGCGTCCGCAACACATCCCTCTCTCAATTTAGCCCTCTCTCGGCAC 692
 QY 678 ACTGCTGAGCTGAAGAGATGCCACCCCTCTGACATTTCTTCCAGCCCTCGCCCC 737
 Db 693 ACTGCTGAAGCTGAAGAGATGCCACCCCTCTGACATTTCTTCCAGCCCTCGCCCC 752
 QY 738 AACCCCGACCTCCCTGAGTGTCTCTGAGGTCCTTTTNTCTGGGTAGGAGCG 797
 Db 753 AACCCCGACCTCCCTGAGTGTCTCTGAGGTCCTTTTNTCTGGGTAGGAGCG 812
 QY 798 GGAGTCGCTGTCT 857
 Db 813 GGAGTCGCTGTCT 872
 QY 858 AATAAATTCACGCTGACGATTTTTCAGTATGCTTAAAGAGAGAGAGTGAAG 917
 Db 873 AATAAATTCACGCTGACGATTTTTCAGTATGCTTAAAGAGAGAGTGAAG 932
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 Db 933 TTTACCCCATGCTGTGTAAACCGAGTCAAGGCGAGAGTCAAGTCTCTAGAA 992
 QY 978 GTCACTGAGGTGGGCACTGCTTTTGTAAAGCCTCCAGTGTCCATTCCTGATGG 1037
 Db 993 GTCACTGAGGTGGGCACTGCTTTTGTAAAGCCTCCAGTGTCCATTCCTGATGG 1052
 QY 1038 GGGCATAGTTTGAAGCTGCAGAGTGAAGTACGTTTCTTAAAGGCTTGAAGGCGCAGTTC 1097
 Db 1053 GGGCATAGTTTGAAGCTGCAGAGTGAAGTACGTTTCTTAAAGGCTTGAAGGCGCAGTTC 1112
 QY 1098 CCACATCAAGGCTCCCTCGCTTGAATTTCAAACTTCCTCTGTAAGAAACATTCCTGCA 1157
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 QY 1158 GCAGATAGT 1217
 Db 1173 GCAGATAGT 1232
 QY 1218 GACTTAAAGCTGGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 1277
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 QY 1338 TCGGT 1397
 Db 1353 TCGGT 1412
 QY 1398 AGGCGGACAGAGCTGCGAGCAACCCGCGAAGCTGTGTGTGTGTGTGTGTGTGTGTGT 1457
 Db 1413 AGGCGGACAGAGCTGCGAGCAACCCGCGAAGCTGTGTGTGTGTGTGTGTGTGTGTGT 1472
 QY 1458 AGGAGGAGGTTGATGACGAGCTGAGTAGAAGAAAGCTCTCGAGAAAGGAGAGATC 1517
 Db 1473 AGGAGGAGGTTGATGACGAGCTGAGTAGAAGAAAGCTCTCGAGAAAGGAGAGATC 1532
 QY 1518 ATGTACGCCCGGAGAGTGAAGCTGTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1577
 Db 1533 ATGTACGCCCGGAGATGAGACTGTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1592
 QY 1578 CTCCGAAATGT 1637
 Db 1593 CTCCGAAATGT 1652
 QY 1638 ACACGAGCAGAGGAG 1697
 Db 1653 ACACGAGCAGAGGAG 1712
 QY 1698 ATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1757
 Db 1713 ATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1772

QY 1758 ATTTTTCAGTGTGACGCTTGTGACGCTTGTGACGCTTGTGACGCTTGTGACGCTTGT 1817
 Db 1773 ATTTTTCAGTGTGACGCTTGTGACGCTTGTGACGCTTGTGACGCTTGTGACGCTTGT 1832
 QY 1818 TTTCAAAACCGGGGAGT 1877
 Db 1833 TTTCAAAACCGGGGAGT 1892
 QY 1878 A 1878
 Db 1893 A 1893
 RESULT 22
 US-09-801-833-7188
 ; Sequence 7188, Application US/09801833
 ; GENERAL INFORMATION:
 ; APPLICANT: Glucksmann, M. Alexandra
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
 ; TITLE OF INVENTION: HUMAN BRAIN LIBRARY
 ; FILE REFERENCE: 1600.1037-005
 ; CURRENT APPLICATION NUMBER: US/09/801,833
 ; PRIOR FILING DATE: 2001-03-13
 ; PRIOR APPLICATION NUMBER: 09/371,168
 ; PRIOR FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: 60/095,907
 ; PRIOR FILING DATE: 1998-08-10
 ; PRIOR APPLICATION NUMBER: 60/103,145
 ; PRIOR FILING DATE: 1998-10-05
 ; NUMBER OF SEQ ID NOS: 8285
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7188
 ; LENGTH: 1917
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-801-833-7188
 Query Match 83.7%; Score 1587; DB 31; Length 1917;
 Best Local Similarity 99.8%; Pred. No. 1.2e-298;
 Matches 1857; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 19 GGTGCTGGGCGCGGAGCGGAGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 78
 Db 33 GGTGCTGGGCGCGGAGCGGAGCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 92
 QY 79 CGGCGATGAGAGGTCGCGAGAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 138
 Db 93 CGGCGATGAGAGGTCGCGAGAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 152
 QY 139 CGGCGAGCAGCGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 198
 Db 153 CGGCGAGCAGCGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 212
 QY 199 CTCGCTGCTGTGCGCTCTGTATGCGCTTGTGCGGCTTGTGCGGCGGCGGAGCTCGGAG 258
 Db 213 CTCGCTGCTGTGCGCTCTGTATGCGCTTGTGCGGCTTGTGCGGCGGCGGAGCTCGGAG 272
 QY 259 AATGTGGTCTTATGAGCTTGTGCGGAGCTTGTGCGGAGCTTGTGCGGAGCTTGTGCGG 318
 Db 273 AATGTGGTCTTATGAGCTTGTGCGGAGCTTGTGCGGAGCTTGTGCGGAGCTTGTGCGG 332
 QY 319 GCTCAATTCAGTGTGACGAGTGTGAAGATTCAGCT-GAACAAGAGCTGTCTCTCC 377
 Db 333 GCTCAATTCAGTGTGACGAGTGTGAAGATTCAGCTGAAACAGAGCTGTCTCTCC 392
 QY 378 CCGAGTTCATTTGTAATTCAGGAGTGAAGCTTCAAGCATGTGTCAAGAAAGAGATGG 437
 Db 393 CCGAGTTCATTTGTAATTCAGGAGTGAAGCTTCAAGCATGTGTCAAGAAAGAGATGG 452
 QY 438 AGCAAAAGTCCGGGATATGTACGCGCAAGTCTGTGTATATACGGGCGCTGTCTATCG 497
 Db 453 AGCAAAAGTCCGGGATATGTACGCGCAAGTCTGTGTATATACGAGGCGCTGTCTATCG 512

QY 319 GCTGCAATTCAGTGTCTTACCAAGTGTGAAGATTTCAGCTGACACAGACGTCCTCTCC 378
| | | | |
Db 1635 GCTGCAATTCAGTGTCTTACCAAGTGTGAAGATTTCAGCTGACACAGACGTCCTCTCC 1576
QY 379 CGAGTTCATTTGTAATTCAGAGTGTGAAGTTCAGACATGTGTGAGAAAGAGATGGA 438
| | | | |
Db 1575 CGAGTTCATTTGTAATTCAGAGTGTGAAGTTCAGACATGTGTGAGAAAGAGATGGA 1516
QY 439 GCAAGTGTGCGGAGTTCATGACGCAAGTGTGTGATCATGACGAGGCTGTCTCATGCG 498
| | | | |
Db 1515 GCAAGTGTGCGGAGTTCATGACGCAAGTGTGTGATCATGACGAGGCTGTCTCATGCG 1456
QY 499 CTGTCGCGGAGTTCAGACGTCCTGTCTGCTCCGAGGAACTGACGTCAGTTGTCATGCTG 558
| | | | |
Db 1455 CTGTCGCGGAGTTCAGACGTCCTGTCTGCTCCGAGGAACTGACGTCAGTTGTCATGCTG 1396
QY 559 CTGCAACACCCCTCTTTGTACGAGGCGCAAGGCGCCAGAAAGGGAAGTTCTGCTGCGC 618
| | | | |
Db 1395 CTGCAACACCCCTCTTTGTACGAGGCGCAAGGCGCCAGAAAGGGAAGTTCTGCTGCGC 1336
QY 619 CCTCAGGCGAGGCGCTCGCCACCACCATCTGTCTCAATTAAGCCCTCTCTGCGACA 678
| | | | |
Db 1335 CCTCAGGCGAGGCGCTCGCCACCACCATCTGTCTCAATTAAGCCCTCTCTGCGACA 1277
QY 679 CTGCTGAAGCTGAAGGAGATGCAACCCCTGCTGATGTCTTCCAGCCCTGCGCCCA 738
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Db 1276 CTGCTGAAGCTGAAGGAGATGCAACCCCTGCTGATGTCTTCCAGCCCTGCGCCCA 1217
QY 729 ACCCCCACTCTCTGATGAGTTCTTCTGCGTCTCTTATTTCTGCTGAGGAGCGG 798
| | | | |
Db 1216 ACCCCCACTCTCTGATGAGTTCTTCTGCGTCTCTTATTTCTGCTGAGGAGCGG 1157
QY 799 GAGTCCGTTCTCTTTTGTCTCTGTGCAATTAATGAAGAGCTCGTAAGCATTCGA 858
| | | | |
Db 1156 GAGTCCGTTCTCTTTTGTCTCTGTGCAATTAATGAAGAGCTCGTAAGCATTCGA 1097
QY 859 ATAAATTCAGCTGACTGAATTTTCAATGATGACTTGAAGAGAGGAGTGAAGAAAGT 918
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Db 1096 ATAAATTCAGCTGACTGAATTTTCAATGATGATGACTTGAAGAGAGGAGTGAAGAAAGT 1037
QY 919 TCACCCCATGCTGTGTATACCGGAGTCAAGGCGAGCTGCGAGAGTCTTACAG 978
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Db 1036 TCACCCCATGCTGTGTATACCGGAGTCAAGGCGAGCTGCGAGAGTCTTACAG 977
QY 979 TCACGAGGAGTGGGAGTGGCTTTTGAAGGCTCCAGATGATTCATCCATCCGATGAG 1038
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QY 1039 GGCATAGTTTGAAGTGCAGAGTGAAGTGAAGTTCCTTAAGGCTGAGAGGCCAGTTCC 1098
| | | | |
Db 916 GGCATAGTTTGAAGTGCAGAGTGAAGTGAAGTTCCTTAAGGCTGAGAGGCCAGTTCC 857
QY 1099 CACTCAAGGCTCCCTGCTTGCATTCATTCATCTCTGAGAAACCATTCCTGAG 1158
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QY 1159 CAGAAATGGCTGTTGCGGCTGAGTGGGCTTGAAGTGCAGTGCAGACTCATGACTGG 1218
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Db 796 CAGAAATGGCTGTTGCGGCTGAGTGGGCTTGAAGTGCAGTGCAGACTCATGACTGG 737
QY 1219 ACTTGAAGTGGGCTGCGGCTGCTGAAAGTGCCTTAAGAAATCTTTCAGTTTCC 1278
| | | | |
Db 736 ACTTGAAGTGGGCTGCGGCTGCTGAAAGTGCCTTAAGAAATCTTTCAGTTTCC 677
QY 1279 TTGCAAGAGACTGGGCGCGGAGAGAGCAAGGCGCTGCGCAAAAGGCGGCTGT 1338
| | | | |
Db 676 TTGCAAGAGACTGGGCGCGGAGAGAGCAAGGCGCGCTGCGCAAAAGGCGGCTGT 617
QY 1339 CGGTGAGTGAAGTGCATGACGAGGAGGCTTCTGAGTGTGAGCTGACGAGACA 1398
| | | | |
Db 616 CGGTGAGTGAAGTGCATGACGAGGAGGCTTCTGAGTGTGAGCTGACGAGACA 557

QY 1399 GCGGAGCAGACAGACCTGACAGAACACCCGCGAAACTGTGCGAGGACACCCGTGTACA 1458
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Db 556 GCGGAGCAGACAGACCTGACAGAACACCCGCGAAACTGTGCGAGGACACCCGTGTACA 497
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Db 496 GAGCGGGTTGATGACCGAGCTGAGGTAGAAAACGTCCTCCAGAAAGGAGAGATGCA 437
QY 1519 TGTACGCGCGGAGTGAAGTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1578
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RESULT 24
US-09-950-083-1914/c
; Sequence 1914, Application US/09950083
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS805
; CURRENT APPLICATION NUMBER: US/09/950,083
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US01/11988
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US00/06043
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06012
; PRIOR FILING DATE: 2000-03-09
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; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06049
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06057
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06824
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: PCT/US00/06765
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: PCT/US00/06792

[illegible]

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PRIOR APPLICATION NUMBER:	PCT/US00/149633
PRIOR FILING DATE:	2000-06-01
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PRIOR APPLICATION NUMBER:	PCT/US00/149288
PRIOR FILING DATE:	2000-06-01
PRIOR APPLICATION NUMBER:	PCT/US00/149344
PRIOR FILING DATE:	2000-06-01
PRIOR APPLICATION NUMBER:	PCT/US00/149733
PRIOR FILING DATE:	2000-06-01
PRIOR APPLICATION NUMBER:	PCT/US00/149654
PRIOR FILING DATE:	2000-06-01
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PRIOR FILING DATE:	2000-09-26
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PRIOR FILING DATE:	2000-09-26
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PRIOR FILING DATE:	2001-04-27
PRIOR APPLICATION NUMBER:	US 60/124,146
PRIOR FILING DATE:	1999-03-12
PRIOR APPLICATION NUMBER:	US 60/167,061
PRIOR FILING DATE:	1999-11-23
PRIOR APPLICATION NUMBER:	US 60/124,093
PRIOR FILING DATE:	1999-03-12
PRIOR APPLICATION NUMBER:	US 60/166,989
PRIOR FILING DATE:	1999-11-23
PRIOR APPLICATION NUMBER:	US 60/124,145
PRIOR FILING DATE:	1999-03-12
PRIOR APPLICATION NUMBER:	US 60/168,654
PRIOR FILING DATE:	1999-12-03
PRIOR APPLICATION NUMBER:	US 60/124,099
PRIOR FILING DATE:	1999-03-12
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PRIOR APPLICATION NUMBER:	US 60/124,096
PRIOR FILING DATE:	1999-03-12
PRIOR APPLICATION NUMBER:	US 60/168,622
PRIOR FILING DATE:	1999-12-03
PRIOR APPLICATION NUMBER:	US 60/124,143
PRIOR FILING DATE:	1999-03-12
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PRIOR FILING DATE:	1999-12-03
PRIOR APPLICATION NUMBER:	US 60/124,095
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PRIOR FILING DATE:	1999-03-19
PRIOR APPLICATION NUMBER:	US 60/138,626
PRIOR FILING DATE:	1999-06-11
PRIOR APPLICATION NUMBER:	US 60/168,662
PRIOR FILING DATE:	1999-12-03
PRIOR APPLICATION NUMBER:	US 60/124,144
PRIOR FILING DATE:	1999-03-12
PRIOR APPLICATION NUMBER:	US 60/138,574

RESULT 25
US-10-105-299-2414/c
; Sequence 2414, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2414
; LENGTH: 1953
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1362)..(1362)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-105-299-2414

Query Match Best Local Similarity 83.6%; Score 1586; DB 40; Length 1953;
Matches 1056; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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DB 1935 GGTGCTCGGCCCCGGAGCGCGAGCGGAGAGCAGAGCCCGGAGCCCGGAGCG 1876
QY 79 CGGGGATGATGAGGCTCCGGAGAGCGGAGCAGCTGCGGCTCTTAAGCTAGCAGCCGTGCTC 138
DB 1875 CGGGGATGATGAGGCTCCGGAGAGCGGAGCAGCTGCGGCTCTTAAGCTAGCAGCCGTGCTC 1816
QY 139 CGCGGAGCAGCGCGGCGGCGGAGCGGAGCAGCTGCGGAGCGGAGCGGAGCGGAGCG 198
DB 1815 CGCGGAGCAGCGCGGCGGCGGAGCGGAGCAGCTGCGGAGCGGAGCGGAGCGGAGCG 1756
QY 199 CTCGCGCTGCTGCGCTCTCTCTGATGCGCTTGCCTCTCCGCGGCGGAGCTCCGCGAG 258
DB 1755 CTCGCGCTGCTGCGCTCTCTCTGATGCGCTTGCCTCTCCGCGGCGGAGCTCCGCGAG 1696
QY 259 AATGAGGATGCTTGAAGCATGCGGAGCTTTTGGGAGATGTTCTTGCTTCCAGGCTTTCG 318
DB 1695 AATGAGGATGCTTGAAGCATGCGGAGCTTTTGGGAGATGTTCTTGCTTCCAGGCTTTCG 1636
QY 319 GCTGCAAAATCCAGTCTACAGTGTGAAGAAATCCAGCTGAACAAGACTGCTCTCCCG 378
DB 1635 GCTGCAAAATCCAGTCTACAGTGTGAAGAAATCCAGCTGAACAAGACTGCTCTCCCG 1576
QY 379 CGAGTTCATTTGATTTGACAGGAGTGAAGCATGTGTGAGAAAGATGATGA 438
DB 1575 CGAGTTCATTTGATTTGACAGGAGTGAAGCATGTGTGAGAAAGATGATGA 1516
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QY 499 CTCTGCGGAGTACAGTCTTCTGCTCCCAAGGAGAACTGAAGTCAAGTTCATCAGCTG 558
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QY 559 CTGCAACACCCCTCTTTTAACAGGAGCCCAAGAAAGAGGAGATTTGCGCTGCGC 618
DB 1335 CTGCAACACCCCTCTTTTAACAGGAGCCCAAGAAAGAGGAGATTTGCGCTGCGC 1336
QY 619 CCTCAGGCGGAGGCTCCGACACCATCTTCTCAATTAAGCCCTCTGCGGAGCA 678
DB 1335 CCTCAGGCGGAGGCTCCGACACCATCTTCTCAATTAAGCCCTCTGCGGAGCA 1277
QY 679 CTGCTGAAGCTGAAGAGATGACACCCCTCTCTGATGTTGTTCTTCAGACCCCTGCGCCCA 738
DB 1276 CTGCTGAAGCTGAAGAGATGACACCCCTCTCTGATGTTGTTCTTCAGACCCCTGCGCCCA 1217

QY 739 ACCCCCCACCTCCCTGAGTGAATTTCTTCTGAGTGTCTTTTATTTCTGGGTAGGAGCGG 798
DB 1216 ACCCCCCACCTCCCTGAGTGAATTTCTTCTGAGTGTCTTTTATTTCTGGGTAGGAGCGG 1157
QY 799 GAGTCCGTTCTCTTTTGTCTGTCGAATTAATGAAGAGCTCGGTAAGCAATTCGA 858
DB 1156 GAGTCCGTTCTCTTTTGTCTGTCGAATTAATGAAGAGCTCGGTAAGCAATTCGA 1097
QY 859 ATAAATTCAGCTGATGAATTTTCAATGATGATGATGAGGAGGAGTGAAGT 918
DB 1096 ATAAATTCAGCTGATGAATTTTCAATGATGATGATGAGGAGGAGTGAAGT 1037
QY 919 TCACCCCATGTCGTGTGAACCGGAGTCAAGCCAGGCTGCAAGTCTGCTTAAG 978
DB 1036 TCACCCCATGTCGTGTGAACCGGAGTCAAGCCAGGCTGCAAGTCTGCTTAAG 977
QY 979 TCACCTGAGTGGGATGCTGCTTTTGTAAAGCTCAAGTGTCAATTCATCCCTGATGGG 1038
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QY 1039 GGCATAGTTTGAAGCTGAGAGTGAAGTACGTTTTTCTTAAGGCTGAGGCGCAGTTCC 1098
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QY 1279 TTGAGAGAGTATGCGCGCGGAGCGGAGCAAGCAAGGCGCTGCAACAAGCGGCGCTGT 1338
DB 676 TTGAGAGAGTATGCGCGCGGAGCGGAGCAAGCAAGGCGCTGCAACAAGCGGCGCTGT 617
QY 1339 CGGTGTGTGATGCGCATGTTAAGCGGAGGCGCTTCTGTTGCTGCTGCGAGCACA 1398
DB 616 CGGTGTGTGATGCGCATGTTAAGCGGAGGCGCTTCTGTTGCTGCTGCGAGCACA 557
QY 1399 GGGGCGAGCAGACCTGCAACGCAACACCCCGGAAACTCTGCGAGGAGCAGCTGTACA 1458
DB 556 GGGGCGAGCAGACCTGCAACGCAACACCCCGGAAACTCTGCGAGGAGCAGCTGTACA 497
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DB 436 TGTACGCCCGGAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 377
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QY 1639 CACGAGCAGGAGGAG 1698
DB 316 CACGAGCAGGAGGAG 257
QY 1699 TAAACCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1758
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DB 196 TTTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACAAGAGAGAGATTAATTAACCTGT 137


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DB 196 TTTTTCAGTGTGGACTTGACAGCTTTCTTCCACAGCAAGAGATTTACACTGT 137
OY 1819 TTCAACCCGGGGAGTTGGCTGTGTTAAAGAACCATTAATGCTTTAGACAGTGA 1878
DB 136 TTCAACCCGGGGAGTTGGCTGTGTTAAAGAACCATTAATGCTTTAGACAGTGA 77

RESULT 27
US-09-950-083-1915/C
: Sequence 1915, Application US/09950083
: GENERAL INFORMATION:
: APPLICANT: Rosen, et. al
: TITLE OF INVENTION: Human Secreted Proteins
: FILE REFERENCE: PS805
: CURRENT APPLICATION NUMBER: US/09/950,083
: CURRENT FILING DATE: 2001-09-12
: PRIOR APPLICATION NUMBER: 60/278,650
: PRIOR FILING DATE: 2001-03-27
: PRIOR APPLICATION NUMBER: 09/833,245
: PRIOR FILING DATE: 2001-04-12
: PRIOR APPLICATION NUMBER: PCT/US01/11988
: PRIOR FILING DATE: 2001-04-12
: PRIOR APPLICATION NUMBER: PCT/US00/06043
: PRIOR FILING DATE: 2000-03-09
: PRIOR APPLICATION NUMBER: PCT/US00/06012
: PRIOR FILING DATE: 2000-03-09
: PRIOR APPLICATION NUMBER: PCT/US00/06058
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: PRIOR APPLICATION NUMBER: PCT/US00/06824
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PRIOR FILING DATE: 2000-06-01
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8 PRIOR FILING DATE: 2000-09-26
9 PRIOR APPLICATION NUMBER: PCT/US00/26337
10 PRIOR FILING DATE: 2000-09-26
11 PRIOR APPLICATION NUMBER: PCT/US01/13318
12 PRIOR FILING DATE: 2001-04-27
13 PRIOR APPLICATION NUMBER: US 60/124,146
14 PRIOR FILING DATE: 1999-03-12
15 PRIOR APPLICATION NUMBER: US 60/167,061
16 PRIOR FILING DATE: 1999-11-23
17 PRIOR APPLICATION NUMBER: US 60/124,093
18 PRIOR FILING DATE: 1999-03-12
19 PRIOR APPLICATION NUMBER: US 60/166,989
20 PRIOR FILING DATE: 1999-11-23
21 PRIOR APPLICATION NUMBER: US 60/124,145
22 PRIOR FILING DATE: 1999-03-12
23 PRIOR APPLICATION NUMBER: US 60/168,654
24 PRIOR FILING DATE: 1999-12-03
25 PRIOR APPLICATION NUMBER: US 60/124,099
26 PRIOR FILING DATE: 1999-03-12
27 PRIOR APPLICATION NUMBER: US 60/168,661
28 PRIOR FILING DATE: 1999-12-03
29 PRIOR APPLICATION NUMBER: US 60/124,096
30 PRIOR FILING DATE: 1999-03-12
31 PRIOR APPLICATION NUMBER: US 60/168,622
32 PRIOR FILING DATE: 1999-12-03
33 PRIOR APPLICATION NUMBER: US 60/124,143
34 PRIOR FILING DATE: 1999-03-12
35 PRIOR APPLICATION NUMBER: US 60/168,663
36 PRIOR FILING DATE: 1999-12-03
37 PRIOR APPLICATION NUMBER: US 60/124,095
38 PRIOR FILING DATE: 1999-03-12
39 PRIOR APPLICATION NUMBER: US 60/138,598
40 PRIOR FILING DATE: 1999-06-11
41 PRIOR APPLICATION NUMBER: US 60/168,665
42 PRIOR FILING DATE: 1999-12-03
43 PRIOR APPLICATION NUMBER: US 60/125,360
44 PRIOR FILING DATE: 1999-03-19
45 PRIOR APPLICATION NUMBER: US 60/138,626
46 PRIOR FILING DATE: 1999-06-11
47 PRIOR APPLICATION NUMBER: US 60/168,662
48 PRIOR FILING DATE: 1999-12-03
49 PRIOR APPLICATION NUMBER: US 60/124,144
50 PRIOR FILING DATE: 1999-03-12
51 PRIOR APPLICATION NUMBER: US 60/138,574
52 PRIOR FILING DATE: 1999-06-11
53 PRIOR APPLICATION NUMBER: US 60/168,667
54 PRIOR FILING DATE: 1999-12-03
55 PRIOR APPLICATION NUMBER: US 60/124,142
56 PRIOR FILING DATE: 1999-03-12
57 PRIOR APPLICATION NUMBER: US 60/138,597
58 PRIOR FILING DATE: 1999-06-11
59 PRIOR APPLICATION NUMBER: US 60/168,666
60 PRIOR FILING DATE: 1999-12-03
61 PRIOR APPLICATION NUMBER: US 60/125,359
62 PRIOR FILING DATE: 1999-03-19
63 PRIOR APPLICATION NUMBER: US 60/168,664
64 PRIOR FILING DATE: 1999-12-03
65 PRIOR APPLICATION NUMBER: US 60/126,051
66 PRIOR FILING DATE: 1999-03-23
67 PRIOR APPLICATION NUMBER: US 60/169,906

```

Query Match	Score	DB	Length
Best Local Similarity	99.8%	Pred. No. 1.9e-298	
Matches 1856; Conservative	0;	Mismatches 3;	Indels 1; Gaps 1

19 GGAGTCGAGCCCGGAGCGGAGAGAGAGAGAGCCCGGAGCGGAGAGCGG 78

Db	1935	GGTCTCTGGCGCCGGGAGGGCGAGCGGGAGGAGACAGACCCGCGAGCCGGGAGGCCGAGCG	1876
Qy	79	CGGGGCGATGAGGCTCTCCGGAGCGGACCTGGGGCTCTCTAACTACGACCGCTGCTTC	138
Db	1875	CGGGCGATGCGAGCTCCGGAGCGGACCGGACCTGGGGCTCTCTAACTACGACCGCTGCTTC	1816
Qy	139	CGGGGCGAGCGCCGGGAGCCCGAGAGCCCGGACCGACCGACCCGCTCACCGGGGACG	198
Db	1815	CGGGGCGAGCGCGGGGGCCCGAGAGCGTCGGGACCGACCGCTGACCGGGGACG	1756
Qy	199	CTCCGCTGCTGCGCTCCTCTGATGCGTTCCTCTCCGGGCCCCGGGACTCCGGAG	258
Db	1755	CTCCGCTGCTGCGCTCCTCTGATGCGTTCCTCTCCGGGCCCCGGGACTCCGGAG	1696
Qy	259	AATGTGGGTCTTGGGCGATCGCGCAACTTTTGGCGATTCTTGGCTTCAGGCTTTGC	318
Db	1695	AATGTGGGTCTTGGGCGATCGCGCAACTTTTGGCGATTCTTGGCTTCAGGCTTTGC	1636
Qy	319	GCTGCAATCCAGTGTACCACTGTGAGAAATTCAGCTGAACAACGACTGCTCTCC	378
Db	1635	GCTGCAATCCAGTGTACCACTGTGAGAAATTCAGCTGAACAACGACTGCTCTCC	1576
Qy	379	CGAGTTCATTTGTAATGACAGGCTGAAGCTTGAAGCATGTGTGAGAAAGATGATGA	438
Db	1575	CGAGTTCATTTGTAATGACAGGCTGAAGCTTGAAGCATGTGTGAGAAAGATGATGA	1516
Qy	439	GCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGC	498
Db	1515	GCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGC	1456
Qy	499	CTCTGCGGGGTACCATGTCCTTGTGCTCCCGAGGAAACGAACTGATTCATCAGCTG	558
Db	1455	CTCTGCGGGGTACCATGTCCTTGTGCTCCCGAGGAAACGAACTGATTCATCAGCTG	1396
Qy	559	CTGCAACACCCCTTTTGTATACGGGCGCAAGGCGCCAGAAAGGGGAATTCTGCTCGC	618
Db	1395	CTGCAACACCCCTTTTGTATACGGGCGCAAGGCGCCAGAAAGGGGAATTCTGCTCGC	1336
Qy	619	CCTCAGGCCAGGGCTCCGCGACACCATCTCTTTCTTCAAAATTAGCCCTTCTGGGACA	678
Db	1335	CCTCAGGCCAGGGCTCCGCGACACCATCTCTTTCTTCAAAATTAGCCCTTCTGGGACA	1277
Qy	679	CTGCGAAGCTGAAGGAGAGGCCACCCCTCTGCAATTTCTTCCAGCCCTCGGCCCA	738
Db	1276	CTGCGAAGCTGAAGGAGAGGCCACCCCTCTGCAATTTCTTCCAGCCCTCGGCCCA	1217
Qy	739	ACCCGCCACCTCCCTGAGTAGTTCCTTCTGGGTCTCTTTATTCTGGGTAGGAGCGG	798
Db	1216	ACCCGCCACCTCCCTGAGTAGTTCCTTCTGGGTCTCTTTATTCTGGGTAGGAGCGG	1157
Qy	799	GAGTCCGATTCCTTTTGTTCCTGCTCAATTAATGAAGAGCTCGTAAACATTCGA	858
Db	1156	GAGTCCGATTCCTTTTGTTCCTGCTCAATTAATGAAGAGCTCGTAAACATTCGA	1097
Qy	859	ATAAATTAGCTGACTGAATTTCACTATGTACTGGAAGGAAGAGGTGAGTGAAGT	918
Db	1096	ATAAATTAGCTGACTGAATTTCACTATGTACTGGAAGGAAGAGGTGAGTGAAGT	1037
Qy	919	TCACCCCATCTGTCTGTAAACCGAGTCAGGCGGAGGCGAGAGTGTCTTAGAG	978
Db	1036	TCACCCCATCTGTCTGTAAACCGAGTCAGGCGGAGGCGAGAGTGTCTTAGAG	977
Qy	979	TCACTAGAGTGGGCACTGCTTTTGAAGCCCTCAGTGTCCATTCCTGATGGG	1038
Db	976	TCACTAGAGTGGGCACTGCTTTTGAAGCCCTCAGTGTCCATTCCTGATGGG	917
Qy	1039	GGCATAGTTGAGACTGACAGAGTGAAGTACGTTTCTTAGGGCTGAGAGGCCAGTTC	1099
Db	916	GGCATAGTTGAGACTGACAGAGTGAAGTACGTTTCTTAGGGCTGAGAGGCCAGTTC	857
Qy	1099	CATCAGAGCTCCCGGCTGACATTAACATTATCTCTTAAACCATTTCTGTGAG	1156


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Db 916 GGCATAGTTGAGACTGCAGAGTAGAGTAGAGTTTCTTAGGGCTGAGGGCCAGTTCC 857
Qy 1099 CACTCAGAGCTCCCTCGCTTGACATTCATCAATCTCATGCTCTGAAAACCATCTCTCGAG 1158
Db 856 CACTCAGAGCTCCCTCGCTTGACATTCATCAATCTCATGCTCTGAAAACCATCTCTCGAG 797
Qy 1159 CAGAAATGGCTGGTTGCGGCTGAGTTGGGCTGAGTACGAGCTCATGACTGAGTGG 1218
Db 796 CAGAAATGGCTGGTTGCGGCTGAGTTGGGCTGAGTACGAGCTCATGACTGAGTGG 737
Qy 1219 ACTTACAGTGGGGCTCGGGCTGCTGAAAAGTCTTAAAGAAATCTTCTCAGTTTCC 1278
Db 736 ACTTACAGTGGGGCTCGGGCTGCTGAAAAGTCTTAAAGAAATCTTCTCAGTTTCC 677
Qy 1279 TTGCAAGAGACTGGGGCGGCGGAGAGAGAGCAAGGGGCGCTGCAGCAAAAGCGGCGCTGT 1338
Db 676 TTGCAAGAGACTGGGGCGGCGGAGAGAGAGCAAGGGGCGCTGCAGCAAAAGCGGCGCTGT 617
Qy 1339 CGGTGGTGGAGTGGCGATGTACGCGCAGGCGCTTCTCGTGGTTGGCGTGTGACAGCAGCA 1398
Db 616 CGGTGGTGGAGTGGCGATGTACGCGCAGGCGCTTCTCGTGGTTGGCGTGTGACAGCAGCA 557
Qy 1399 GCGCGAGCAGCAGCAGCTGCGAGCAACACCGCGGAACTGCTGCGAGAGACACCGTGTACA 1458
Db 556 GCGCGAGCAGCAGCAGCTGCGAGCAACACCGCGGAACTGCTGCGAGAGACACCGTGTACA 497
Qy 1459 GAGAGCGGCTGTATGACCCGAGCTGAGGTAGAAAAAGCTCTCCGAGAGAGGAGAGAGATCA 1518
Db 496 GAGAGCGGCTGTATGACCCGAGCTGAGGTAGAAAAAGCTCTCCGAGAGAGGAGAGAGATCA 437
Qy 1519 TGTACGCCCGGAAGTAGAGACTGTGTCAGATCGTGTGGTTGGCCGAGCCAGCATGATCC 1578
Db 436 TGTACGCCCGGAAGTAGAGACTGTGTCAGATCGTGTGGTTGGCCGAGCCAGCATGATCC 377
Qy 1579 TCCGAATCTGTTGGGCTGACAGCATAGCGCAATGTCAACAATTCAGCCCTGGGCGAGA 1638
Db 376 TCCGAATCTGTTGGGCTGACAGCATAGCGCAATGTCAACAATTCAGCCCTGGGCGAGA 317
Qy 1639 CACGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1698
Db 316 CACGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 257
Qy 1699 TAAACCATATAATATTATAGCCCTCTGTTCTGTGCTTACTGCGCAGGAATGTATCCAA 1758
Db 256 TAAACCATATAATATTATAGCCCTCTGTTCTGTGCTTACTGCGCAGGAATGTATCCAA 197
Qy 1759 TTTTTCAGTGTGAGCTTTCACAGCTTCTTTTGGCCACAGAGAGAGAGATTTAAACACTGT 1818
Db 196 TTTTTCAGTGTGAGCTTTCACAGCTTCTTTTGGCCACAGAGAGAGAGATTTAAACACTGT 137
Qy 1819 TTCAAACCCGGGAGTGTGCTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGA 1878
Db 136 TTCAAACCCGGGAGTGTGCTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGA 77

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RESULT 29
US-10-108-260A-197
Sequence 197, Application US/10108260A

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 197
LENGTH: 1832
TYPE: DNA
ORGANISM: Homo sapiens
US-10-108-260A-197

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Query Match      80.4%; Score 1526; DB 40; Length 1832;
Best Local Similarity 99.8%; Pred. No. 8e-287;
Matches 1676; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 199 CTCGGCTGCTGTGGCTCTCTGATGAGCTTGGCCCTCTCCCGGCGGAGACTCCGGAG 258
Db 154 CTCGGCTGCTGTGGCTCTCTGATGAGCTTGGCCCTCTCCCGGCGGAGACTCCGGAG 213
Qy 259 AATGTGGTCTGATGAGCTATCGCGCAACTTTTGGCGATTTGTTCTTCTTCAGAGCTTTCG 318
Db 214 AATGTGGTCTGATGAGCTATCGCGCAACTTTTGGCGATTTGTTCTTCTTCAGAGCTTTCG 273
Qy 319 GCTGCAATCCAGTGTACAGAGTGAAGATTCACAGTGAACAGAGCTCTCTCC 378
Db 274 GCTGCAATCCAGTGTACAGAGTGAAGATTCACAGTGAACAGAGCTCTCTCC 333
Qy 379 CAGATTTATGTGAATGTCAGAGTGAAGATTCACAGTGAAGATTCAGAGTGAAG 438
Db 334 CAGATTTATGTGAATGTCAGAGTGAAGATTCACAGTGAAGATTCAGAGTGAAG 393
Qy 439 GCAAGTGGCGGATCATGTATCCGCAAGTCTGTGATCATCAGAGGCGCTGTCTATCCG 498
Db 394 GCAAGTGGCGGATCATGTATCCGCAAGTCTGTGATCATCAGAGGCGCTGTCTATCCG 453
Qy 499 CTCTGCGGGGTACCAAGTCTTCTGCTCCCGAGGAACTGACACTGTTGATCAGCTG 558
Db 454 CTCTGCGGGGTACCAAGTCTTCTGCTCCCGAGGAACTGACACTGTTGATCAGCTG 513
Qy 559 CTGCAACACCCCTTTTGTATAGGGGCCAAGGCCCAAGAGAGAGAGAGAGAGAGAGAG 618
Db 514 CTGCAACACCCCTTTTGTATAGGGGCCAAGGCCCAAGAGAGAGAGAGAGAGAGAGAG 573
Qy 619 CCTCAGGCGAGGGCTCCGACACACATCTGTTCTGCAATTAAGCCCTCTTCTCGGACA 678
Db 574 CCTCAGGCGAGGGCTCCGACACACATCTGTTCTGCAATTAAGCCCTCTTCTCGGACA 633
Qy 679 CTGCTGAAGCTGAAGAGAGATCCACCCCTCTGATGATGTTCTTCCAGCCCTGCCCCA 738
Db 634 CTGCTGAAGCTGAAGAGAGATCCACCCCTCTGATGATGTTCTTCCAGCCCTGCCCCA 693
Qy 739 ACCGCCACCTCCCTGATGAGTGTCTTCTGAGGCTCTTATTTTGGGTAGGAGAGCGG 798
Db 694 ACCGCCACCTCCCTGATGAGTGTCTTCTGAGGCTCTTATTTTGGGTAGGAGAGCGG 753
Qy 799 GAGTCCGCTGCTCTTGTGCTGTCGCAATAATGAAGAGCTCGGTAAGCATCTGA 858
Db 754 GAGTCCGCTGCTCTTGTGCTGTCGCAATAATGAAGAGCTCGGTAAGCATCTGA 813
Qy 859 ATTAATTCAGCTGATGATGATTTTCAATGATGATGATGATGATGATGATGATGATGAT 918
Db 814 ATTAATTCAGCTGATGATGATTTTCAATGATGATGATGATGATGATGATGATGATGAT 873
Qy 919 TCACCCCATGCTGTGTGAACCGAGTCAAGGCGCAGAGCTGCAAGCTCTTATAG 978
Db 874 TCACCCCATGCTGTGTGAACCGAGTCAAGGCGCAGAGCTGCAAGCTCTTATAG 933
Qy 979 TCATGAGTGGGATCTGCTTTTGTAAAGCTTCAGATGATTCATTCATCCGTATGG 1038
Db 934 TCATGAGTGGGATCTGCTTTTGTAAAGCTTCAGATGATTCATTCATCCGTATGG 993
Qy 1039 GGCATAGTTTGAAGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1098
Db 994 GGCATAGTTTGAAGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1053
Qy 1099 CACTCAGAGCTCCCTCGCTTACATTCATTAATGCTCTGAAAACATCTCTCAG 1158
Db 1054 CACTCAGAGCTCCCTCGCTTACATTCATTAATGCTCTGAAAACATCTCTCAG 1113
Qy 1159 CAGAAATGGCTGGTTGCGGCTGAGTTGGGCTGTAGTGCAGACTCAATGACTGG 1218
Db 1114 CAGAAATGGCTGGTTGCGGCTGAGTTGGGCTGTAGTGCAGACTCAATGACTGG 1173
Qy 1219 ACTTACAGTGGGGCTCGGCTGCTGAAAAGTCTTAAAGAAATCTTCTCAGTTCTCC 1278

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Db 1174 ACTTAGACTGGGGCTCGGCTCGCTCTGAAAAAGTCTTAAGAAAAATCTTTCAGTTCTCC 1233
Oy 1279 TTGCGAGAGACGCGCGCGGGGACGCGAGACACACGCGCGCTGCACAAAGGGGCGCTGT 1338
Db 1234 TTGCGAGAGACGCGCGCGGGGACGCGAGACACACGCGCGCTGCACAAAGGGGCGCTGT 1293
Oy 1339 CGGTGGTGGAGTGCATGTACGCGCGACGCGCTTCTCGTGGTGGCGGTGCTGCAGCGACA 1398
Db 1294 CGGTGGTGGAGTGCATGTACGCGCGACGCGCTTCTCGTGGTGGCGGTGCTGCAGCGACA 1353
Oy 1399 GCGCGACACACACACCTGCACAGAAACACCGCGCAACTGCTGCAGAGACACCGTGTACA 1458
Db 1354 GCGCGACACACACACCTGCACAGAAACACCGCGCAACTGCTGCAGAGACACCGTGTACA 1413
Oy 1459 GGAGCGGGTGTGATGACGAGCTGAGAGTGAAGAAACGTCTCCGAGAAAGGGAGAGATCA 1518
Db 1414 GGAGCGGGTGTGATGACGAGCTGAGAGTGAAGAAACGTCTCCGAGAAAGGGAGAGATCA 1473
Oy 1519 TGTACGCCCGGAAAGTACGCTCGCTCAGTGTGCTTGGTGGCGCGACCGCATGATCC 1578
Db 1474 TGAACGCCCGGAAAGTACGCTCGCTCAGTGTGCTTGGTGGCGCGACCGCATGATCC 1533
Oy 1579 TCCGAAATGTGTTGGGCTTCCAGCATACGCCAATGTACAAACATCAGCCCTGGGAGA 1638
Db 1534 TCCGAAATGTGTTGGGCTTCCAGCATACGCCAATGTACAAACATCAGCCCTGGGAGA 1593
Oy 1639 CACGAGCGCGGAGAGACAGAGAGAAAGAAACACAGCATGAGAACACAGTAAATGAA 1698
Db 1594 CACGAGCGGAGAGAGAGACAGAGAGAAAGAAACACAGCATGAGAACACAGTAAATGAA 1653
Oy 1699 TAAACCATAAATATTTTATGACCCCTCTGTTCTGTGCTTACTGCGCAGAGAAATGTTACCA 1758
Db 1654 TAAACCATAAATATTTTATGACCCCTCTGTTCTGTGCTTACTGCGCAGAGAAATGTTACCA 1713
Oy 1759 TTTTCACTGTGAGCTTGTGACAGCTTCTTTCACACAGAGAGAGAAATTTAACACTGT 1818
Db 1714 TTTTCACTGTGAGCTTGTGACAGCTTCTTTCACACAGAGAGAGAAATTTAACACTGT 1773
Oy 1819 TTCAAAACCGGGGAGTGTGCTGTGTTAAAGAAACCATTAATGCTTTAGACAGTGT 1877
Db 1774 TTCAAAACCGGGGAGTGTGCTGTGTTAAAGAAACCATTAATGCTTTAGACAGTGT 1832

RESULT 30
US-09-526-994-1070/c
; Sequence 1070, Application US/09526994
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: 1600.1090-001
; CURRENT APPLICATION NUMBER: US/09/526,994
; EARLIER FILING DATE: 2000-03-15
; EARLIER APPLICATION NUMBER: 60/125,564
; EARLIER FILING DATE: 1999-03-22
; EARLIER APPLICATION NUMBER: 60/135,678
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1070
; LENGTH: 2535
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-526-994-1070

Query Match 79.5%: Score 1509: DB 19: Length 2535:
Best Local Similarity 99.9%: Pred. No. 1.4e-283:
Matches 1609: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

Oy 19 GGTGCTGGGCGCGGAGCGCGAGCGAGAGACCGCGAGCGCGGAGCGCGAGCG 78
Db 2503 GGTGCTGGGCGCGGAGCGCGAGCGAGAGACCGCGAGCGCGGAGCGCGAGCG 2444

Oy 79 CGGGCGATGACAGGCTCCGGGAGGCGACCTGCGGCTCTCTAAGCTACAGACGCTGCTC 138
Db 2443 CGGGCGATGACAGGCTCCGGGAGGCGACCTGCGGCTCTCTAAGCTACAGACGCTGCTC 2384
Oy 139 CGGCGACGAGCGGCGCGCCACGACGCTTGGGAGGCGACGCGCGCTGCAGCGCGGCGAGC 198
Db 2383 CGGCGACGAGCGGCGCGCCACGACGCTTGGGAGGCGACGCGCGCTGCAGCGCGGCGAGC 2324
Oy 199 CTCCGCTGTGTGCGCTCTCTGATGCGCTTGGCTTCCCGGCGCGGAGACTCCGGGAG 258
Db 2323 CTCCGCTGTGTGCGCTCTCTGATGCGCTTGGCTTCCCGGCGCGGAGACTCCGGGAG 2264
Oy 259 AATGTGGGCTCTAGAGCATGCGCGCACTTTTTCGCAATGTTTCTGCTTCAGGCTTGC 318
Db 2263 AATGTGGGCTCTAGAGCATGCGCGCACTTTTTCGCAATGTTTCTGCTTCAGGCTTGC 2204
Oy 319 GCTGCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGACACAGACGCTGCTCCGCC 378
Db 2203 GCTGCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGACACAGACGCTGCTCCGCC 2144
Oy 379 CGAGTTCATTTGTGAATTCACGCGTAAACGTTTCAAGACATGTGCAGAAAGAAAGTATGA 438
Db 2143 CGAGTTCATTTGTGAATTCACGCGTAAACGTTTCAAGACATGTGCAGAAAGAAAGTATGA 2084
Oy 439 GCAAGTGGCGGGATCATGTATACGCGCAAGCTGTGATATATCAGCGCGCTGTCTATCC 498
Db 2083 GCAAGTGGCGGGATCATGTATACGCGCAAGCTGTGATATATCAGCGCGCTGTCTATCC 2024
Oy 499 CTGCGCGGTACAGTCTCTTGTCTGCCAGGAGAACTGAATCAGTTTGCATCAGCTG 558
Db 2023 CTGCGCGGTACAGTCTCTTGTCTGCCAGGAGAACTGAATCAGTTTGCATCAGCTG 1964
Oy 559 CTGCAACACCCCTTTTGTATACGGGCCAAGGCCAAGAAAGGGAGATTCGCTCGGC 618
Db 1963 CTGCAACACCCCTTTTGTATACGGGCCAAGGCCAAGAAAGGGAGATTCGCTCGGC 1904
Oy 619 CCTCAGCGCGGCGCTCGCACACATCCGTTTCTCAATTAATGACCTCTGTCGGGACA 678
Db 1903 CCTCAGCGCGGCGCTCGCACACATCCGTTTCTCAATTAATGACCTCTGTCGGGACA 1844
Oy 679 CTGCTGAAGCTGAAGAGATGACACCCCTCTGCAATGTTTCTCCAGCCCTCGCCCCA 738
Db 1843 CTGCTGAAGCTGAAGAGATGACACCCCTCTGCAATGTTTCTCCAGCCCTCGCCCCA 1784
Oy 739 ACCGCCACCTCCCTAGAGAGTTCCTTCTGGGTGCTTTTATTTTGGGTAGGAGCGG 798
Db 1783 ACCGCCACCTCCCTAGAGAGTTCCTTCTGGGTGCTTTTATTTTGGGTAGGAGCGG 1724
Oy 799 GAGTCCGTGTTCTTTTGTCTGCTGCAAAATTAAGAAAGCTGGTAAAGCATTCGA 858
Db 1723 GAGTCCGTGTTCTTTTGTCTGCTGCAAAATTAAGAAAGCTGGTAAAGCATTCGA 1664
Oy 859 ATTAATTCAGCTGACTGAATTTTTCAGTATGTACTTGAAGAGAGAGTGAAGTGAAGT 918
Db 1663 ATTAATTCAGCTGACTGAATTTTTCAGTATGTACTTGAAGAGAGAGTGAAGTGAAGT 1604
Oy 919 TCACCCCATGCTGTGTACCGGAGTCAAGGCGAGGCGGAGAGTGTCTTCTTAGAG 978
Db 1603 TCACCCCATGCTGTGTACCGGAGTCAAGGCGAGGCGGAGAGTGTCTTCTTAGAG 1544
Oy 979 TCACGAGGTGGGATCTGCTTTTGTAAAGCTCCAGTGTCCATTCATCCCTGATGG 1038
Db 1543 TCACGAGGTGGGATCTGCTTTTGTAAAGCTCCAGTGTCCATTCATCCCTGATGG 1484
Oy 1039 GGCATAGTTTGAAGCTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1098
Db 1483 GGCATAGTTTGAAGCTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1424
Oy 1099 CACTCAAGGCTCCCTGCTTGAATTCAAATTCATGCTCGGAAACCATTCCTGCGAG 1158
Db 1423 CACTCAAGGCTCCCTGCTTGAATTCAAATTCATGCTCGGAAACCATTCCTGCGAG 1364

Qy	1340	GGTGGTGAAGACCAATGATACGGGCGAGGGCCCTCTGTGGTTGGGGTGGTGCAGGAGAC	13399
Db	1201	GGTGGTGAATGCGCATGTACGGCCAGGGCGCTTCTGTGTGGTGGCTGTGCAGGAGAC	12600
Qy	1400	GGCGACACACAGCACCTGTACGAACACCCGCGAATCTCTGCGAGGACACCCGTATAC	1459
Db	1261	GGCGACACACAGCACCTGTACGAACACCCGCGAATCTCTGCGAGGACACCCGTATAC	1320
Qy	1460	GAGCGGTTGATGACCCGAGCTGAGTAGAAAAACGTCTCCGAAGAGGGAGAGGATCAT	1519
Db	1321	GAGCGGTTGATGACCCGAGCTGAGTAGAAAAACGTCTCCGAAGAGGGAGAGGATCAT	1380
Qy	1520	GTAACGCCCCGAAAGTAGAGCACTGCTCCAGTGTGTCTGGTTTGGCCGACGCCATGATCT	1579
Db	1381	GTAACGCCCCGAAAGTAGAGCACTGCTCCAGTGTGTCTGGTTTGGCCGACGCCATGATCT	1440
Qy	1580	CCGAATCTGGTTGGGCATTCACAGATACGGCCAAATGTCAACAATACAGCCCTGGGACAC	1639
Db	1441	CCGAATCTGGTTGGGCATTCACAGATACGGCCAAATGTCAACAATACAGCCCTGGGACAC	1500
Qy	1640	ACGAGCAGAGGAGGAGACACGAGA	1663
Db	1501	ACGAGCAGAGGAGGAGACACGAGA	1524

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: RESULT 34
: US-10-216-162-15
: Sequence 15. Application US/10216162
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Deenoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: APPLICANT: Wood, William J.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIC
: FILE REFERENCE: P9530PIC2
: CURRENT APPLICATION NUMBER: US/10/216,162
: CURRENT FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: 10/119,480
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/079294
: PRIOR FILING DATE: 1998-03-25
: PRIOR APPLICATION NUMBER: 60/079656
: PRIOR FILING DATE: 1998-03-26
: PRIOR APPLICATION NUMBER: 60/079728
: PRIOR FILING DATE: 1998-03-27
: Remaining Prior Application data removed - See file Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 246
: SEQ ID NO 15
: LENGTH: 1524
: TYPE: DNA
: ORGANISM: Homo Sapien
: JS-10-216-162-15

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Query Match	75.0%;	Score 1422;	DB 42;	Length 1524;
Best Local Similarity	99.9%;	Pred. No. 1.2e-266;		
Matches 1522;	Conservative 0;	Mismatches 2;	Indels 0;	Caps 0;

OY	140	GCAGCAGACGCGCCGGCCCCAGCACGCCCTCGCGAGCCACAAGCCGTCAACCGGGGAGCC	199
Db	1	GCGGCAGCAGCGCGGGCCCCAGCACGCCCTCGCGAGCCACAAGCCGTCAACCGGGGAGCC	60
OY	200	TCCGCTGCTGTCGACCCTCTGATGCGCTTGGCCCTCTCCCGGCCCGCGGACTCCGGAGA	259
Db	61	TCCGCTGCTGTCGACCCTCTCTGATGCGCTTGCCCTCTCCCGGCCCGCGGACTCCGGAGA	120
OY	260	ATGTGGGTCTTAGCATTCGGGGCAACTTTTGGGGATTGTTCTTGCTTCAGGCTTTGGC	319
Db	121	ATGTGGGTCTTAGGCATTCGGGGCAACTTTTGGGGATTGTTCTTGCTTCAGGCTTTGGC	180
OY	320	CTGCAAAATCCAGTCTACCAAGTGAAGAATTCACCTGTAACAAGACATGTCCTCCCC	379
Db	181	CTGCAAAATCCAGTCTACCAAGTGAAGAATTCACCTGTAACAAGACATGTCCTCCCC	240
OY	380	GAGTTCATTTGAAATTGCACGGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAG	439
Db	241	GAGTTCATTTGAAATTGCACGGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAG	300
OY	440	CAAAGTCCGGGGATCATGTACCCAGTCTGTGTGATCATCAGCGGCTGTCTATCGCC	499
Db	301	CAAAGTCCGGGGATCATGTACCCAGTCTGTGTGATCATCAGCGGCTGTCTATCGCC	360
OY	500	TCTGCGGGGTACAGTCTCTTCTGCTGCCCGAGGAACTAACATCAGTTGATCAGTGC	559
Db	361	TCTGCGGGGTACAGTCTCTTCTGCTGCCCGAGGAACTAACATCAGTTGATCAGTGC	420
OY	560	TGCAACACACCTCTTTTGTAAAGGGCCACAGGCCACAGAAAAGGGAAATTCTGCTCGSCC	619
Db	421	TGCAACACACCTCTTTTGTAAAGGGCCACAGGCCACAGAAAAGGGAAATTCTGCTCGSCC	480
OY	620	CTCAGGCGAGGGCTCCGACACCACTTCCTCTCAAAATTAGCCCTCTCTCGGCAAC	679
Db	481	CTCAGGCGAGGGCTCCGACACCACTTCCTCTCAAAATTAGCCCTCTCTCGGCAAC	540
OY	680	TGCTGAAGCTGAAGAGATGCCAACCCCTCTGCAATTGTTCTTCAGCCCTGCCCCAA	739
Db	541	TGCTGAAGCTGAAGAGATGCCAACCCCTCTGCAATTGTTCTTCAGCCCTGCCCCAA	600
OY	740	CCCCCAACCTCCGAGTAGTTCCTTCGGGTGTCCTTTATTCGGGTAGGAGCGGG	799
Db	601	CCCCCAACCTCCGAGTAGTTCCTTCGGGTGTCCTTTATTCGGGTAGGAGCGGG	660
OY	800	AGTCCGTTCTCTTTTGTTCCTGCTCAATAATGAAGAAGTCGTAAGAAGATCTGAA	859
Db	661	AGTCCGTTCTCTTTTGTTCCTGCTCAATAATGAAGAAGTCGTAAGAAGATCTGAA	720
OY	860	TAAATTCAGCTGACGTAAATTTTCAGATGATCTTGAAAGGAAGAGGTGAGTGAAGTT	919
Db	721	TAAATTCAGCTGACGTAAATTTTCAGATGATCTTGAAAGGAAGAGGTGAGTGAAGTT	780
OY	920	CACCCCATGCTGTGTAAACCGGAGTCAAGGCCAGGCTGGCAGATCMGTCTTGAAGT	979
Db	781	CACCCCATGCTGTGTAAACCGGAGTCAAGGCCAGGCTGGCAGATCMGTCTTGAAGT	840
OY	980	CACGTAGGTGGGCATGCTCTTTTGTAAAGCCTCCAGTGTCCATTTCATCCCTGATGGG	1039
Db	841	CACGTAGGTGGGCATGCTCTCTTTTGTAAAGCCTCCAGTGTCCATTTCATCCCTGATGGG	900
OY	1040	GCATAGTTTGAAGTGCAGAGTGAAGTACGTTTTCTTAGGGCTGAAGGGCCAGTTCCC	1099
Db	901	GCATAGTTTGAAGTGCAGAGTGAAGTACGTTTTCTTAGGGCTGAAGGGCCAGTTCCC	960
OY	1100	ACTTAAGGCTCCCTCGGTTTACATTTCAAACTTCANCTCTCAAAAACATTTCTGACG	1159
Db	961	ACTTAAGGCTCCCTCGGTTTACATTTCAAACTTCANCTCTCTAAAAACATTTCTGACG	1020
OY	1160	AGAAATGGCTTGTTTGGCGCCTGAAGTTTGGGCTCTAAGTACTCGAGACTCAATGACTGGGA	1219

Db	841	CACATAGGTGGGCATCTGACCTTTTGTAAAGCCCTCAGTGGCATTCATCCCTGATGGGG	900
Qy	1040	GCATAGCTTTGAGACTGCGAGAGTGAAGATGACGTTTTCTTAAGGCTTGGAGGCCACTGCC	1099
Db	901	GCATAGTTTGAGACTGCGAGAGTGAAGATGACGTTTTCTTAAGGCTTGGAGGCCACTGCC	960
Qy	1100	ACTCAAGGCTCCCTCGGCTTACATTCAAATTCATCTCTCGTGAACCAATTCCTGCAGC	1159
Db	961	ACTCAAGGCTCCCTCGGCTTACATTCAAATTCATCTCTCGTGAACCAATTCCTGCAGC	1020
Qy	1160	AGAAATGGCTGTTTCCGCGCTGAGTTGGGCTCTAATGACTGAGACTCAATGACTGGGA	1219
Db	1021	AGAAATGGCTGTTTCCGCGCTGAGTTGGGCTCTAATGACTGAGACTCAATGACTGGGA	1080
Qy	1220	CTTAGACAGCGGGGCTCGGCTCGGCTCGGCTTAAGAAATCTTCTGACTCTCTCT	1279
Db	1081	CTTAGACAGCGGGGCTCGGCTCGGCTCGGCTTAAGAAATCTTCTGACTCTCTCTCT	1140
Qy	1280	TGCAGAGACTGCGCGCCGGAGCGCGAAGACACGCGGCGCTGCACAAAGCGGCGCTGTC	1339
Db	1141	TGCAGAGACTGCGCGCCGGAGCGCGAAGACACGCGGCGCTGCACAAAGCGGCGCTGTC	1200
Qy	1340	GCTGATGAGAGCGGCATGTCAGGGGAGCGGCTTCTGCTGTTGGGCTGTGCAGCGACAG	1399
Db	1201	GCTGATGAGAGCGGCATGTCAGGGGAGCGGCTTCTGCTGTTGGGCTGTGCAGCGACAG	1260
Qy	1400	GCAGCAGACACAGCACCTGTCAGCAACACCCGCGCAAACTGCTCGAGAGACACCGTATAC	1459
Db	1261	GCAGCAGACACAGCACCTGTCAGCAACACCCGCGCAAACTGCTCGAGAGACACCGTATAC	1320
Qy	1460	GAGGGGGTTGATGACCGAGCTGAGGTAGAAAAACGTTCTCCGAAAGGGAGGAGGATCAT	1519
Db	1321	GAGGGGGTTGATGACCGAGCTGAGGTAGAAAAACGTTCTCCGAAAGGGAGGAGGATCAT	1380
Qy	1520	GTACGCCCGGAGTAGAGCACTCGTCCAGTCTGCTGCTGGGTTTGGCGCGGAGCCATGATCT	1579
Db	1381	GTACGCCCGGAGTAGAGCACTCGTCCAGTCTGCTGCTGGGTTTGGCGCGGAGCCATGATCT	1440
Qy	1580	CCGAATCTGTTGGGCAATCCAGCATACGGCCAAATGTCACAAACATCAGCCCTGGGCGAC	1639
Db	1441	CCGAATCTGTTGGGCAATCCAGCATACGGCCAAATGTCACAAACATCAGCCCTGGGCGAC	1500
Qy	1640	ACGAGCAGAGGGAGGAGACAGAGA	1663
Db	1501	ACGAGCAGAGGGAGGAGACAGAGA	1524
RESULT 36			
US-10-216-164-15			
: Sequence 15, Application US/10216164			
: GENERAL INFORMATION:			
: APPLICANT: Baker, Kevin P.			
: APPLICANT: Desnoyers, Luc			
: APPLICANT: Gerritsen, Mary			
: APPLICANT: Goddard, Audrey			
: APPLICANT: Godowski, Paul J.			
: APPLICANT: Grimaldi, J. Christopher			
: APPLICANT: Gurney, Austin L.			
: APPLICANT: Smith, Victoria			
: APPLICANT: Stephan, Jean-Philippe F.			
: APPLICANT: Watanabe, Colin L.			
: APPLICANT: Wood, William I.			
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
: FILE OF INVENTION: ACIDS ENCODING THE SAME			
: FILE REFERENCE: P3530P1C5			
: CURRENT APPLICATION NUMBER: US/10/216.164			
: CURRENT FILING DATE: 2002-08-09			
: PRIOR APPLICATION NUMBER: 10/119.480			
: PRIOR FILING DATE: 2002-04-09			
: PRIOR APPLICATION NUMBER: 60/059113			
: PRIOR FILING DATE: 1997-09-17			
: PRIOR APPLICATION NUMBER: 60/062287			
: PRIOR FILING DATE: 1997-10-17			

?	PRIOR APPLICATION NUMBER: 60/063549	?
?	PRIOR FILING DATE: 1997-10-28	?
?	PRIOR APPLICATION NUMBER: 60/064103	?
?	PRIOR FILING DATE: 1997-10-31	?
?	PRIOR APPLICATION NUMBER: 60/069873	?
?	PRIOR FILING DATE: 1997-12-17	?
?	PRIOR APPLICATION NUMBER: 60/078910	?
?	PRIOR FILING DATE: 1998-03-20	?
?	PRIOR APPLICATION NUMBER: 60/079294	?
?	PRIOR FILING DATE: 1998-03-25	?
?	PRIOR APPLICATION NUMBER: 60/079656	?
?	PRIOR FILING DATE: 1998-03-26	?
?	PRIOR APPLICATION NUMBER: 60/079728	?
?	PRIOR FILING DATE: 1998-03-27	?
?	Remaining Prior Application data removed - See file Wrapper or PALM.	?
?	NUMBER OF SEQ ID NOS: 246	?
?	SEQ ID NO: 15	?
?	LENGTH: 1524	?
?	TYPE: DNA	?
?	ORGANISM: Homo Sapien	?
?	US-10-216-164-15	?
Query Match	75.0%: Score 1422; DB 42; Length 1524;	
Best Local Similarity	99.9%: Pred. No. 1.2e+26;	
Matches 1522; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
QY	140 GCGGACAGCAGCGGGGGCCCCCAGCAGCCCTCGCGAGCCACAGCGCTGACAGCGGGGACGCC	199
Db	1 GCGGACAGCAGCGGGGGCCCCCAGCAGCCCTCGCGAGCCACAGCGCGCTGACAGCGGGGACGCC	60
QY	200 TCCGCTGCTGTGCGCTCTCTGTATGCGCTTGGCCCTCTCCGGCCCCGGGACTCGGGAGA	259
Db	61 TCCGCTGCTGTGCGCTCTCTGTATGCGCTTGGCCCTCTCCGGCCCCGGGACTCGGGAGA	120
QY	260 ATGTGGTCTTATGGCATGCGCGCAACTTTTTCGGGATTTGTTGCTTCCTTCAGACTTTGGC	319
Db	121 ATGTGGTCTTATGGCATGCGCGCAACTTTTTCGGGATTTGTTGCTTCCTTCAGACTTTGGC	180
QY	320 CTGCAATTCAGTGTACCAAGTGTGAAGAATTCAGCTGAACAGACTGCTCTCCGCC	379
Db	181 CTGCAATTCAGTGTGTACCAAGTGTGAAGAATTCAGCTGAACAGACTGCTCTCCGCC	240
QY	380 GAGTTCATTGTGAATTTGACAGCGGTGAACCTTCAAGACATGTGTCAAAAAGAAATGATGGAG	439
Db	241 GAGTTCATTGTGAATTTGACAGCGGTGAACCTTCAAGACATGTGTCAAAAAGAAATGATGGAG	300
QY	440 CAAAGTGGCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTATCGCC	499
Db	301 CAAAGTGGCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTATCGCC	360
QY	500 TCTGGCGGGTACCAATCCTTCTGTCTCTCCAGGGAACTGAATCAAGTTGCATCAGCTGTC	559
Db	361 TCTGGCGGGTACCAATCCTTCTGTCTCTCCAGGGAACTGAATCAAGTTGCATCAGCTGTC	420
QY	560 TGCACACACCCCTCTTTTGAACGGGCGCAAGGCCCAAGAAAAGGGGAAGTTTGTGCCCGGCC	619
Db	421 TGCACACACCCCTCTTTTGAACGGGCGCAAGGCCCAAGAAAAGGGGAAGTTTGTGCCCGGCC	480
QY	620 CTGACGGCCAGGGGCTCGCAGCACCAATCTCTGTTCCTCAAAATTAAGCCCTCTTCGGCACAC	679
Db	481 CTGACGGCCAGGGGCTCGCAGCACCAATCTCTGTTCCTCAAAATTAAGCCCTCTTCGGCACAC	540
QY	680 TGTGTAACCTTAAGAGATGTGCACCCCTCTCGATGTCTTCACAGCCCTTCGCCCCAA	739
Db	541 TGTGTAACCTTAAGAGATGTGCACCCCTCTCGATGTCTTCACAGCCCTTCGCCCCAA	600
QY	740 CCCCCACACCTCCAGATGAGTTCTTCTGGGTGTCTTTTATTTCTGGGTAGGAGCGGG	799
Db	601 CCCCCACACCTCCAGATGAGTTCTTCTGGGTGTCTTTTATTTCTGGGTAGGAGCGGG	660
QY	800 AGTCGCGTTCTCTTTTGTCTCTGTGCAAAATTAAGAAAGACCTGGTAAACATTTCTGAA	859
Db	661 AGTCGCGTTCTCTTTTGTCTCTGTGCAAAATTAAGAAAGACCTGGTAAACATTTCTGAA	720


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QY 680 TCGTGAAGCTGAAGAGATGCCACCCCTCTGTCATGTTCTTCCAGCCCTGCCCCCAA 739
    |||
Db 541 TCGTGAAGCTGAAGAGATGCCACCCCTCTGTCATGTTCTTCCAGCCCTGCCCCCAA 600
QY 740 CCCCCACCTCCCTGAGTGAAGTTCTTCTGGGTCCTTTTATTCGGGTAGGAGCGGG 799
    |||
Db 601 CCCCCACCTCCCTGAGTGAAGTTCTTCTGGGTCCTTTTATTCGGGTAGGAGCGGG 660
QY 800 AGTCCGTGTTCTTCTTGTTCCTGTCATAATATGAAGAGCCGGTAAAGCATTCGTGA 859
    |||
Db 661 AGTCCGTGTTCTTCTTGTTCCTGTCATAATATGAAGAGCCGGTAAAGCATTCGTGA 720
QY 860 TAAATTCAGCTGACTGAATTTTCACTATGTAAGAGAGAGAGTGAAGTT 919
    |||
Db 721 TAAATTCAGCTGACTGAATTTTCACTATGTAAGAGAGAGTGAAGTT 780
QY 920 CACCCCATGTCGTGTAACCCGAGTCAAGGCCAGGCTGGCAGAGTCMCTCTTAGAAT 979
    |||
Db 781 CACCCCATGTCGTGTAACCCGAGTCAAGGCCAGGCTGGCAGAGTCMCTCTTAGAAT 840
QY 980 CACTGAGGTGGCATCTGCCCTTTTAAAGCCCTCAGTGTCCATTCATCCCTGATGGG 1039
    |||
Db 841 CACTGAGGTGGCATCTGCCCTTTTAAAGCCCTCAGTGTCCATTCATCCCTGATGGG 900
QY 1040 GCATAGTTGAGACTGCACAGTGAAGTACGTTTCTTAGGGCTGAGGGCAGTTCC 1099
    |||
Db 901 GCATAGTTGAGACTGCACAGTGAAGTACGTTTCTTAGGGCTGAGGGCAGTTCC 960
QY 1100 ACTCAAGGCTCCCTGCTTGATTAACCTTCATCCTCTTCAAAAACCTTCTCTGCAC 1159
    |||
Db 961 ACTCAAGGCTCCCTGCTTGATTAACCTTCATCCTCTTCAAAAACCTTCTCTGCAC 1020
QY 1160 AGAATTTGCTGTTTGCCTCTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGA 1219
    |||
Db 1021 AGAATTTGCTGTTTGCCTCTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGA 1080
QY 1220 CTTAGCTGAGGCTGAGGCTCTGCTCTGAAAAAGTCTTAAAGAAATCTTCTCAGTTCT 1279
    |||
Db 1081 CTTAGCTGAGGCTGAGGCTCTGCTCTGAAAAAGTCTTAAAGAAATCTTCTCAGTTCT 1140
QY 1280 TGCAGAGGACTGCGCGCGGAGCGGAGCAACGGGCGCTGCACAAAGCGGCGCTGTC 1339
    |||
Db 1141 TGCAGAGGACTGCGCGCGGAGCGGAGCAACGGGCGCTGCACAAAGCGGCGCTGTC 1200
QY 1340 GGTGTGAGTGCAGATGTACGCGGAGGCGCTTCTGTTGGGTGCTGAGGAGCAG 1399
    |||
Db 1201 GGTGTGAGTGCAGATGTACGCGGAGGCGCTTCTGTTGGGTGCTGAGGAGCAG 1260
QY 1400 GGGGAGGACACACCTGTCAGCAACCCCGGAAATGCTGCGAGGACACCGGTACAG 1459
    |||
Db 1261 GGGGAGGACACACCTGTCAGCAACCCCGGAAATGCTGCGAGGACACCGGTACAG 1320
QY 1460 GAGCGGTTGATGACGAGCTGAGGTAGAAAAAGCTCTCCGGAAGGGAGAGATCAT 1519
    |||
Db 1321 GAGCGGTTGATGACGAGCTGAGGTAGAAAAAGCTCTCCGGAAGGGAGAGATCAT 1380
QY 1520 GTTACGCGCGGAGTAAGGACCTGTCAGTCTGTTGGTTTGGCGGAGCCATGATCT 1579
    |||
Db 1381 GTTACGCGCGGAGTAAGGACCTGTCAGTCTGTTGGTTTGGCGGAGCCATGATCT 1440
QY 1580 CCGAATTCGTTGGGCTTCACACATACGCGCAATGTCACACAAATCAGCCCTGGGAGAC 1639
    |||
Db 1441 CCGAATTCGTTGGGCTTCACACATACGCGCAATGTCACACAAATCAGCCCTGGGAGAC 1500
QY 1640 ACGAGCAGGAGGAGAGACAGAGA 1663
    |||
Db 1501 ACGAGCAGGAGGAGAGACAGAGA 1524

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RESULT 38
 US-10-216-166-15
 ; Sequence 15, Application us/10216166
 ; GENERAL INFORMATION:

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C9
; CURRENT APPLICATION NUMBER: US/10/216,166
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; REMAINING PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-216-166-15

Query Match 75.0%; Score 1422; DB 42; Length 1524;
Best Local Similarity 99.9%; Pred. No. 1,2e-266;
Matches 1522; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 140 GCGGAGCAGCGCGGCGCCAGCAGCCTCGGACAGCCAGAGCGGCTGCGAGCGGGAGCC 199
    |||
Db 1 GCGGAGCAGCGCGGCGCCAGCAGCCTCGGACAGCCAGAGCGGCTGCGAGCGGGAGCC 60
QY 200 TCCGCTGCTGCTCCTCTGATGCGCTTGCCCTGCCGGGCCCGGAGCTCGGGAGA 259
    |||
Db 61 TCCGCTGCTGCTCCTCTGATGCGCTTGCCCTGCCGGGCCCGGAGCTCGGGAGA 120
QY 260 ATGTGGGTCCTAGGATCGGGGCAACTTTTGGCGATTTGCTTCTGCTTCCAGGCTTGGC 319
    |||
Db 121 ATGTGGGTCCTAGGATCGGGGCAACTTTTGGCGATTTGCTTCTGCTTCCAGGCTTGGC 180
QY 320 CTGCAATTCAGTCTACAGTGTGAAGAAATTCAGCTGAACAAGCAAGCACTCTCTCCCC 379
    |||
Db 181 CTGCAATTCAGTCTACAGTGTGAAGAAATTCAGCTGAACAAGCAAGCACTCTCTCCCC 240
QY 380 GAGTTCAATTTGAATTTGACGCGTGAACGTTCAAGACATGTGTGAGAAAAGATGATGAG 439
    |||
Db 241 GAGTTCAATTTGAATTTGACGCGTGAACGTTCAAGACATGTGTGAGAAAAGATGATGAG 300
QY 440 CAAAGTGGGGATCATGTACCGCAAGTCTGTGTCATCATCAGAGGCGCTCTCATCGCC 499
    |||
Db 301 CAAAGTGGGGATCATGTACCGCAAGTCTGTGTCATCATCAGAGGCGCTCTCATCGCC 360
QY 500 TCTGCGGATACAGTCTTCTGCTCCCGAGGGAACTGAATCAATGTTGATCAGCTGC 559

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|||||
Db 361 TCTGCCGGTACCACTCTTCTCTCTCCAGGAACTGAATCGATTGCATCAGCTGC 420
|||
Qy 560 TCGAACACCCCTCTTGTAAAGGGCCAAAGGCCAAAGAAAGGAGTTCTGCTCGGCC 619
|||
Db 421 TCGAACACCCCTCTTGTAAAGGGCCAAAGGCCAAAGAAAGGAGTTCTGCTCGGCC 480
|||
Qy 620 CTCAGGCCAGGGCTCCGACACCATCTCTTCTCAATTAAGCCCTTCTGCGACAC 679
|||
Db 481 CTCAGGCCAGGGCTCCGACACCATCTCTTCTCAATTAAGCCCTTCTGCGACAC 540
|||
Qy 680 TCTGAGCTGAAGAGATGCCACCCCTCTGATGTTCTTCCAGCCCTCGCCCAA 739
|||
Db 541 TCTGAGCTGAAGAGATGCCACCCCTCTGATGTTCTTCCAGCCCTCGCCCAA 600
|||
Qy 740 CCCCCACCTCCCTGAGTGAAGTTCTTCTGCTCTTCTTCTTCTGAGGAGCGGG 799
|||
Db 601 CCCCCACCTCCCTGAGTGAAGTTCTTCTGCTCTTCTTCTTCTGAGGAGCGGG 660
|||
Qy 800 ACTCGCTCTCTTCTTCTGCTGCAATTAAGAGAGCTCGGTAAGCATCTGAA 859
|||
Db 661 ACTCGCTCTCTTCTTCTGCTGCAATTAAGAGAGCTCGGTAAGCATCTGAA 720
|||
Qy 860 TAAATTCACCTGATGAATTTTCTGATATGATCTGAAGAGAGAGTGAAGT 919
|||
Db 721 TAAATTCACCTGATGAATTTTCTGATATGATCTGAAGAGAGAGTGAAGT 780
|||
Qy 920 CACCCCATCTCTGTGTAAAGCGGAGTCAAGCCAGGCTGCGAGTCTGCTTAAGAGT 979
|||
Db 781 CACCCCATCTCTGTGTAAAGCGGAGTCAAGCCAGGCTGCGAGTCTGCTTAAGAGT 840
|||
Qy 980 CACTGAGGGGAGTCTGCTTCTTCTTCTGAAAGCTCTGATCTCATTCCTGATGAGG 1039
|||
Db 841 CACTGAGGGGAGTCTGCTTCTTCTTCTGAAAGCTCTGATCTCATTCCTGATGAGG 900
|||
Qy 1040 GCATGATTTGAGACTGACAGAGTGAAGTGAAGTCTTCTTCTGAGGCTGAGGCGCAATTC 1099
|||
Db 901 GCATGATTTGAGACTGACAGAGTGAAGTGAAGTCTTCTTCTGAGGCTGAGGCGCAATTC 960
|||
Qy 1100 ACTCAAGGCTCCCTGCTGTTGATCAATTCATGCTCTCTGAAAGAACATTTCTGACGC 1159
|||
Db 961 ACTCAAGGCTCCCTGCTGTTGATCAATTCATGCTCTCTGAAAGAACATTTCTGACGC 1020
|||
Qy 1160 AGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1219
|||
Db 1021 AGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
|||
Qy 1220 CTTAGACTGGGCTGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1279
|||
Db 1081 CTTAGACTGGGCTGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
|||
Qy 1280 TGCAGAGAGCTGGGCTGCGGAGCGGAGGAGCAAGGAGGCTGCTGCTGCTGCTGCTGCTGCT 1339
|||
Db 1141 TGCAGAGAGCTGGGCTGCGGAGCGGAGGAGCAAGGAGGCTGCTGCTGCTGCTGCTGCTGCT 1200
|||
Qy 1340 GGTGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1399
|||
Db 1201 GGTGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
|||
Qy 1400 GCGGAGCAGACACCTGACAGACACCCGCGAAACTGCTGCGAGGACACCGTGTACAG 1459
|||
Db 1261 GCGGAGCAGACACCTGACAGACACCCGCGAAACTGCTGCGAGGACACCGTGTACAG 1320
|||
Qy 1460 GAGCGGTTGATGATGACGAGCTAGGTAGAAAACGTTCTCCGAGAGGAGAGATCAT 1519
|||
Db 1321 GAGCGGTTGATGATGACGAGCTAGGTAGAAAACGTTCTCCGAGAGGAGAGATCAT 1380
|||
Qy 1520 GTACGCGCCGGAAGTGAAGACCTGCTCAGTCTGCTTGGTTGGCGGAGCATATCTCT 1579
|||
Db 1381 GTACGCGCCGGAAGTGAAGACCTGCTCAGTCTGCTTGGTTGGCGGAGCATATCTCT 1440
|||
Qy 1580 CCGAATCTGTGGGATCAGCATACGCGCAATGTCAACAAATCAGCCCTGCGGAGAC 1639
|||

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Db 1441 CCGAATCTGTGGTGGCATCCAGCATAGCGCCAAATGTCAACAATCAGCCCTGGGAGAC 1500
Qy 1640 ACGAGCAGAGGAGGAGACAGAGA 1663
|||
Db 1501 ACGAGCAGAGGAGGAGACAGAGA 1524
|||
RESULT 39
US-10-216-167-15
; Sequence 15, Application US/10216167
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C4
; CURRENT APPLICATION NUMBER: US/10/216,167
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-167-15
Query Match 75.0%; Score 1422; DB 42; Length 1524;
Best Local Similarity 99.9%; Pred. No. 1,2e-266;
Matches 1522; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 140 GCGGAGCAGAGCGGGGCCCGACAGAGCTGAGGACACAGCCGCTGACGCGGGGAGCC 199
|||
Db 1 GCGGAGCAGAGCGGGGCCCGACAGAGCTGAGGACACAGCCGCTGACGCGGGGAGCC 60
|||
Qy 200 TCCGCTCTGTGCGCTCTCTGATGCGCTTCCCTTCCGCGGCGCGGGGAGTCCGAGAGA 259
|||
Db 61 TCCGCTCTGTGCGCTCTCTGATGCGCTTCCCTTCCGCGGCGCGGGGAGTCCGAGAGA 120
|||
Qy 260 ATGAGGCTCTAGCAGTACGCGGCAACTTTTGGGATTTCTTCTGCTTCCAGGCTTTGCG 319
|||
Db 121 ATGAGGCTCTAGCAGTACGCGGCAACTTTTGGGATTTCTTCTGCTTCCAGGCTTTGCG 180
|||
Qy 320 CTGCAATCTGCTCTACCACTGTGAAGAAATTCAGCTGAACAAGACGCTCTCCGCC 379
|||

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Db 181 CTGCAATTCAGTCTACCAAGTGTGAAGATTCCAGCTGAACAGACAGCTGCTCCCCC 240
Qy 380 GAGTTCATTGTGAATTGACAGGTGAACGTTTCAAGACATGTGTGAGAAAGATGATGAG 439
Db 241 GAGTTCATTGTGAATTGACAGGTGAACGTTTCAAGACATGTGTGAGAAAGATGATGAG 300
Qy 440 CAAAGTCCGGGATTCATGTACCCGAAGTCTGTGCAATCAGCGGCTGTCTCATGCGC 499
Db 301 CAAAGTCCGGGATTCATGTACCCGAAGTCTGTGCAATCAGCGGCTGTCTCATGCGC 360
Qy 500 TCTGCGGGGATTCAGTCTGTCTCCCGGAGAACTGAACCTGATTGCAATCAGCTGCG 559
Db 361 TCTGCGGGGATTCAGTCTGTCTCCCGGAGAACTGAACCTGATTGCAATCAGCTGCG 420
Qy 560 TGCAGACCCCTCTTGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 619
Db 421 TGCAGACCCCTCTTGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Qy 620 CTGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 679
Db 481 CTGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Qy 680 TGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 739
Db 541 TGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Qy 740 CCCCCACCTCCCTGAGTGTCTTCTGAGTGTCTTCTTATCTGAGGAGGAGGAGGAG 799
Db 601 CCCCCACCTCCCTGAGTGTCTTCTGAGTGTCTTCTTATCTGAGGAGGAGGAGGAG 660
Qy 800 AGTCCGATCT 859
Db 661 AGTCCGATCT 720
Qy 860 TAAATTCAGCTGAGTGAATTTTCAATGATGATGATGATGATGATGATGATGATGAT 919
Db 721 TAAATTCAGCTGAGTGAATTTTCAATGATGATGATGATGATGATGATGATGATGAT 780
Qy 920 CACCCCATGCTGTGTAAACGGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 979
Db 781 CACCCCATGCTGTGTAAACGGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Qy 980 CACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1039
Db 841 CACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Qy 1040 GCATAGTTGAGAGCTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1099
Db 901 GCATAGTTGAGAGCTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 960
Qy 1100 ACTCAAGGCTCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1159
Db 961 ACTCAAGGCTCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1020
Qy 1160 AGAATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1219
Db 1021 AGAATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1080
Qy 1220 CTGAGAGTGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1279
Db 1081 CTGAGAGTGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1140
Qy 1280 TGCAGAGAGTGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1339
Db 1141 TGCAGAGAGTGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1200
Qy 1340 GGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1399
Db 1201 GGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1260
Qy 1400 GGGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1459
Db 1261 GGGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1320

Qy 1460 GAGCGGTTGATGACGAGCTGAGTGAAGAAACGCTCCGAGAGGAGGAGGATCAT 1519
Db 1321 GAGCGGTTGATGACGAGCTGAGTGAAGAAACGCTCCGAGAGGAGGAGGATCAT 1380
Qy 1520 GTAGCCCCGGAAGTAGAAGCTGTCAGTGTGCTTGGGTTGGCCGAGCATGATCT 1579
Db 1381 GTAGCCCCGGAAGTAGAAGCTGTCAGTGTGCTTGGGTTGGCCGAGCATGATCT 1440
Qy 1580 CGAATCTGTGGGATTCAGCATACGCGCAATGTCAACAATCAGCCTGGGAGAC 1639
Db 1441 CGAATCTGTGGGATTCAGCATACGCGCAATGTCAACAATCAGCCTGGGAGAC 1500
Qy 1640 ACGAGAGGAGGAG 1663
Db 1501 ACGAGAGGAGGAG 1524

RESULT 40
US-10-216-168-15
Sequence 15, Application US/10216168
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C10
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 15
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo Sapien
US-10-216-168-15

Query Match 75.0% Score 1422; DB 42; Length 1524;
Best Local Similarity 99.9% Pred. No. 1.2e-266;
Matches 1522; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 140 GGGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 199
Db 1 GGGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 60

OY	200	TCGCCTGCTGCGGCTCCCTGTATGCGGTTGGCCCTCCCGGCCCGCGGAGCTCCGGAGA	259
Db	61	TCGCCTGCTGCGGCTCCCTGTATGCGGTTGGCCCTCCCGGCCCGCGGAGCTCCGGAGA	120
OY	260	ATGTGGGTCCTAGGCATCGCGGCAACTTTTGTGGGATTTGTCCTTCCAGGCTTTGGC	319
Db	121	ATGTGGGTCCTAGGCATCGCGGCAACTTTTGTGGGATTTGTCCTTCCAGGCTTTGGC	180
OY	320	CTGAATTCAGAGCTCTACAGTGTGAAAGATTCCAGCTGAACAAGACGTGCTCCCTCCC	379
Db	181	CTGAATTCAGAGCTCTACAGTGTGAAAGATTCCAGCTGAACAAGACGTGCTCCCTCCC	240
OY	380	GAGTTCATTGTGAATTGACAGCGTGAACGTTTCAAGACATGTCTCAGAAAGAAAGTGTAG	439
Db	241	GAGTTCATTGTGAATTGACAGCGTGAACGTTTCAAGACATGTCTCAGAAAGAAAGTGTAG	300
OY	440	CAAAAGTGGCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTATCGCC	499
Db	301	CAAAAGTGGCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTATCGCC	360
OY	500	TCCTGCGGGGTACGAGTCTTCTGTGCCCCAGGGAAACTGAACTCAGTTGGATCAGCTGC	559
Db	361	TCCTGCGGGGTACGAGTCTTCTGTGCCCCAGGGAAACTGAACTCAGTTGGATCAGCTGC	420
OY	560	TGCAACAACCCCTCTTTGTAAACGGGCCCCAGAGCCCAAGAAAAGGGGAAGTTCTGCCTGCGC	619
Db	421	TGCAACAACCCCTCTTTGTAAACGGGCCCCAGAGCCCAAGAAAAGGGGAAGTTCTGCCTGCGC	480
OY	620	CTCAGGCGCAGGGGCTCGGCACACACATCCGTTCCCTAAATTAGCCCTCTCTCGGCGACAC	679
Db	481	CTCAGGCGCAGGGGCTCGGCACACACATCCGTTCCCTAAATTAGCCCTCTCTCGGCGACAC	540
OY	680	TGCTGAAGCTGAAGAGATGCCAACCCCTCTGTCATTGTTCTTCCAGCCCTGCCCCCAA	739
Db	541	TGCTGAAGCTGAAGAGATGCCAACCCCTCTGTCATTGTTCTTCCAGCCCTGCCCCCAA	600
OY	740	CCCCCACCCCTCCGAGTGAATTTCTTCGCGGTCCCTTATTCGGGTAGGAGCGGG	799
Db	601	CCCCCACCCCTCCGAGTGAATTTCTTCGCGGTCCCTTATTCGGGTAGGAGCGGG	660
OY	800	AGTCGTGTTCTCTTTTGTTCCTGCTGCAATAATATGAAGAGCTCGGTAAAGCATCTGAA	859
Db	661	AGTCGTGTTCTCTTTTGTTCCTGCTGCAATAATATGAAGAGCTCGGTAAAGCATCTGAA	720
OY	860	TAAATTACGCTGACTGAATTTTCAGTATGTACTTAAGAGAGAGGTGAGTGAAGTT	919
Db	721	TAAATTACGCTGACTGAATTTTCAGTATGTACTTAAGAGAGAGGTGAGTGAAGTT	780
OY	920	CACCCCATGTCTGTATACCGGAGTGAAGGCAAGGCTGGAGAGTCTTGAAGT	979
Db	781	CACCCCATGTCTGTATACCGGAGTGAAGGCAAGGCTGGAGAGTCTTGAAGT	840
OY	980	CAGTGAAGTGGGCAATCGCCTTTTGTAAAGCTTCAGTGTCCATTCATCCCTGATGGGG	1039
Db	841	CAGTGAAGTGGGCAATCGCCTTTTGTAAAGCTTCAGTGTCCATTCATCCCTGATGGGG	900
OY	1040	GCATGTTTGAAGACTGAGAGGTAGAGTACGTTTCTTAAGGCTGGAGGCACTGTCC	1099
Db	901	GCATGTTTGAAGACTGAGAGGTAGAGTACGTTTCTTAAGGCTGGAGGCACTGTCC	960
OY	1100	ACTCAAGGCTCCCTCGGCTTGACATTCAAACCTTCATCTCCTGAAACCAATTCCTGCAAC	1159
Db	961	ACTCAAGGCTCCCTCGGCTTGACATTCAAACCTTCATCTCCTGAAACCAATTCCTGCAAC	1020
OY	1160	AGAATTGGCTGTGTTTCGCGCTGAGTTGGGCTTAAGTACTGAGACTAATGACTGGGA	1219
Db	1021	AGAATTGGCTGTGTTTCGCGCTGAGTTGGGCTTAAGTACTGAGACTAATGACTGGGA	1080
OY	1220	CTTAGAGCGGGGCTCGGCGTCCGCTGTAAAGAGCTTAAAGAAAATTTCTCAGTTCTCT	1279
Db	1081	CTTAGAGCGGGGCTCGGCGTCCGCTGTAAAGAGCTTAAAGAAAATTTCTCAGTTCTCT	1140

```

Oy 1280 TGCAGAGAGACTGGGGCGCCGGGAGCCGAAAGAGCAACGGGCGCTGCACAAAGCGGGCGCTGC
Db 1141 TGCAGAGAGACTGGGGCGCCGGGAGCCGAAAGAGCAACGGGCGCTGCACAAAGCGGGCGCTGC
Oy 1340 GGTGTGTGAGTGGCCATGATACGGCGCAGGCGCTTCTGTTGGCGTGTGTGCAGCGACAG
Db 1201 GGTGTGTGAGTGGCCATGATACGGCGCAGGCGCTTCTGTTGGCGTGTGTGCAGCGACAG
Oy 1400 GCGCGAGCAGACAGACCTGTGCACGAACACCCGCGGAAACTGCTGTGCAGAGACACCGTGTACAG
Db 1261 GCGCGAGCAGACAGCCTGTGCACGAACACCCGCGGAAACTGCTGTGCAGAGACACCGTGTACAG
Oy 1460 GAGGGGGTGTGATGCACGAGCTGAGGTAGAAAAACGTCTCGAAGAAAGGGAGGAGGATCAT
Db 1321 GAGGGGGTGTGATGCACGAGCTGAGGTAGAAAAACGTCTCGAAGAAAGGGAGGAGGATCAT
Oy 1520 GTACGCCCGGAAGTACGACCTCTGTCCAGTCTGTCTTGGGTTTGGCCGAGCCATGATCCT
Db 1381 GTACGCCCGGAAGTACGACCTCTGTCCAGTCTGTCTTGGGTTTGGCCGAGCCATGATCCT
Oy 1580 CCGAATCTGTTGGGCGATCCAGCATATACGGCCAAATGTACAAACATACAGCCCTGGGCGACAG
Db 1441 CCGAATCTGTTGGGCGATCCAGCATATACGGCCAAATGTACAAACATACAGCCCTGGGCGACAG
Oy 1640 ACGAGCAGAGGAGGAGACAGACAGA 1663
Db 1501 ACGAGCAGAGGAGGAGACAGACAGA 1524

RESULT 41
US-10-218-612-15
; Sequence 15, Application US/10218612
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gunney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C21
; CURRENT APPLICATION NUMBER: US/10/218,612
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524

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;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 246
;; SEQ ID NO: 15
;; LENGTH: 1524
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-10-218-631-15

Query Match 75.0%; Score 1422; DB 42; Length 1524;
Best Local Similarity 99.9%; Freq. No. 1.2e-266;
Matches 1522; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 140 GCGGAGCAGCGCGGCGCCGACGACGCTCGGAGCAGCAGCGGCTGCAAGCGGAGCGCC 199
DB 1 GCGGAGCAGCGCGGCGCCGACGACGCTCGGAGCAGCAGCGGCTGCAAGCGGAGCGCC 60
QY 200 TCCGCTGCTGTCGCTCTCTGATGCGCTTCCGCTCCCGGCGCGGAGCTCCGAGAGA 259
DB 61 TCCGCTGCTGTCGCTCTCTGATGCGCTTCCGCTCCCGGCGCGGAGCTCCGAGAGA 120
QY 260 ATGTGGTCTCTAGGATCGCGGCACTTTTGGGATTTGTTCTGCTTCCAGAGCTTTCG 319
DB 121 ATGTGGTCTCTAGGATCGCGGCACTTTTGGGATTTGTTCTGCTTCCAGAGCTTTCG 180
QY 320 CTGCAATTCAGATGCTACGAGTGTGAAGATTCAGCTGAACAAGACTGCTCTCCGCC 379
DB 181 CTGCAATTCAGATGCTACGAGTGTGAAGATTCAGCTGAACAAGACTGCTCTCCGCC 240
QY 380 GAGTTCATTGTGAATTCAGAGTGAACGTTCAAGACATGTGTGAGAAAGAGATGAGAG 439
DB 241 GAGTTCATTGTGAATTCAGAGTGAACGTTCAAGACATGTGTGAGAAAGAGATGAGAG 300
QY 440 CAAAGTCCGCGGATCATGTACGCAAGTCTGTGATCATGCGGCGCTGTCTCATTCGCC 499
DB 301 CAAAGTCCGCGGATCATGTACGCAAGTCTGTGATCATGCGGCGCTGTCTCATTCGCC 360
QY 500 TCTGCGGCTGACAGTCTCTGCTGCTCCGAGGAACTGAATCTGATCTGCTGCTGCTG 559
DB 361 TCTGCGGCTGACAGTCTCTGCTGCTCCGAGGAACTGAATCTGATCTGCTGCTGCTG 420
QY 560 TCGCAACACCCCTCTTTTGAAGCGGCGCAAGGCCCAAGAAAGGAGGAGTTCCTCGGCC 619
DB 421 TCGCAACACCCCTCTTTTGAAGCGGCGCAAGGCCCAAGAAAGGAGGAGTTCCTCGGCC 480
QY 620 CTCAGGCGCGGCTCCGCGACCAACATCTGTCTCAAAATTCGCCCTTCTCGGCGACAC 679
DB 481 CTCAGGCGCGGCTCCGCGACCAACATCTGTCTCTCAAAATTCGCCCTTCTCGGCGACAC 540
QY 680 TCTGAGCTGAAGAGATGACACCCCTCTGATTTGTTCTTCAGGCTTCGCCGCCAA 739
DB 541 TCTGAGCTGAAGAGATGACACCCCTCTGATTTGTTCTTCAGGCTTCGCCGCCAA 600
QY 740 CCCCCCAGCTCTCTGAGTGAATTTCTTGGGTCTCTTTATTTCTGGGTAGGAGCGGG 799
DB 601 CCCCCCAGCTCTCTGAGTGAATTTCTTGGGTCTCTTTATTTCTGGGTAGGAGCGGG 660
QY 800 AGTCCGCTGCTCTTTTGTGTTGCAAAATATGAAGAGCTCGTAAAGATCTGAA 859
DB 661 AGTCCGCTGCTCTTTTGTGTTGCAAAATATGAAGAGCTCGTAAAGATCTGAA 720
QY 860 TAAATTCAGCTGAGTGAATTTTCAATGATGATGAAGAGAGGAGGAGTGAATTT 919
DB 721 TAAATTCAGCTGAGTGAATTTTCAATGATGATGAAGAGAGGAGGAGTGAATTT 780
QY 920 CACCCCATGCTGTGTAAACGAGTCAAGGCGAGCTGCGAGAGTCTGCTTGAAGT 979

DB 781 CACCCCATGCTGTGTAAACGAGTCAAGGCGAGCTGCGAGAGTCTGCTTGAAGT 840
QY 980 CACTGAGTGGGATCGCTCTTTTGAAGCTTCAGTGTCAATTCATCCCTGATGGG 1039
DB 841 CACTGAGTGGGATCGCTCTTTTGAAGCTTCAGTGTCAATTCATCCCTGATGGG 900
QY 1040 GCATAGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1099
DB 901 GCATAGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 960
QY 1100 ACTCAAGCTCTCTCTGCTTACATTTCAATCTATGCTCTGAAACATCTCTGAC 1159
DB 961 ACTCAAGCTCTCTCTGCTTACATTTCAATCTATGCTCTGAAACATCTCTGAC 1020
QY 1160 AGAATGGCTGCTTTCGCGCTGAGTGGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1219
DB 1021 AGAATGGCTGCTTTCGCGCTGAGTGGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080
QY 1220 CTGAGCTGGGCTCGGCTCTGCTGAAAGTCTTAAAGAAATCTTCTCAATCTCTCT 1279
DB 1081 CTGAGCTGGGCTCGGCTCTGCTGAAAGTCTTAAAGAAATCTTCTCAATCTCTCTCT 1140
QY 1280 TCGAGAGACTGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1339
DB 1141 TCGAGAGACTGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1340 GGTGGTGAAGTGCATGTACGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1399
DB 1201 GGTGGTGAAGTGCATGTACGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1400 GCGGAGCAGACAGCAGCTGCAAGAACCCCGCAAACTGCTGCGAGAGACCTGTACAG 1459
DB 1261 GCGGAGCAGACAGCAGCTGCAAGAACCCCGCAAACTGCTGCGAGAGACCTGTACAG 1320
QY 1460 GAGCGGCTGATGACCGAGCTGAGGTGAGAAAGCTTCCGAGAAAGGAGAGAGATCAT 1519
DB 1321 GAGCGGCTGATGATGACCGAGCTGAGGTGAGAAAGCTTCCGAGAAAGGAGAGATCAT 1380
QY 1520 GTACGCCCGGAGTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1579
DB 1381 GTACGCCCGGAGTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
QY 1580 CCGAATCTGTTGGGATTCAGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAG 1639
DB 1441 CCGAATCTGTTGGGATTCAGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAG 1500
QY 1640 ACGAGCAG 1663
DB 1501 ACGAGCAG 1524

RESULT 43
US-10-218-765-15
; Sequence 15; Application US/10218765
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C19
; CURRENT APPLICATION NUMBER: US/10/218,765
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: 60/059113	PRIOR FILING DATE: 1997-09-10
PRIOR FILING DATE: 1997-09-17	PRIOR APPLICATION NUMBER: 60/100038
PRIOR APPLICATION NUMBER: 60/062287	PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1997-10-17	PRIOR APPLICATION NUMBER: 60/100385
PRIOR APPLICATION NUMBER: 60/063549	PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1997-10-28	PRIOR APPLICATION NUMBER: 60/100399
PRIOR APPLICATION NUMBER: 60/064103	PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1997-10-31	PRIOR APPLICATION NUMBER: 60/100627
PRIOR APPLICATION NUMBER: 60/069873	PRIOR FILING DATE: 1998-09-16
PRIOR FILING DATE: 1997-12-17	PRIOR APPLICATION NUMBER: 60/100848
PRIOR APPLICATION NUMBER: 60/078910	PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/100919
PRIOR APPLICATION NUMBER: 60/079294	PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-03-25	PRIOR APPLICATION NUMBER: 60/101477
PRIOR APPLICATION NUMBER: 60/079656	PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-03-26	PRIOR APPLICATION NUMBER: 60/101738
PRIOR APPLICATION NUMBER: 60/079728	PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/101744
PRIOR APPLICATION NUMBER: 60/081819	PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/101786
PRIOR APPLICATION NUMBER: 60/081955	PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/101914
PRIOR APPLICATION NUMBER: 60/082804	PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/101922
PRIOR APPLICATION NUMBER: 60/084441	PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/106178
PRIOR APPLICATION NUMBER: 60/085333	PRIOR FILING DATE: 1998-10-28
PRIOR FILING DATE: 1998-05-13	PRIOR APPLICATION NUMBER: 60/106248
PRIOR APPLICATION NUMBER: 60/085579	PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/106466
PRIOR APPLICATION NUMBER: 60/086392	PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-05-22	PRIOR APPLICATION NUMBER: 60/106905
PRIOR APPLICATION NUMBER: 60/089532	PRIOR FILING DATE: 1998-11-03
PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/108787
PRIOR APPLICATION NUMBER: 60/089538	PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/108801
PRIOR APPLICATION NUMBER: 60/089905	PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-06-18	PRIOR APPLICATION NUMBER: 60/108849
PRIOR APPLICATION NUMBER: 60/090472	PRIOR FILING DATE: 1998-11-18
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/112422
PRIOR APPLICATION NUMBER: 60/090557	PRIOR FILING DATE: 1998-12-15
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/113296
PRIOR APPLICATION NUMBER: 60/090691	PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/113605
PRIOR APPLICATION NUMBER: 60/090695	PRIOR FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/113621
PRIOR APPLICATION NUMBER: 60/091982	PRIOR FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-07-07	PRIOR APPLICATION NUMBER: 60/115558
PRIOR APPLICATION NUMBER: 60/095302	PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1998-08-04	PRIOR APPLICATION NUMBER: 60/115565
PRIOR APPLICATION NUMBER: 60/095318	PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1998-08-04	PRIOR APPLICATION NUMBER: 60/115733
PRIOR APPLICATION NUMBER: 60/095916	PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1998-08-10	PRIOR APPLICATION NUMBER: 60/119549
PRIOR APPLICATION NUMBER: 60/096146	PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1998-08-11	PRIOR APPLICATION NUMBER: 60/123618
PRIOR APPLICATION NUMBER: 60/096791	PRIOR FILING DATE: 1999-03-10
PRIOR FILING DATE: 1998-08-17	PRIOR APPLICATION NUMBER: 60/125255
PRIOR APPLICATION NUMBER: 60/097986	PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1998-08-26	PRIOR APPLICATION NUMBER: 60/125775
PRIOR APPLICATION NUMBER: 60/098544	PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1998-08-31	PRIOR APPLICATION NUMBER: 60/126773
PRIOR APPLICATION NUMBER: 60/099596	PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1998-09-09	PRIOR APPLICATION NUMBER: 60/127887
PRIOR APPLICATION NUMBER: 60/099598	PRIOR FILING DATE: 1999-04-05
PRIOR FILING DATE: 1998-09-09	PRIOR APPLICATION NUMBER: 60/130232
PRIOR APPLICATION NUMBER: 60/099803	PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1998-09-10	PRIOR APPLICATION NUMBER: 60/131022
PRIOR APPLICATION NUMBER: 60/099811	PRIOR FILING DATE: 1999-04-26
PRIOR FILING DATE: 1998-09-10	PRIOR APPLICATION NUMBER: 60/131270
PRIOR APPLICATION NUMBER: 60/099812	PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1998-09-10	PRIOR APPLICATION NUMBER: 60/131291
PRIOR APPLICATION NUMBER: 60/099816	PRIOR FILING DATE: 1999-04-27

Sequence 15, Application US/10218784
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC18
CURRENT APPLICATION NUMBER: US/10/218,784
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-08-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-22
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-08-17
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PRIOR FILING DATE: 1998-08-31
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PRIOR FILING DATE: 1998-09-09
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PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
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PRIOR FILING DATE: 1998-12-23
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PRIOR FILING DATE: 1998-12-23
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PRIOR FILING DATE: 1999-01-12
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PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12

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Db 1441 CCGAATCTGGTGGGCATCCAGCATACGGCCATGTCTCACAACATTCAGCCCTGGGACAGAC 1500
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OY 1640 ACGACGAGGAGGAGAGACAGAGA 1663
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Db 1501 ACGACGAGGAGGAGAGACAGAGA 1524
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Job time : 4268.69 secs

697

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:16:33 : Search time 52.9982 Seconds
(without alignments)
3937.596 Million cell updates/sec

Title: US-09-970-966-214

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Scoring table: OLIGO_NMC
Gapop 60.0 , Gapext 60.0

Searched: 193892 seqs, 55004114 residues

Word size : 10

Total number of hits satisfying chosen parameters: 75239

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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- 3: /cgn2_6/ptodata/1/pna/US07_NEM_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1422	75.0	1524	6 US-10-230-437-15	Sequence 15, App1
2	24	1.3	1337	6 US-10-125-928A-215	Sequence 215, App
3	24	1.3	2057	6 US-10-266-829-15	Sequence 15, App1
4	24	1.3	2305	6 US-10-240-425-1530	Sequence 1530, App
5	23	1.2	102	5 US-09-513-999C-20982	Sequence 20982, A
6	23	1.2	198	5 US-09-907-907A-23	Sequence 23, App1
7	23	1.2	286	6 US-10-266-131-1361	Sequence 1361, App
8	23	1.2	315	5 US-09-907-907A-21	Sequence 31, App1
9	23	1.2	504	6 US-10-240-425-758	Sequence 758, App
10	23	1.2	523	6 US-10-240-425-525	Sequence 525, App
11	23	1.2	574	6 US-10-264-237-114	Sequence 114, App
12	23	1.2	785	6 US-10-264-237-1055	Sequence 1055, App
13	23	1.2	1001	6 US-10-264-237-687	Sequence 687, App
14	23	1.2	1092	1 PCR-US02-33408-5	Sequence 5, App1
15	23	1.2	1092	6 US-10-264-237-563	Sequence 563, App
16	23	1.2	1326	6 US-10-264-237-40	Sequence 40, App1
17	23	1.2	1539	6 US-10-264-237-995	Sequence 995, App
18	23	1.2	1571	6 US-10-264-237-1007	Sequence 1007, App
19	23	1.2	1593	5 US-09-602-472A-1	Sequence 1, App1
20	23	1.2	1689	6 US-10-264-237-457	Sequence 457, App
21	23	1.2	1740	6 US-10-260-046-19	Sequence 19, App1
22	23	1.2	1765	6 US-10-264-237-890	Sequence 890, App
23	23	1.2	1998	6 US-10-145-087A-136	Sequence 136, App
24	23	1.2	1998	6 US-10-143-031A-136	Sequence 136, App
25	23	1.2	1998	6 US-10-145-092A-136	Sequence 136, App
26	23	1.2	1998	6 US-10-162-522A-136	Sequence 136, App

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27	23	1.2	1998	6 US-10-165-038A-136	Sequence 136, App
28	23	1.2	1998	6 US-10-165-353-136	Sequence 136, App
29	23	1.2	1998	6 US-10-170-461A-136	Sequence 136, App
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33	23	1.2	1998	6 US-10-145-129A-136	Sequence 136, App
34	23	1.2	1998	6 US-10-125-923A-53	Sequence 53, App1
35	23	1.2	1998	6 US-10-165-353A-136	Sequence 136, App
36	23	1.2	2136	6 US-10-125-923A-227	Sequence 227, App
37	23	1.2	2680	6 US-10-145-087A-136	Sequence 136, App
38	23	1.2	2680	6 US-10-143-031A-156	Sequence 156, App
39	23	1.2	2680	6 US-10-145-092A-156	Sequence 156, App
40	23	1.2	2680	6 US-10-162-522A-156	Sequence 156, App
41	23	1.2	2680	6 US-10-165-038A-156	Sequence 156, App
42	23	1.2	2680	6 US-10-165-353-156	Sequence 156, App
43	23	1.2	2680	6 US-10-170-481A-156	Sequence 156, App
44	23	1.2	2680	6 US-10-172-039A-156	Sequence 156, App
45	23	1.2	2680	6 US-10-145-016A-156	Sequence 156, App

RESULT 1
US-10-230-437-15
Sequence 15, Application US/10230437
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C94
CURRENT FILING DATE: 2002-08-28
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 15
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo Sapien
US-10-230-437-15
Query Match 75.0%; Score 1422; DB 6; Length 1524;

Best Local Similarity 99.9%: Pred. No. 0:
 Matches 1522: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

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 DB 61 TCCGCTGCTGTCGCTCTCTGATGAGCGCTTCCCTCCCGGCGGCGGAGTCCGGGAGA 120

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 DB 121 ATGTGGGTCTAGAGCATGCGGCACTTTTGGGATGTTCTTGTCCAGGCTTTGCG 180

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QY 380 GAGTTCATTTGTAATGACGGGTGAAGCTCAAGCATGTGTCAAGAAAGATGATGAG 439
 DB 241 GAGTTCATTTGTAATGACGGGTGAAGCTCAAGCATGTGTCAAGAAAGATGATGAG 300

QY 440 CAAAGTGGCGGATCATGTACCGCAAGTCTGTGCATCATGACGGGCTGTCTATCGCC 499
 DB 301 CAAAGTGGCGGATCATGTACCGCAAGTCTGTGCATCATGACGGGCTGTCTATCGCC 360

QY 500 TGTGCGGCTACCAATCTCTTCTGCTCCCGAGGAAACTGAACTGATTCATGACTGCG 559
 DB 361 TGTGCGGCTACCAATCTCTTCTGCTCCCGAGGAAACTGAACTGATTCATGACTGCG 420

QY 560 TGCACACACCTCTTTTGTAAACGGGCAAGGCGCAAGAAAGGAGTTCGCTCGGCC 619
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QY 680 TGTGTAAGTGAAGAGATGCGACCCCTCTCTGCTTCTTCCAGGCTCGGCCCAA 739
 DB 541 TGTGTAAGTGAAGAGATGCGACCCCTCTCTGCTTCTTCCAGGCTCGGCCCAA 600

QY 740 CCCCCACCTCCCTGAGTGAATTTCTTCCGGTGCCTTTTATTCGGTGAAGAGCGGG 799
 DB 601 CCCCCACCTCCCTGAGTGAATTTCTTCCGGTGCCTTTTATTCGGTGAAGAGCGGG 660

QY 800 AGTCCGCTCTCTTTTGTCTGTGCAAAATTAAGAGAGCTCGTAAAGCATTTGAA 859
 DB 661 AGTCCGCTCTCTTTTGTCTGTGCAAAATTAAGAGAGCTCGTAAAGCATTTGAA 720

QY 860 TAAATTCACCTGAGTGAATTTTCAATATGTAAGAGAGAGGAGTGAATTAATTT 919
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QY 920 CACCCCATGCTGTGTAAACCGAGTCAAGGCGGAGCTGCGAGATCTGCTTGAAGT 979
 DB 781 CACCCCATGCTGTGTAAACCGAGTCAAGGCGGAGCTGCGAGATCTGCTTGAAGT 840

QY 980 CACTGAGTGGGCACTCTGCTTTTGTAAAGCTCAAGTGTCCATTCCTGATGGGG 1039
 DB 841 CACTGAGTGGGCACTCTGCTTTTGTAAAGCTCAAGTGTCCATTCCTGATGGGG 900

QY 1040 GCATAGTTGAGACGACAGAGAGAGAGTGTCTTTTCTTGAAGGCGGAGGCGCATTTCC 1099
 DB 901 GCATAGTTGAGACGACAGAGAGAGAGTGTCTTTTCTTGAAGGCGGAGGCGCATTTCC 960

QY 1100 ACTCAAGGCTCCCTGCTGTGACATTCAAACTCATGCTCTCAAAAACATTTCTGACGC 1159
 DB 961 ACTCAAGGCTCCCTGCTGTGACATTCAAACTCATGCTCTCAAAAACATTTCTGACGC 1020

QY 1160 AGAATTTGCTGTTGCGCCCTGAGTGGGCTGTAGTGAATCAGACTCAATGACTGGGA 1219
 DB 1160 AGAATTTGCTGTTGCGCCCTGAGTGGGCTGTAGTGAATCAGACTCAATGACTGGGA 1219

DB 1021 AGAATTTGCTGTTTTCGCGGCTGATGTTGGGCTCTAGTGAATCAGACTCAATGACTGGGA 1080

QY 1220 CTTAGACTGGGCTCGGCTCTGCTCTGAAAAGTCTTAAGAAAATCTTCTGCTCTCT 1279

DB 1081 CTTAGACTGGGCTCGGCTCTGCTCTGAAAAGTCTTAAGAAAATCTTCTGCTCTCT 1140

QY 1280 TGCAGAGACTGCGCGCGGAGCGCAAGAGCAACGGGCGCTGCAACAAAGCGGCGCTGTC 1339

DB 1141 TGCAGAGAGACTGCGCGCGGAGCGCAAGAGCAACGGGCGCTGCAACAAAGCGGCGCTGTC 1200

QY 1340 GGTGTGAGTGGGCTGATGACGCGCAAGCGGCTTCTGCTGTTGGGCTGCTGCAAGCAGAG 1399

DB 1201 GGTGTGAGTGGGCTGATGACGCGCAAGCGGCTTCTGCTGTTGGGCTGCTGCAAGCAGAG 1260

QY 1400 GCGGACACAGACACGCGCAAGCAACCGCGGAACTGCTGCGAGAGACCGCTGTACAG 1459

DB 1261 GCGGACACAGACACGCGCAAGCAACCGCGGAACTGCTGCGAGAGACCGCTGTACAG 1320

QY 1460 GAGCGGTTGATGACCGAGCTGAGTGAAGAAACGCTCTCGAGAAAGGAGAGAGATCAT 1519

DB 1321 GAGCGGTTGATGACCGAGCTGAGTGAAGAAACGCTCTCGAGAAAGGAGAGAGATCAT 1380

QY 1520 GTACGCGCGGAGTGAAGACTCTGCTCAAGTGTCTTGGGTTGGCGGACCATGATCTCT 1579

DB 1381 GTACGCGCGGAGTGAAGACTCTGCTCAAGTGTCTTGGGTTGGCGGACCATGATCTCT 1440

QY 1580 CCGAATCTGTTGGGCTATCCAGCATAGGCCAATGTACAAACATCAGCCCTGGGAGAG 1639

DB 1441 CCGAATCTGTTGGGCTATCCAGCATAGGCCAATGTACAAACATCAGCCCTGGGAGAG 1500

QY 1640 ACGAGCAGAGGAGGAGAGACAGAGA 1663

DB 1501 ACGAGCAGAGGAGGAGAGACAGAGA 1524

RESULT 2
 US-10-125-923A-215
 : Sequence 215, Application US/10125923A
 : GENERAL INFORMATION:
 : APPLICANT: Baker, Kevin P.
 : APPLICANT: Chen, Jian
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Pan, James
 : APPLICANT: Smith, Victoria
 : APPLICANT: Watanabe, Colin K.
 : APPLICANT: Wood, William I.
 : TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 : FILE REFERENCE: P3430R1C79
 : CURRENT APPLICATION NUMBER: US/10/125, 923A
 : PRIOR FILING DATE: 2002-01-15
 : PRIOR APPLICATION NUMBER: 10/052586
 : PRIOR FILING DATE: 2002-01-15
 : PRIOR APPLICATION NUMBER: 60/059263
 : PRIOR FILING DATE: 1997-09-18
 : PRIOR APPLICATION NUMBER: 60/059266
 : PRIOR FILING DATE: 1997-09-18
 : PRIOR APPLICATION NUMBER: 60/062250
 : PRIOR FILING DATE: 1997-10-17
 : PRIOR APPLICATION NUMBER: 60/063120
 : PRIOR FILING DATE: 1997-10-24
 : PRIOR APPLICATION NUMBER: 60/063121
 : PRIOR FILING DATE: 1997-10-24
 : PRIOR APPLICATION NUMBER: 60/063486
 : PRIOR FILING DATE: 1997-10-21
 : PRIOR APPLICATION NUMBER: 60/063540
 : PRIOR FILING DATE: 1997-10-28
 : PRIOR APPLICATION NUMBER: 60/063541
 : PRIOR FILING DATE: 1997-10-28

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; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; SEQ ID NO 215
; LENGTH: 1337
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-125-923A-215

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Qy 1874 GTGTAACAAAAA 1897
Db 1298 GTGTAACAAAAA 1321

RESULT 3
US-10-266-829-15
; Sequence 15, Application US/10266829
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 29 Human secreted proteins
; FILE REFERENCE: P2041P1
; CURRENT APPLICATION NUMBER: US/10/266,829
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 09/756,168
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/US00/19735
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/145,220
; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 2057
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-266-829-15

Query Match
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1907 GTGTAACAAAAA 1930

RESULT 4
US-10-240-425-1530/c
; Sequence 1530, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Metzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1530
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; LENGTH: 2305
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. X06374
US-10-240-425-1530

Query Match
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1874 GTGTAACAAAAA 1897
Db 1626 GTGTAACAAAAA 1603

RESULT 5
US-09-513-999C-20982
; Sequence 20982, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59,US2,REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent-pm
; SEQ ID NO 20982
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-20982

Query Match
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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1875 TGTAAAAA 1897
Db 73 TGTAAAAA 95

RESULT 6
US-09-907-907A-23
; Sequence 23, Application US/09907907A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Ieszyńska, Magdalena
; TITLE OF INVENTION: GENES DISPLAYING ENHANCED EXPRESSION DURING CELLULAR SENESECE
; FILE REFERENCE: A34584-A-PCT-USA (070050,1664)
; CURRENT APPLICATION NUMBER: US/09/907,907A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: US 09/243,277
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 21
; OTHER INFORMATION: a or c or g or t
US-09-907-907A-23

Query Match
Best Local Similarity 1.2%; Score 23; DB 5; Length 198;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAA 1897
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Db 160 TGTAAAAAAAAAAAAAAAAA 182

RESULT 7
US-10-266-131-1361/c
; Sequence 1361, Application US/10266131
; GENERAL INFORMATION:
; APPLICANT: Friedlich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: Novel Murine Polynucleotide Tags and
; FILE REFERENCE: LEX-0030-USA
; CURRENT APPLICATION NUMBER: US/10/266.131
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/09/617.675
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/143,878
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 2908
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1361
; LENGTH: 286
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(286)
; OTHER INFORMATION: n = A,T,C or G
US-10-266-131-1361

Query Match 1.2%; Score 23; DB 6; Length 286;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAA 1897
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Db 24 TGTAAAAAAAAAAAAAAAAA 2

RESULT 8
US-09-907-907A-31
; Sequence 31, Application US/09907907A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.

; APPLICANT: Leszczynska, Magdalena
; TITLE OF INVENTION: GENES DISPLAYING ENHANCED EXPRESSION DURING CELLULAR SENESCENCE A
; FILE REFERENCE: A34584-A-PCT-USA (070050.1664)
; CURRENT APPLICATION NUMBER: US/09/907.907A
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: US 09/243,277
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-907A-31

Query Match 1.2%; Score 23; DB 5; Length 315;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAA 1897
|||||
Db 290 TGTAAAAAAAAAAAAAAAAA 312

RESULT 9
US-10-240-425-758/c
; Sequence 758, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.

; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240.425
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 758
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AI675419
US-10-240-425-758

Query Match 1.2%; Score 23; DB 6; Length 504;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAA 1897
|||||
Db 23 TGTAAAAAAAAAAAAAAAAA 1

RESULT 10
US-10-240-425-525/c
; Sequence 525, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240.425
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 525
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AI262104
US-10-240-425-525

Query Match 1.2%; Score 23; DB 6; Length 523;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAA 1897

DB 52 TGTAAAAAAAAAAAAAAAAAAAA 30

RESULT 11
US-10-264-237-114

; Sequence 114, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 114
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-114

Query Match 1.2%; Score 23; DB 6; Length 574;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
DB 551 TGTAAAAAAAAAAAAAAAAAAAA 573

RESULT 12
US-10-264-237-1055

; Sequence 1055, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1055
; LENGTH: 785
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc-feature
; LOCATION: (74)..(74)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1055

Query Match 1.2%; Score 23; DB 6; Length 785;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
DB 734 TGTAAAAAAAAAAAAAAAAAAAA 756

RESULT 13
US-10-264-237-687
; Sequence 687, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 687
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-687

Query Match 1.2%; Score 23; DB 6; Length 1001;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
DB 974 TGTAAAAAAAAAAAAAAAAAAAA 996

RESULT 14
PCT-US02-33408-5/c

; Sequence 5, Application PC/TUS0233408
; GENERAL INFORMATION:
; APPLICANT: HAYASHI, Yasunori
; TITLE OF INVENTION: NR3B Receptor Subunit Compositions and Related Methods
; FILE REFERENCE: M00656,70068 WO
; CURRENT APPLICATION NUMBER: PCT/US02/33408
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US 60/344,545
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1040
; TYPE: DNA
; ORGANISM: Rattus norvegicus
PCT-US02-33408-5

Query Match 1.2%; Score 23; DB 1; Length 1040;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
DB 42 TGTAAAAAAAAAAAAAAAAAAAA 20

RESULT 15
US-10-264-237-563
; Sequence 563, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 563
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Homo sapiens

```

: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (57)..(57)
: OTHER INFORMATION: n equals a,t,g, or c
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (227)..(227)
: OTHER INFORMATION: n equals a,t,g, or c
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1078)..(1078)
: OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-563

```

Query Match	1.2%	Score 23	DB 6	Length 1092
Best Local Similarity	100.0%	Pred. No. 0.076		
Matches 23	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Oy	1875	TGTAAAAAAAAAAAAAAAAA	1897	
Db	1037	TGTAAAAAAAAAAAAAAAAA	1059	

```

RESULT 16
US-10-264-237-40/c
: Sequence 40, Application US/10264237
: GENERAL INFORMATION:
: APPLICANT: Btise et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PA31PI
: CURRENT APPLICATION NUMBER: US/10/264,237
: PRIOR FILING DATE: 2002-10-04
: PRIOR APPLICATION NUMBER: PCT/US01/16450
: PRIOR FILING DATE: 2001-05-18
: PRIOR APPLICATION NUMBER: US 60/205,515
: PRIOR FILING DATE: 2000-05-19
: NUMBER OF SEQ ID NOS: 2876
: SOFTWARE: PatentIn Ver. 3.1
: SEQ ID NO 40
: LENGTH: 1326
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (912)..(912)
: OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-40

```

```

Query Match 23; DB 6; Length 1326;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
      |||||
Db 54 TGTAAAAAAAAAAAAAAAAAAAAA 32

RESULT 17
US-10-264-237-995
: Sequence 995, Application US/10264237
: GENERAL INFORMATION:
: APPLICANT: Birse et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PA131P1
: CURRENT APPLICATION NUMBER: US/10/264,237
: CURRENT FILING DATE: 2002-10-04
: PRIOR APPLICATION NUMBER: PCT/US01/16450
: PRIOR FILING DATE: 2001-05-18
: PRIOR APPLICATION NUMBER: US 60/205,515
: PRIOR FILING DATE: 2000-05-19
: NUMBER OF SEQ ID NOS: 2876
: SOFTWARE: PatentIn Ver. 3.1
: SEQ ID NO 995

```

```

; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-995

```

```
Query Match      1.2%; Score 23; DB 6; Length 1539;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	1875	TGTAACAAAAA	1897
Db	1509	TGTAACAAAAA	1531

```

RESULT 18
US-10-264-237-1007
: Sequence 1007, Application US/10264237
: GENERAL INFORMATION:
:   APPLICANT: Birse et al.
:   TITLE OR INVENTION: Nucleic Acids, Proteins, and Antibodies
:   FILE REFERENCE: PA131PI
:   CURRENT APPLICATION NUMBER: US/10/264,237
:   CURRENT FILING DATE: 2002-10-04
:   PRIOR APPLICATION NUMBER: PCT/US01/16450
:   PRIOR FILING DATE: 2001-05-18
:   PRIOR APPLICATION NUMBER: US 60/205,515
:   PRIOR FILING DATE: 2000-05-19
:   NUMBER OF SEQ ID NOS: 2876
:   SOFTWARE: PatentIn Ver. 3.1
:   SEQ ID NO 1007
:   LENGTH: 1571
:   TYPE: DNA
:   ORGANISM: Homo sapiens
US-10-264-237-1007

```

Query Match 1.28; Score 23; DB 6; Length 1571;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy	1875	TGTA	1897
Db	1539	TGTA	1561

```

US-09-602-472A-1
RESULT 19
US-09-602-472A-1
: Sequence 1, Application US/09602472A
: GENERAL INFORMATION:
: APPLICANT: Bidney, Dennis L.
: APPLICANT: Hu, Xu
: APPLICANT: Li, Guibua
: TITLE OF INVENTION: Sunflower Disease Resistance Genes
: FILE REFERENCE: 35718/200630
: CURRENT APPLICATION NUMBER: US/09/602.472A
: PRIORITY FILING DATE: 2000-06-23
: PRIOR APPLICATION NUMBER: 60/140, 876
: PRIOR FILING DATE: 1999-06-24
: NUMBER OF SEQ ID NOS: 64
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 1593
: TYPE: DNA
: ORGANISM: Helianthus annuus
: FEATURE:
US-09-602-472A-1

```

```
Query Match      1.2%; Score 23; DB 5; Length 1593;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

QY	1875	TGTA	1897
Db	1571	TGTA	1593

RESULT 20
US-10-264-237-457
; Sequence 457, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 457
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-457

Query Match 1.2%; Score 23; DB 6; Length 1689;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAA 1897
|||||
Db 1654 TGTAAAAA 1676

RESULT 21
US-10-260-046-19
; Sequence 19, Application US/10260046
; GENERAL INFORMATION:
; APPLICANT: Dhugga, Kanwarpal S.
; TITLE OF INVENTION: Manipulation of Plant Polysaccharide
; FILE REFERENCE: 1296
; CURRENT APPLICATION NUMBER: US/10/260,046
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/325,614
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Zea mays
US-10-260-046-19

Query Match 1.2%; Score 23; DB 6; Length 1740;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAA 1897
|||||
Db 1711 TGTAAAAA 1733

RESULT 22
US-10-264-237-890
; Sequence 890, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18

; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 890
; LENGTH: 1765
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-890

Query Match 1.2%; Score 23; DB 6; Length 1765;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAA 1897
|||||
Db 1739 TGTAAAAA 1761

RESULT 23
US-10-145-087A-136
; Sequence 136, Application US/10145087A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuop, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumms, Daniel
; APPLICANT: Williams, P. Mickey
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C47
; CURRENT APPLICATION NUMBER: US/10/145,087A
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 136
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-10-145-087A-136

Query Match 1.2%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 24

US-10-143-031A-136
Sequence 136, Application US/10143031A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C39
CURRENT APPLICATION NUMBER: US/10/143.031A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 136
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-10-143-031A-136

Query Match 1.2%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 25

US-10-145-092A-136
Sequence 136, Application US/10145092A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C45
CURRENT APPLICATION NUMBER: US/10/145.092A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11

```
;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 624
;; SEQ ID NO 136
;; LENGTH: 1998
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-145-092A-136

Query Match          1.2%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
    |||
Db 1974 TGTAAAAAAAAAAAAAAAAAAAAA 1996

RESULT 26
US-10-162-522A-136
; Sequence 136, Application US/10162522A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James.
; APPLICANT: Peoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC56
; CURRENT APPLICATION NUMBER: US/10/162,522A
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
```

```
;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 624
;; SEQ ID NO 136
;; LENGTH: 1998
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-162-522A-136

Query Match          1.2%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
    |||
Db 1974 TGTAAAAAAAAAAAAAAAAAAAAA 1996

RESULT 27
US-10-165-038A-136
; Sequence 136, Application US/10165038A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James.
; APPLICANT: Peoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC29
; CURRENT APPLICATION NUMBER: US/10/165,038A
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
```

PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 136
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-10-165-038A-136

Query Match 1.2%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAA 1897
Db 1974 TGTAAAAA 1996

RESULT 28

US-10-165-353-136
Sequence 136, Application US/10165333

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C40
CURRENT APPLICATION NUMBER: US/10/165,353
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 136
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-10-165-353-136

Query Match 1.2%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAA 1897
Db 1974 TGTAAAAA 1996

RESULT 29

US-10-170-481A-136
Sequence 136, Application US/10170481A

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C53
CURRENT APPLICATION NUMBER: US/10/170,481A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11

```
;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 624
;; SEQ ID NO 136
;; LENGTH: 1998
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-170-481A-136
```

Query Match 1.2%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.073;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
    |||
Db 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996
```

RESULT 30

US-10-172-039A-136

Sequence 136, Application US/10172039A

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630PIC30

CURRENT APPLICATION NUMBER: US/10/172,039A

PRIOR FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649

PRIOR FILING DATE: 1998-03-11

```
;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 624
;; SEQ ID NO 136
;; LENGTH: 1998
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-172-039A-136
```

Query Match 1.2%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.073;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
    |||
Db 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996
```

RESULT 31

US-10-145-016A-136

Sequence 136, Application US/10145016A

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630PIC52

CURRENT APPLICATION NUMBER: US/10/145,016A

PRIOR FILING DATE: 2001-10-18

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 136
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-10-145-016A-136

Query Match 1.2%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
|||||
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 32
US-10-145-088A-136
Sequence 136, Application US/10145088A
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C49
CURRENT APPLICATION NUMBER: US/10/145.088A
PRIOR FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 136
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-10-145-088A-136

Query Match 1.2%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
|||||
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 33
US-10-145-129A-136
Sequence 136, Application US/10145129A
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C51
CURRENT APPLICATION NUMBER: US/10/145.129A
PRIOR FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11

```

; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 136
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-145-129A-136

Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 1998;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
|||||
Db 1974 TGTAAAAAAAAAAAAAAAAAAAAA 1996

RESULT 34
US-10-125-923A-53
; Sequence 53, Application US/10125923A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C79
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 53
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-125-923A-53

Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 1998;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
|||||
```

```

Db 1974 TGTAAAAAAAAAAAAAAAAAAAAA 1996

RESULT 35
US-10-165-353A-136
; Sequence 136, Application US/10165353A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C40
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 136
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-165-353A-136

Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 1998;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
|||||
```

DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 36

US-10-125-923A-227 Application US/10125923A

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C79
CURRENT APPLICATION NUMBER: US/10/125.923A
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 227
LENGTH: 2136
TYPE: DNA
ORGANISM: Homo Sapien
US-10-125-923A-227

Query Match 1.2%; Score 23; DB 6; Length 2136;
Best Local Similarity 100.0%; Pred. No. 0.073;

Matches 23; Conservative 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897

DB 2061 TGTAAAAAAAAAAAAAAAAAAAA 2083

RESULT 37

US-10-145-087A-156

Sequence 156, Application US/10145087A

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C47
CURRENT APPLICATION NUMBER: US/10/145.087A
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/07450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/07632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/07641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/07791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 156
LENGTH: 2680
TYPE: DNA
ORGANISM: Homo sapiens
US-10-145-087A-156

Query Match 1.2%; Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.072;

Matches 23; Conservative 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897

DB 2655 TGTAAAAAAAAAAAAAAAAAAAA 2677

RESULT 38

US-10-143-031A-156

Sequence 156, Application US/10143031A

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang

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: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James?
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630PIC39
: CURRENT APPLICATION NUMBER: US/10/143,031A
: PRIOR FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/064249
: PRIOR FILING DATE: 1997-11-03
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066364
: PRIOR FILING DATE: 1997-11-21
: PRIOR APPLICATION NUMBER: 60/077450
: PRIOR FILING DATE: 1998-03-10
: PRIOR APPLICATION NUMBER: 60/077632
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077641
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077649
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077791
: PRIOR FILING DATE: 1998-03-12
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 624
: SEQ ID NO 156
: LENGTH: 2680
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-143-031A-156

Query Match
Best Local Similarity 1.2%; Score 23; DB 6; Length 2680;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
Db 2655 TGTAAAAAAAAAAAAAAAAAAAAA 2677

RESULT 39
US-10-145-092A-156
: Sequence 156, Application US/10145092A
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
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: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James?
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630PIC45
: CURRENT APPLICATION NUMBER: US/10/145,092A
: PRIOR FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/064249
: PRIOR FILING DATE: 1997-11-03
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066364
: PRIOR FILING DATE: 1997-11-21
: PRIOR APPLICATION NUMBER: 60/077450
: PRIOR FILING DATE: 1998-03-10
: PRIOR APPLICATION NUMBER: 60/077632
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077641
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077649
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077791
: PRIOR FILING DATE: 1998-03-12
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 624
: SEQ ID NO 156
: LENGTH: 2680
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-145-092A-156

Query Match
Best Local Similarity 1.2%; Score 23; DB 6; Length 2680;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
Db 2655 TGTAAAAAAAAAAAAAAAAAAAAA 2677

RESULT 40
US-10-162-522A-156
: Sequence 156, Application US/10162522A
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
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: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James.
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630PIC40
: CURRENT APPLICATION NUMBER: US/10/165,353
: PRIOR FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/064249
: PRIOR FILING DATE: 1997-11-03
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066364
: PRIOR FILING DATE: 1997-11-21
: PRIOR APPLICATION NUMBER: 60/077450
: PRIOR FILING DATE: 1998-03-10
: PRIOR APPLICATION NUMBER: 60/077632
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077641
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077649
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077791
: PRIOR FILING DATE: 1998-03-12
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 624
: SEQ ID NO 156
: LENGTH: 2680
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-165-353-156

Query Match          1.2%: Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%: Pred. No. 0.072;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
    |||||||||||||||||||
Db 2655 TGTAAAAAAAAAAAAAAAAAAAAA 2677

RESULT 43
US-10-170-481A-156
: Sequence 156, Application US/10170481A
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Flavaro, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
```

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: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James.
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630PIC53
: CURRENT APPLICATION NUMBER: US/10/170,481A
: PRIOR FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/064249
: PRIOR FILING DATE: 1997-11-03
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066364
: PRIOR FILING DATE: 1997-11-21
: PRIOR APPLICATION NUMBER: 60/077450
: PRIOR FILING DATE: 1998-03-10
: PRIOR APPLICATION NUMBER: 60/077632
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077641
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077649
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077791
: PRIOR FILING DATE: 1998-03-12
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 624
: SEQ ID NO 156
: LENGTH: 2680
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-170-481A-156

Query Match          1.2%: Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%: Pred. No. 0.072;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
    |||||||||||||||||||
Db 2655 TGTAAAAAAAAAAAAAAAAAAAAA 2677

RESULT 44
US-10-172-039A-156
: Sequence 156, Application US/10172039A
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Flavaro, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
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APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C30
CURRENT APPLICATION NUMBER: US/10/172.039A
PRIOR FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/07450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 156
LENGTH: 2680
TYPE: DNA
ORGANISM: Homo sapiens
US-10-172-039A-156

Query Match 1.2%; Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAA 1897
DB 2655 TGTAAAAA 2677

RESULT 45
US-10-145-016A-156
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
```

```
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C52
CURRENT APPLICATION NUMBER: US/10/145.016A
PRIOR FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/07450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 156
LENGTH: 2680
TYPE: DNA
ORGANISM: Homo sapiens
US-10-145-016A-156

Query Match 1.2%; Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAA 1897
DB 2655 TGTAAAAA 2677
```

Search completed: November 8, 2002, 02:04:42
Job time : 105.998 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:51:07 ; Search time 4825.36 Seconds
(without alignments)
11441.218 Million cell updates/sec

Title: US-09-970-966-214

Perfect score: 1897

Sequence: 1 gccaaactccgagagctctg.....aaaaaaaaaaaaaaaaaaaaa 1897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vl:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.ph:*
24: em.pl:*
25: em.ro:*
26: em.sts:*
27: em.un:*
28: em.vl:*
29: em.vl:*
30: em.htg.hum:*
31: em.htg.inv:*
32: em.htg.other:*
33: em.htg.mus:*
34: em.htg.pln:*
35: em.htg.rtd:*
36: em.htg.mam:*
37: em.htg.vrt:*
38: em.sy:*
39: em.htgo.hum:*
40: em.htgo.mus:*
41: em.htgo.other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1826	96.3	1890	6	AX136281 Sequence
2	1725	90.9	1832	9	AK094501 Homo sapi
3	1523.2	80.3	1524	6	AX358762 Sequence
4	1523.2	80.3	1524	6	AX362255 Sequence
5	1430	75.4	129676	9	AC079773 Homo sapi
6	1322.2	69.7	2528	6	AX319944 Sequence
7	908.6	47.9	945	9	BC017318 Homo sapi
8	857.8	45.2	1797	10	AB041649 Mus muscu
9	800.2	42.2	826	9	BC011449 Homo sapi
10	643.4	33.9	209885	2	AC124493 Mus muscu
11	550.4	29.0	591	6	AX136556 Sequence
12	508.6	26.8	1362	6	AX319942 Sequence
13	508.6	26.8	1362	6	AF034633 Homo sapi
14	498.8	25.3	92874	2	AC112072 Rattus no
15	480.4	25.3	587	6	AX136698 Sequence
16	413.4	21.8	444	6	AX093191 Sequence
17	368.8	19.4	366	6	AX093191 Sequence
18	365.4	19.3	369	6	AX093191 Sequence
19	298.4	15.7	147131	9	AC010974 Homo sapi
20	228.8	12.1	190503	2	AC128363 Rattus no
21	120.8	6.4	190503	2	AC128363 Rattus no
22	80.2	4.2	136799	2	AC110334 Rattus no
23	69.2	3.6	127714	9	AL590677 Human DNA
24	63.4	3.3	125020	9	AF429315 Homo sapi
25	59.8	3.2	3917	10	AB017027 Mus muscu
26	59.4	3.1	58930	2	AC098321 Rattus no
27	58.2	3.1	1254	6	E11480 cDNA encodl
28	58.2	3.1	1257	6	AX280911 Sequence
29	58.2	3.1	4131	9	HSNEURA
30	57.8	3.0	125020	9	AF429315 Homo sapi
31	56.4	3.0	1140	6	E37240 Novel physl
32	56.4	3.0	1140	6	E63120 Peptide der
33	56.4	3.0	1148	9	AF100206 Macaca mu
34	56.4	3.0	1583	9	HS003642 Homo sapi
35	56.4	3.0	1754	9	BC032688 Homo sapi
36	56.4	3.0	1801	9	HS03108P
37	56.4	3.0	1872	6	AR107256 Sequence
38	56.4	3.0	1872	6	AR194356 Sequence
39	56.4	3.0	169216	2	AC090238 Homo sapi
40	56.4	3.0	171744	9	AP001786 Homo sapi
41	55.8	2.9	139627	2	AC016779 Oryza sat
42	55.8	2.9	154078	2	AC101929 Mus muscu
43	55.6	2.9	159	9	GIBHONTPEA
44	55.6	2.9	216	9	HUMHNTPEA
45	55.6	2.9	477	6	AR165922 Sequence

ALIGNMENTS

RESULT 1
LOCUS AX136281 1890 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 203 from Patent EP1067182.
ACCESSION AX136281
VERSION AX136281.1 GI:14272687
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1890)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein

Pred. No. is the number of results predicted by chance to have a

QY 1201 CGAGACTCATGACTGGGACTTGAAGTGGGGCTGGGCTCTGCTTGAAGTGGTTAGA 1260
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Db 1156 CGAGACTCAATGACTGGGACTTGAAGTGGGGCTGGGCTCTGCTTGAAGTGGTTAGA 1215
1261 AATATCTTCTGCTTCTGCTTCAAGAGACTGGGCGCGGGAGCGGCAAGACAGCGGGCT 1320
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Db 1216 AATATCTTCTGCTTCTGCTTCAAGAGACTGGGCGCGGGAGCGGCAAGACAGCGGGCT 1275
1321 GCAGAAAGCGGGCGCTGCTGGTGGTGAAGTGGCGCATGTAGCGCGAGCGCTTCTGCTGT 1380
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Db 1276 GCAGAAAGCGGGCGCTGCTGGTGGTGAAGTGGCGCATGTAGCGCGAGCGCTTCTGCTGT 1335
1381 TGGGCTGTGAGAGGAGGAGGCGGAGCAGACAGTGGTGAAGTGGCGCATGTAGCGCGAG 1440
1336 TGGGCTGTGAGAGGAGGAGGCGGAGCAGACAGTGGTGAAGTGGCGCATGTAGCGCGAG 1395
1441 GCGAGACACCGCTGTACAGAGCGGGTTGATGACCGAGTGGTGAAGTGGCGCATGTAGCG 1500
1396 GCGAGACACCGCTGTACAGAGCGGGTTGATGACCGAGTGGTGAAGTGGCGCATGTAGCG 1455
1501 AGAAGGGGAGGAGGATCATGTAGCGCGGAGTGAAGTGGCGCATGTAGCGCGAGTGGGTT 1560
1456 AGAAGGGGAGGAGGATCATGTAGCGCGGAGTGAAGTGGCGCATGTAGCGCGAGTGGGTT 1515
1561 TGGCGCGCATGTATCTCTCGAATCTGTGGGCTATCCAGCATAGCGCGCAATGTCAAA 1620
1516 TGGCGCGCATGTATCTCTCGAATCTGTGGGCTATCCAGCATAGCGCGCAATGTCAAA 1575
1621 CAATGAGCCCTGGGCGAGACAGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
1576 CAATGAGCCCTGGGCGAGAGAGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1635
1681 GAGAACACAGTAATGATTAATAACCATTAATATTAGCCCTCTGTCTGTCTTACTG 1740
1636 GAGAACACAGTAATGATTAATAACCATTAATATTAGCCCTCTGTCTGTCTTACTG 1695
1741 GCCAGGAATGTACCAATTTTTCAGTGTGGAGCTTGACAGCTTCTTGGCACAAGCAA 1800
1686 GCCAGGAATGTACCAATTTTTCAGTGTGGAGCTTGACAGCTTCTTGGCACAAGCAA 1755
1801 GAGAACATTTAACAACCTGTTTCAAAACCGGGGAGTGGCTGTGTTAAAGAAAGCAATTA 1860
1756 GAGAACATTTAACAACCTGTTTCAAAACCGGGGAGTGGCTGTGTTAAAGAAAGCAATTA 1815
QY 1861 AATGCTTTAGACAGTGT 1877
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Db 1816 AATGCTTTAGACAGTGT 1832

RESULT 3
AX358762 1524 bp DNA linear PAT 13-FEB-2002
LOCUS AX358762
DEFINITION Sequence 15 from Patent WO0193983.
ACCESSION AX358762
VERSION AX358762.1 GI:18675282
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
1 Godowski, P.J., Grimaldi, J.C., Gunney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K., and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0193983-A 15 13-DEC-2001.
Genentech Inc. (US)
FEATURES
Source Location/Qualifiers
1..1524
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 321 a 433 c 435 g 335 t

ORIGIN
Query Match 80.3%; Score 1523.2; DB 6; Length 1524;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1522; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 140 GCGGAGAGAGCGGGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 199
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Db 1 GCGGAGAGAGCGGGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
200 TCCGCTGCTGTCGCTCTCTCTGATGCGCTTCCGCGCGCGGAGACTCCGAGAGA 259
Db 61 TCCGCTGCTGTCGCTCTCTCTGATGCGCTTCCGCGCGCGGAGACTCCGAGAGA 120
QY 260 ATGTGGCTCTAGGAGATGCGGAGACTTTTGGGATTTTCTTGGCTTTCAGGCTTTCG 319
121 ATGTGGCTCTAGGAGATGCGGAGACTTTTGGGATTTTCTTGGCTTTCAGGCTTTCG 180
QY 320 CTGCAATCGAGTACGAGTGTGAAGTTCAGCTGAACAGAGAGAGAGAGAGAGAGAGAGAG 379
181 CTGCAATCGAGTACGAGTGTGAAGTTCAGCTGAACAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 380 GAGTTCATGTAATTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 439
241 GAGTTCATGTAATTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 440 CAAGTGGCGGAGATCATGTATCCGAGAGTCTGTGATCATACAGGCGCTGTCTCATGCGC 499
301 CAAGTGGCGGAGATCATGTATCCGAGAGTCTGTGATCATACAGGCGCTGTCTCATGCGC 360
QY 500 TCTGCGGGAGACAGATCTTCTCTCCAGGAGAACTAAGTGTGATCATAGCTGC 559
361 TCTGCGGGAGACAGATCTTCTCTCCAGGAGAACTAAGTGTGATCATAGCTGC 420
QY 560 TGCAGACCCCTCTTGTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 619
421 TGCAGACCCCTCTTGTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 620 CTGAGGCGAGAGGCTCGGAG 679
481 CTGAGGCGAGAGGCTCGGAG 540
QY 680 TGTGGAAGTGAAG 739
541 TGTGGAAGTGAAG 600
QY 740 CCCCCACCTCCTGAGTGAAGTCTTCTGAGTCTTATTTATTTGGGTAGAGAGAGAG 799
601 CCCCCACCTCCTGAGTGAAGTCTTCTGAGTCTTATTTATTTGGGTAGAGAGAGAGAG 660
QY 800 AGTCCGCTCTCTTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 859
661 AGTCCGCTCTCTTCTTCT 720
QY 860 TAAATTCAGCTGACTGAATTTTCACTATGACTTGAAGAGAGAGAGAGAGAGAGAGAGAG 919
721 TAAATTCAGCTGACTGAATTTTCACTATGACTTGAAGAGAGAGAGAGAGAGAGAGAGAG 780
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781 CACCCCACTGCTGTGTAAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 980 CACTGAGAGTGGAGATCTGCTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1039
841 CACTGAGAGTGGAGATCTGCTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 1040 GCATAGTTGAGAGTGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1099
901 GCATAGTTGAGAGTGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 960
QY 1100 ACTCAAGGCTCCTCGCTTGAATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGAT 1159
961 ACTCAAGGCTCCTCGCTTGAATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 1020

Db 1141 TGCAGAGGACTGGCGCCGGAGCGGAGAGACGAGCGGCGTTCACAAAGCGGCGTGTCTC 1200

Qy 1340 GGTGCTGAGATGCGCATATACGCCGAGCGCTTCTCGTGGTGGCGTCTGACGACAG 1339

Db 1201 GGTGCTGAGATGCGCATATACGCCGAGCGCTTCTCGTGGTGGCGTCTGACGACAG 1250

Qy 1400 GCGGAGAGACGACGACCTTCAGAACACCGCGCAACTGCTGGCGAGCAGCGTGTACAG 1459

Db 1261 GCGGAGAGACGACGACCTTCAGAACACCGCGCAACTGCTGGCGAGCAGCGTGTACAG 1320

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Db 1321 GAGCGGCTTGTATGACCGAGCTGAGGTAGAAAACGCTCTCCAGAAAGGAGAGAGATCAT 1380

Qy 1520 GTACGCGCGGAGATGAGACCTCTGCTGCTGCTGGTGGTGGCGGAGCAGATGCTCT 1579

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Qy 1580 CCGATCTGCTGGGATCTCCAGCATACGCGCAATGTCAACAATACAGCCCTGGGAGAGAC 1639

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Qy 1640 ACGAGCAGAGGAGAGAGACAGAGA 1663

Db 1501 ACGAGCAGAGGAGAGAGAGAGAGA 1524

RESULT 5

AC079773/c

LOCUS AC079773 129676 bp DNA linear PRI 09-JAN-2002

DEFINITION Homo sapiens BAC clone RP11-258B17 from 2, complete sequence.

ACCESSION AC079773

VERSION AC079773.8 GI:15145561

KEYWORDS HTG.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 129676)

Sulston, J.E. and Waterston, R.

Toward a complete human genome sequence

Genome Res. 8 (11), 1097-1108 (1998)

MEDLINE

PUBMED

9847074

REFERENCE

AUTHORS

2 (bases 1 to 129676)

Shah, N., Meyer, R., Boyer, F. and Dignan, G.

The sequence of Homo sapiens BAC clone RP11-258B17

Unpublished (2001)

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

4 (bases 1 to 129676)

Waterston, R.H.

Direct Submission

Submitted (09-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

5 (bases 1 to 129676)

Waterston, R.

Direct Submission

Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

On Aug 9, 2001 this sequence version replaced g1:14408388.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: sapiens@wustl.wustl.edu

Summary Statistics

Center project name: H_NH0258B17

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Taten, M., Catanes, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: PBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1L22; the clone sequenced to the right is RP11-159N20. 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-258B17; actual end is at base position 60003 of RP11-159N20.

RP11-258B17 contains a single plasmid region from 1230 to 1239.

FEATURES

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Location/Qualifiers

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/chromosome="2"

/map="2"

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941..1253

/note="match to EST BF804362 (NID:912133351)"

1388..1412

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1397..3331

/rpt_family="L1"

2346..2370

/rpt_family="(TTTG)n"

9444..9466

/rpt_family="AT_rich"

11961..11969

/note="match to EST A1054234 (NID:93322021) q177b02.x1"

12697..12739

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14016..14171

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14175..14337

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15532..15842

/rpt_family="Alu"

16269..16505

/rpt_family="MALR"

16629..16712

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16810..16939

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Db 119905 AGGACTGGCGCCGGGAGCGAAGAGCAACGGCGCTGACACAAAGCGGCGCTGCTGGTG 119846
 QY 1345 TGGAGTGGGATGTACGGGAGGGCGCTTCTGTGGTGGCTGCTGACAGCAGCGGGCC 1404
 Db 119845 TGGAGTGGGATGTACGGGAGGGCGCTTCTGTGGTGGCTGCTGACAGCAGCGGGCC 119786
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 QY 1465 GGTGTATGACCGAGCTGAGTAGAAGAAAGCTCCGAGAGAGGAGAGATCATGTACG 1524
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 QY 1645 CAGGAGGAG 1704
 Db 119545 CAGGAGGAG 119486
 QY 1705 CATTAATATTAG 1764
 Db 119485 CATTAATATTAG 119426
 QY 1765 AGTGTGGAGCTGAG 1824
 Db 119425 AGTGTGGAGCTGAG 119366
 QY 1825 CCCGGGAGAGTGGCTGTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1878
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RESULT 6

AXJ19944/c 2528 bp DNA linear PAT 14-DEC-2001
 LOCUS AXJ19944 2528 bp DNA linear PAT 14-DEC-2001
 DEFINITION Sequence 3 from Patent WO0181634.
 ACCESSION AXJ19944
 VERSION AXJ19944.1 GI:17901491
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1
 Galvin, K.A. and Rudolph-Owen, L.A.
 Methods and compositions for the diagnosis and treatment of
 cardiovascular and tumorigenic disease using 4941
 Patent: WO 0181634-A 3 01-NOV-2001;
 Millennium Pharmaceuticals, Inc. (US)
 FEATURES
 source location/Qualifiers
 1..2528
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 42..1403
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 ARROTIIFRLIVTLAVCMPPNRIIRIMAAKPKHMTSYRAYKILLIPSESTFY
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CDS

BASE COUNT 516 a 766 c 677 g 567 t 2 others
 ORIGIN
 Query Match 69.7%; Score 1322.2; DB 6; Length 2528;
 Best Local Similarity 99.5%; Pred. No.: 6.9e-296;
 Matches 1324; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 308 CCGAGCTTTGGCTGGGAATCCAGTGTACAGTGTGAAGAAATCCAGTGAACAGCAG 367
 Db 2219 CAAGGCTTTGGCTGGGAATCCAGTGTACAGTGTGAAGAAATCCAGTGAACAGCAG 2160
 QY 368 TGGCTCTCCCGCCAGTTCATTTGTAATTCACAGTGAACAGTTCAGACATGTGTAGAAA 427
 Db 2159 TGGCTCTCCCGCCAGTTCATTTGTAATTCACAGTGAACAGTTCAGACATGTGTAGAAA 2100
 QY 428 GAAGTATGAGCAAAAGTGGCGGATCATGTACAGCAGTCTGTGATCATACAGCGGC 487
 Db 2099 GAAGTATGAGCAAAAGTGGCGGATCATGTACAGCAGTCTGTGATCATACAGCGGC 2040
 QY 488 TGTCTCATGCGCTTGGCGGCTACAGTCTCTGTCTCCGAGGAAATGAACTCAGTT 547
 Db 2039 TGTCTCATGCGCTTGGCGGCTACAGTCTCTGTCTCCGAGGAAATGAACTCAGTT 1980
 QY 548 TGCATCAGCTGTGCAACAACCCCTCTTTGTAAACGGGCCAAGGCCCAAGAAAGGGAGT 607
 Db 1979 TGCATCAGCTGTGCAACAACCCCTCTTTGTAAACGGGCCAAGGCCCAAGAAAGGGAGT 1920
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 Db 1919 TGTGCTCGGCGCTCAGGCCAGGGCTCCGACACCATCTGTCTCAAAATTAAGCCCTC 1860
 QY 668 TTCTCGGCACTGTGCAAGCTGAAGAGATGCGACACCCCTCTGTGATGTTCTTCCAC 727
 Db 1859 TTCTCGGCACTGTGCAAGCTGAAGAGATGCGACACCCCTCTGTGATGTTCTTCCAC 1800
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 Db 1679 AAGCATTTCAATAAATTCAGCTGTGACTGAATTTGATGATGACTTGAAGAAGAGAGT 1620
 QY 908 GGAAGTGAAGTCAACCCCATGTCTGTGTAAACCGAGTCAAGGCGAGCTGCAGAGTCW 967
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 QY 1088 GGGCGCAATTCACCTCAAGGCTCCCTGCTTGCATTAATTAATTAATTAATTAATTA 1147
 Db 1439 GGGCGCAATTCACCTCAAGGCTCCCTGCTTGCATTAATTAATTAATTAATTAATTA 1380
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 QY 1208 CAATGACTGGAGCTTGAAGTGGGCTCGGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1267
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 QY 1268 CTCAGTTCTCTTGCAGAGAGCTGGGCGCGGAGCGCAAGAGCAACGGCGCTGCACAAA 1327

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Qy	1448	CACCGTGTACAGAGAGCGGGTGTGATGACCGAGCTGAGGTAGAAAAACGCTCTCGAGAAAGG	1507
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Qy	1508	GAGGAGGATTCATGTACGGCCCGGAATAGAGACCTGCTCAGTCGTCGTCCTTGGTTGGCCGC	1567
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Qy	1628	CCCTGGGCAGA	1638
Db	899	CCTCAGGAGA	889

RESULT	7
BC017318	
LOCUS	946 bp mRNA linear PRI_09-NOV-2001
DEFINITION	Homo sapiens, clone MGC:23643 IMAGE:3641660, mRNA, complete cds.
ACCESSION	BC017318
VERSION	BC017318.1 GI:16878239
KEYWORDS	MGC.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens

REFERENCE AUTHORS TITLE JOURNAL	
1 (bases 1 to 946) Straussberg, R. Direct Submission Submitted (03-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	

REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk

CNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland,
Web site: [http://www.nisc.nih.gov/
nisc_mgc/hg1.nih.gov](http://www.nisc.nih.gov/nisc_mgc/hg1.nih.gov)
Contact: Stevechen, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-T., Karlins, E., Legaspi, R.,
Lim, M., Maduro, O.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Statulipop, S., Thomas, P.J.,
Tlonegon, E.E., Touchman, J.W., Tsurgoun, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLNC at: <http://image.lnl.gov>
Series: IRAL Plate: 39 Row: B Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

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SOURCE

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Db	260	AATGAGGGGCTCTAGGCAATCGGGGCAACTTTTGGGGATGTGTTCTTGCTTCCAGGCTTGC	319				
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 REFERENCE
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUL-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-7590,
 USA
 REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 COMMENT Contact: MGC help desk
 Email: gcgabs-rt@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTF

CDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadansystembiology.org
 Anup Madan, Rachel Dickhoff, Jessica Fahy, Stephanie Ford, Julia
 Greene, Mark Kettelman and Anuradha Madan
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 25 Row: n Column: 18
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 analysis.
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 McPherson, J.D. and Waterston, R.H.
 The sequence of Mus musculus clone
 Unpublished
 2 (bases 1 to 209885)
 McPherson, J.D. and Waterston, R.H.
 Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 3 (bases 1 to 209885)
 McPherson, J.D. and Waterston, R.H.
 Direct Submission
 Submitted (05-JUL-2002) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 On Jul 5, 2002 this sequence version replaced gi:21426614.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 Contact: submissions@wustl.wustl.edu
 Project Information
 Center project name: M_BA0462P13

 Summary Statistics
 Sequencing vector: M13: 0%
 Chemistry: Dye-terminator Big Dye: 100% of reads
 Assembly program: Phrap: version 0.990319
 Consensus quality: 208484 bases at least Q40
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 Consensus quality: 209285 bases at least Q20
 Insert size: 206000; agarose-IP
 Insert size: 212112; sum-of-contrigs
 Quality coverage: 0.00 in Q20 bases; agarose-IP
 Quality coverage: 11.62 in Q20 bases; sum-of-contrigs

 NOTE: This is a 'working draft' sequence. It currently
 consists of 5 contrigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contrigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
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ORIGIN					

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OY	1184	GTGGGCTCTAGTACTGAGACTCAATGACTGGACATTAGACTGGGGCTGGCTCGCT	1243
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VERSION	AF034633	complete cds.	
KEYWORDS	AF034633.1	GI:2654160	
SOURCE	.		
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	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		

REFERENCE	1 (bases 1 to 1362)
AUTHORS	McGee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D., Hreniuk,D.L., Smith,R.G., Howard,A.D. and Van der Ploeg,L.H.
TITLE	Cloning and characterization of two human G protein-coupled receptor genes (GPR38 and GPR39) related to the growth hormone secretagogue and neuropeptide receptors
JOURNAL	Genomics 46 (3), 426-434 (1997)
MEDLINE	98110578
PUBMED	9441746
REFERENCE	2 (bases 1 to 1362)
AUTHORS	McGee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D., Hreniuk,D.L., Smith,R.G., Van Der Ploeg,L.H.T. and Howard,A.D.
TITLE	Direct Submission
JOURNAL	Submitted (17-NOV-1997) Biochemistry and Physiology, Merck and Co., Inc., PO Box 2000, Rahway, NJ 07065, USA
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FEATURES	location/Qualifiers
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CDS	1. .1362

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AC112072									
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ACCESSION	AC112072								
VERSION	AC112072.3	GI:21744373							
KEYWORDS	HTG: HTGS. PHASE1.								
SOURCE	HTG: HTGS. PHASE1.								
ORGANISM	Rattus norvegicus								
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AUTHORS	Muzny D.M., Adams C., Adio-Oduola B., All-oman F.R., Allen C., Alshrocks S.L., Amaralunge H.C., Are J.R., Ayele M., Banks T., Barbata J., Benton J., Blimage K., Blankenburg K., Bonaldi N., Bouck J., Bowle S., Brileva M., Brown E., Brown M., Bryant D., Burch J., Burck P., Burkett C., Burrell K.L., Byrd N., P., Cannon T.F., Carter M., Cavazos S., R., Chacko J., Chavez D., Chen G., Chen R., Chen Z., Chowdhury I., Christopoulos C., Cleveland C.D., Cox C., Coyle M.D., Dathorne S.R., David R., Dellany M.L., Davis C., Davy-Carroll L., Dederich D.A., Delaney K.R., Delgado O., Dem A.L., Ding X., Dim H.H., Douthwaite K.J., Draper H., Dugan-Rocha S., Durbin K.J., Earhart C., Edgar D., Edwards C.C., Elhaj C., Escoto M., Falls T., Ferraguto D., Flagg N., Ford J., Foster P., Frantz P., Gabriel A., Gao J., Garcia A., Garner T., Garza N., Gill R., Gorrell J.H., Guevara M., Gunaratne P., Hale S., Hamilton K., Harris C., Harris K., Hart M., Havlak P., Hawes A., Hernandez J., Hernandez O., Hodgson A., Hogues M., Holloway C., Hollins B., Homsl F., Howard S., Huber J., Huylk S., Hume J., Jackson L.E., Jacobson B., Jia Y., Johnson R., Jolivet S., Joudah S., Kallstrom E., Kelly S., Khan U., King L., Korvah J., Kovar C., Kretovic J., Kureshi A., Landry N., Leal B., Lewis L.C., Lewis L., Li J., Li Z., Lichteberg O., Lieu C., Liu J., Liu M., Lounseged H., Locado R.J., Lu X., Lucier A., Lucier R., Luna R., Ma J., Maheshwari M., Mapua P., Martin R., Martindale A., Martinez E., Massey E., Mawhinney E., McLeod M.P., Meador M., Mel G., Metker M., Miner G., Miner Z., Mitchell T., Mohabhat R., Morgan M., Morris S., Moser M., Neal D., Newton J., Newton N., Nguyen A., Nguyen N., Nguyen N., Nickerson E., Nwokweto S., Ogbu M., Okunolu G., Ogunyeye N., Oviedo R., Pace A., Payton B., Peery J., Perez L., Peters L., Pickens R., Primus E., Pul L.L., Quties M., Ren Y., Rives M., Rojas A., Rojudoan I., Roite M., Ruiz S., Severy G., Scherer S., Scott G., Shen H., Shoostari N., Sisson I., Sodergren E., Sonalke T., Sparks A., Stanley H., Stone H., Sulton A., Svatek A., Tabor P., Tameris A., Tameris K., Tang H., Tamey J., Taylor C., Taylor T., Telford B., Thomas N., Thomas S., Usmani K., Vasquez L., Vera V., Villalob D., Vinson R., Wang Q., Wang S., Ward-Moore S., Warren R., Washington C., Wallington S., Williams G., Williamson A., Wleczyk R., Wooden S., Worley K., Wu C., Wu Y., Wu Y.F., Zhou J., Zorrilla S., Nelson D., Weinstock G. and Gibbs R.								
TITLE	Journal	Unpublished							
REFERENCE	2 (bases 1 to 92874)								
AUTHORS	Worley K.C.								
TITLE	Direct Submission								
JOURNAL	Submitted (19-FEB-2002)	Human Genome Sequencing Center, Department							

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REFERENCE
AUTHORS
TITLE
JOURNAL

of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 92874)
Worley, R.C.
Direct Submission
Submitted (17-Jul-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 13, 2002 this sequence version replaced gi:20303189.

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Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

-----
Project Information
Center project name: GRD
Center clone name: CH230-286021

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Summary Statistics
Sequencing vector: Plasmid;
Assembly: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 32512 bases at least Q40
Consensus quality: 34515 bases at least Q30
Consensus quality: 35930 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html)
* NOTE: This is a 'working draft' sequence. It currently
* consists of 50 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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1058 1057: contig of 1057 bp in length
1158 1157: gap of unknown length
2411 2410: contig of 1253 bp in length
2511 2510: gap of unknown length
3571 3571: contig of 1061 bp in length
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25657 26711: contig of 1055 bp in length
26712 26811: gap of unknown length

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of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 92874)

Worley, R.C.

Direct Submission

Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 13, 2002 this sequence version replaced gi:20303189.

Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: GRD

Center clone name: CH230-286021

Summary Statistics

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap: version 0.990329

Consensus quality: 32512 bases at least Q40

Consensus quality: 34515 bases at least Q30

Consensus quality: 33930 bases at least Q20

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)

NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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ACCESSION AX136698
VERSION AX136698.1 GI:14273102
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Hayashi,K.
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Patent: EP 1067182-A 620 10-JAN-2001;
Helix Research Institute (JP)
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Oy 1414 CCGTGCACGAACCGCGGAACTGCTGCGAGGACACCGGTACAGAGCGGGTGTGATGA 1473
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GenCore version 5.1.3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1845.8	97.3	1956	22	AAF64188
5	1826	96.3	1890	22	AAF33845
6	1606.2	84.7	1619	24	ABT03277
7	1606.2	84.7	1619	24	ABT03281
8	1606.2	84.7	1619	24	ABL40345
9	1606.2	84.7	1619	24	ABL40349

10	1523.2	80.3	1524	24	ABK33543	CDNA encoding huma
11	1405.6	74.1	1608	24	ABO54231	Human ovarian anti
12	1323.2	69.7	2528	22	AAO18690	Human G protein co
13	624	32.9	625	24	ABT03280	Human ovarian carc
14	624	32.9	625	24	ABL40348	Human ovarian carc
15	624	32.9	625	24	ABL87898	Human ovarian carc
16	566.4	29.9	1010	24	ABT03282	Human ovarian carc
17	566.4	29.9	1010	24	ABL40350	Human ovarian carc
18	550.4	29.0	591	22	AAF94044	Ovarian carcinoma
19	508.6	26.8	1362	24	ABT03279	Primer specific fo
20	508.6	26.8	1362	24	ABL40347	Human ovarian carc
21	480.4	25.3	480	22	AAF94186	Ovarian carcinoma
22	476.8	25.1	480	24	ABT03283	Primer specific fo
23	476.8	25.1	480	24	ABL40351	Human ovarian carc
24	433.2	22.8	558	24	ABL79397	Ovarian carcinoma
25	413.4	21.8	444	22	AAH50766	Human ovarian carc
26	396.4	20.9	409	24	ABL81262	Human tumour assoc
27	378.6	20.0	430	24	ABL81273	Human ovarian carc
28	368.8	19.4	396	22	AAF94818	Human ovarian carc
29	368.8	19.4	396	24	ABT03085	Human ovarian carc
30	368.8	19.4	396	24	ABL40385	Human ovarian carc
31	365.4	19.3	369	22	AAF95007	Ovarian carcinoma
32	365.4	19.3	369	22	ABT03274	Human ovarian carc
33	365.4	19.3	369	24	ABL48956	Human ovarian carc
34	362	19.1	373	24	ABL78538	Human ovarian carc
35	354	18.7	390	24	ABL78554	Human ovarian carc
36	341.8	18.0	381	24	ABL84848	Human ovarian carc
37	310.2	16.4	349	24	ABL79431	Human ovarian carc
38	175.4	9.2	468	22	AAK54063	Human ovarian carc
39	171.2	9.0	201	24	ABL85916	Murine transport a
40	60	3.2	60	24	ABN41977	Human ovarian carc
41	58.2	3.1	1254	17	AAAT3127	Human spliced tran
42	58.2	3.1	1257	23	ABT98007	Human neurotensin
43	58.2	3.1	4149	23	AAK76503	Non-endogenous hum
44	58	3.1	3609	22	AAK94581	DNA encoding novel
45	56.4	3.0	1140	20	AAK83839	Human full-length
						G protein-coupled

ALIGNMENTS

RESULT 1	
ID	ABT03284 standard; CDNA; 1897 BP.
XX	
AC	ABT03284;
XX	
DT	05-SEP-2002 (first entry)
XX	
DE	Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.
XX	
KW	Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
KW	cytoskeletal; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200239885-A2.
XX	
PD	23-MAY-2002.
XX	
PF	13-NOV-2001; 2001WO-US45395.
XX	
PR	14-NOV-2000; 2000US-0713550.
XX	
PR	03-APR-2001; 2001US-0825294.
XX	
PR	02-OCT-2001; 2001US-0970966.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Xu J, Stolk JA, Algate PA, Filing SP, Molesch DA;
XX	
DR	WPI; 2002-500186/53.
XX	
PT	Novel ovarian cancer polypeptide and polynucleotide; useful for

XX	RESULT 2
ABLA0352	ID ABLA0352 standard; cDNA; 1897 BP.
XX	AC ABLA0352;
XX	DT 28-JUN-2002 (first entry)
XX	Ovarian carcinoma O1034C/0591S consensus nucleotide sequence.
DE	Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer; ss.
KW	Homo sapiens.
XX	OS Homo sapiens.
XX	Key Location/Qualifiers
FT CDS	260..685
FT	/tag= "a"
FT	/product= "Ovarian carcinoma protein O1034C/0591S"
FN	US2002004491-A1.
PD	10-JAN-2002.
XX	03-APR-2001; 2001US-0825294.
PR	10-SEP-1999; 99US-0394374.
PR	01-MAY-2000; 2000US-0561778.
PR	15-AUG-2000; 2000US-0640173.
PR	07-SEP-2000; 2000US-0656668.
PR	14-NOV-2000; 2000US-0713550.
XX	(XUJ/) XU J.
PA	(STOL/) STOLK J A.
PA	(ALGA/) ALGATE P A.
PA	(FLIN/) FLING S P.
PI	Xu J, Stolk JA, Algate PA, Fling SP;
DR	WP1; 2002-171027/22.
DR	P-PSDB; ABB09417.
XX	Ovarian tumour polypeptide and polynucleotide useful in diagnosis, prevention and/or treatment of cancer, especially ovarian cancer -
PT	Claim 1a; Page 127-128; 131pp; English.
XX	The invention relates to ovarian tumour polynucleotides and polypeptides that may be utilised in cancer therapy, for example in a vaccine or gene therapy. Polypeptides and polynucleotides of the invention are useful for detecting a cancer in a patient, for stimulating and/or expanding T-cells specific for a tumour protein, and for inhibiting the development of a cancer in a patient. They are also useful for stimulating an immune response in a patient, and for treating a cancer in a patient and for determining the presence of a cancer in a patient. The isolated polynucleotides of the invention are useful for their ability to selectively form duplex molecules with complementary stretches of the entire desired gene or gene fragments, and for designing and preparing ribozyme molecules for inhibiting expression of tumour polypeptides in tumour cells. Polypeptides and polynucleotides of the invention are also useful in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. The current sequence represents the ovarian carcinoma O1034C/0591S consensus nucleotide sequence.
SO	Sequence 1897 BP: 435 A: 521 C: 532 G: 407 T: 2 other:
Query Match	100.0%; Score 1896.2; DB 24; Length 1897;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1897; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
GC	CGCACCTCCGAGGCTGTGTCGTGGCCCGGAGACCGAGCGGAGAGACGACCGG 60

Db	1	GGCAACCTCCGGAGGCGTCTGGTGTCTGGCCCGGGAGCGCAAGCGGAGGAGCAGAGACCCG	60
Qy	61	CAGCCGGAGACCCGACGCGCGGGCGATGCAGAGCTCCGCGAGCGGCACCTCGGCTCTCTTA	120
Db	61	CAGCCGGAGACCCGACGCGCGGGCGATGCAGAGCTCCGCGAGCGGCACCTCGGCTCTCTTA	120
Qy	121	ACCTACGACCGTCGTCTCCGGGGAGAGGCGGGGCCCAAGACGCTCGGGCAGCCAGAC	180
Db	121	ACCTACGACCGTCGTCTCCGGGGAGAGGCGGGGCCCAAGACGCTCGGGCAGCCAGAC	180
Qy	181	CGCTACACCGGGGAGCGCTCCGCTGTCTGGCTCCTCGATGAGCGCTTGCCCTCCCG	240
Db	181	CGCTACACCGGGGAGCGCTCCGCTGTCTGGCTCCTCGATGAGCGCTTGCCCTCCCG	240
Qy	241	GGCCCGGGAATCTCCGGAGATGTGGTCTCAAGGCATCGCGCAACTTTTGGGATGT	300
Db	241	GGCCCGGGAATCTCCGGAGATGTGGTCTCAAGGCATCGCGCAACTTTTGGGATGT	300
Qy	301	CTTGGTTCAGGCTTTGGCGTGCAGAAATCCAGTGTACAGTGTGAAGATTTCCAGTGA	360
Db	301	CTTGGTTCAGGCTTTGGCGTGCAGAAATCCAGTGTACAGTGTGAAGATTTCCAGTGA	360
Qy	361	CAACACATGCTCTCCGCCGAGTTGATTTGAATTCAGCAGTTAAAGTTCAAGACATGTG	420
Db	361	CAACACATGCTCTCTCCGCCGAGTTGATTTGAATTCAGCAGTTAAAGTTCAAGACATGTG	420
Qy	421	TCAGAAAGATGATGAGCAAGATGCCGGGATCATGTACCGCAAGTCTGTGATCATC	480
Db	421	TCAGAAAGATGATGAGCAAGATGCCGGGATCATGTACCGCAAGTCTGTGATCATC	480
Qy	481	AGCGGCGTGTCTCATCGCTCTGCGGGGTACAGTCTCTGTCTCCCAAGGAACTGAA	540
Db	481	AGCGGCGTGTCTCATCGCTCTGCGGGGTACAGTCTCTGTCTCCCAAGGAACTGAA	540
Qy	541	CTCAGTTTGATCATAGCTGTCTGCAACACCCCTTTGTAACGGGCGCAAGGCCCAAGAAAG	600
Db	541	CTCAGTTTGATCATAGCTGTCTGCAACACCCCTTTGTAACGGGCGCAAGGCCCAAGAAAG	600
Qy	601	GGGAAGTTCTGCTCGCGGCTTCAGAGCGCGAGGCTCCGACACCATCTGTTCTCAAAAT	660
Db	601	GGGAAGTTCTGCTCGCGGCTTCAGAGCGCGAGGCTCCGACACCATCTGTTCTCAAAAT	660
Qy	661	AGCCTCTTTTCGCGCACATGCTGTAAGCTTAAGAGATGCCACCCCTCTGCAATTTGTC	720
Db	661	AGCCTCTTTTCGCGCACATGCTGTAAGCTTAAGAGATGCCACCCCTCTGCAATTTGTC	720
Qy	721	TTCCAGGCCCTGGCCCCAACCCCCCACTCCGATGTAGATTTCTTGGGATCTCTTTT	780
Db	721	TTCCAGGCCCTGGCCCCAACCCCCCACTCCGATGTAGATTTCTTGGGATCTCTTTT	780
Qy	781	ATTCTGGGTAGGAGACGGAGATCCGTTTCTTTTGTTCCTGTGCAAAATATTAAGAAAG	840
Db	781	ATTCTGGGTAGGAGACGGAGATCCGTTTCTTTTGTTCCTGTGCAAAATATTAAGAAAG	840
Qy	841	CTCGGTAAAGCATTTCTGAATTAATTCAGCTGACTGAATTTTCAATGTACTGAAGA	900
Db	841	CTCGGTAAAGCATTTCTGAATTAATTCAGCTGACTGAATTTTCAATGTACTGAAGA	900
Qy	901	AGGAGGTGAGTGAAGGTACCCCACTGTCTGTGAACCGGAGTCAAGGCCAGGCTGGC	960
Db	901	AGGAGGTGAGTGAAGGTACCCCACTGTCTGTGAACCGGAGTCAAGGCCAGGCTGGC	960
Qy	961	AGAGTCGTCCTTTGAGATCACTGAGTGGGCAATCGCCTTTTGTAAAGCCCTCCAGTTC	1020
Db	961	AGAGTCGTCCTTTGAGATCACTGAGTGGGCAATCGCCTTTTGTAAAGCCCTCCAGTTC	1020
Qy	1021	CATTCATCCTGATGGGGGCAATGTTGAGACTGACAGTGAAGAGTGAACGTTTCTTGA	1080
Db	1021	CATTCATCCTGATGGGGGCAATGTTGAGACTGACAGTGAAGAGTGAACGTTTCTTGA	1080
Qy	1081	GGCTGGAGGGCAATTCGCCACTCAAGGCTCCCTGCTTGAACATTCATCATGCTCT	1140
Db	1081	GGCTGGAGGGCAATTCGCCACTCAAGGCTCCCTGCTTGAACATTCATCATGCTCT	1140


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Db 853 CTCGGTAAGCATCTGTAATTAATTCAGCTGACTGAATTTTCACTATGTAAGTGAAGA 912
Qy 901 AGGAGGTGAGTGAAGATTACACCCCATGTCTGTAAACCGAGATCAAGGCGAGCTGGC 960
Db 913 AGGAGGTGAGTGAAGATTACACCCCATGTCTGTAAACCGAGATCAAGGCGAGCTGGC 972
Qy 961 AGAGTCMGTCCTTAGAAGTCACTGAGTGGGCGATCGCTTTTGTAAAGCCCTCCAGTGC 1020
Db 973 AGAGTCMGTCCTTAGAAGTCACTGAGTGGGCGATCGCTTTTGTAAAGCCCTCCAGTGC 1032
Qy 1021 CATTCATCCCTGATGAGGCGCATAGTTTGAGACTGACAGTGAAGTGAAGTCTTTTAG 1080
Db 1033 CATTCATCCCTGATGAGGCGCATAGTTTGAGACTGACAGTGAAGTGAAGTCTTTTAG 1092
Qy 1081 GCGTGGAGGCGCATGTTCCACTCAAGGCTCCCTCGTTGACTTAAACTTATCTCTCT 1140
Db 1093 GCGTGGAGGCGCATGTTCCACTCAAGGCTCCCTCGTTGACTTAAACTTATCTCTCT 1152
Qy 1141 GAAACCATTCCTGACAGAGAAATGGGCTGTTGCGCGCTGATGGGCTCTAGTGA 1200
Db 1153 GAAACCATTCCTGACAGAGAAATGGGCTGTTGCGCGCTGATGGGCTCTAGTGA 1212
Qy 1201 CGAGACTCAATGACTGAGACTTGAAGTGGGCTCGGCTCCCTCTGAAAAGTCTTAAGA 1260
Db 1213 CGAGACTCAATGACTGAGACTTGAAGTGGGCTCGGCTCCCTCTGAAAAGTCTTAAGA 1272
Qy 1261 AATCTCTCAATGCTT-CCTTGACAGAGACTGGCGCGGAGCGCAAGAGCAGCGGCGC 1319
Db 1273 AATCTCTCAATGCTTCCCTTGACAGAGACTGGCGCGGAGCGCAAGAGCAGCGGCGC 1332
Qy 1320 TGCACAAACGCGGCGCTGTCGGTGGTGGAGTGCATGATGACGAGGCGCTTCCTG 1379
Db 1333 TGCACAAACGCGGCGCTGTCGGTGGTGGAGTGCATGATGACGAGGCGCTTCCTG 1392
Qy 1380 TTGGCGTGTGACGACGACAGGCGGACGACAGACCTGACAGAACACCCGCGAAATGC 1439
Db 1393 TTGGCGTGTGACGACGACAGGCGGACGACAGACCTGACAGAACACCCGCGAAATGC 1452
Qy 1440 TGGGAGACACCGTGTACAGAGACCGGCTGATGACGAGCTGATGAGTAAAGAACTCC 1499
Db 1453 TGGGAGACACCGTGTACAGAGACCGGCTGATGACGAGCTGATGAGTAAAGAACTCC 1512
Qy 1500 GAGAAAGGAGAGAGATCATGTACGCCGGAAGTAGAGACTGTCAGTCTGTGGGT 1559
Db 1513 GAGAAAGGAGAGAGATCATGTACGCCGGAAGTAGAGACTGTCAGTCTGTGGGT 1572
Qy 1560 TTGGCGGACGACATGATCTCCGAATCTGGTGGGATCCAGCATACGCGCAATGTACA 1619
Db 1573 TTGGCGGACGACATGATCTCCGAATCTGGTGGGATCCAGCATACGCGCAATGTACA 1632
Qy 1620 ACAATAGCCCTGGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1679
Db 1633 ACAATAGCCCTGGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1692
Qy 1680 TGAGAACACAGTAAATGAATTAACCATTAATTTAGCCCTCTGTCTGTCTGTACT 1739
Db 1693 TGAGAACACAGTAAATGAATTAACCATTAATTTAGCCCTCTGTCTGTCTGTACT 1752
Qy 1740 GGGCAGAAATGTTACCAATTTTTCAGTGTGACTGACAGCTTCTTTGCCACAAGCA 1799
Db 1753 GGGCAGAAATGTTACCAATTTTTCAGTGTGACTGACAGCTTCTTTGCCACAAGCA 1812
Qy 1800 AGAGAAATTTTAACACTGTTTAAACCCGCGGAGTGGCTGTGTTAAAGAAAGACCAT 1859
Db 1813 AGAGAAATTTTAACACTGTTTAAACCCGCGGAGTGGCTGTGTTAAAGAAAGACCAT 1872
Qy 1860 AATGCTTTAGACAGTGT 1877
Db 1873 AATGCTTTAGACAGTGT 1890

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ABT03277
ID ABT03277 standard; cDNA; 1619 BP.
XX
AC ABT03277;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 205.
XX
KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
KW cytosolic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200239885-A2.
XX
PD 23-MAY-2002.
XX
PF 13-NOV-2001; 2001WO-US45395.
XX
PR 14-NOV-2000; 2000US-0713550.
PR 03-APR-2001; 2001US-0825294.
PR 02-OCT-2001; 2001US-0970966.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX
DR WPI; 2002-500186/53.
XX
PT Novel ovarian cancer polypeptide and polynucleotide, useful for
PT detecting the presence of ovarian cancer in a patient, and in
PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
PT
XX
PS Claim 2; Page 189-190; 197pp; English.
XX
CC The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention.
XX
SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;
Query Match 84.7%; Score 1606.2; DB 24; Length 1619;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1616; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
Qy 280 GGCACATTTTGGGATTTGTTCTTCCAGGCTTTGCGTGAATTCAGTGTACCA 339
Db 1 GGCACATTTTGGGATTTGTTCTTCCAGGCTTTGCGTGAATTCAGTGTACCA 60
Qy 340 GTGTGAAGATTTCCAGTGAAGACGACTGCTCTCCCGGAGTCAATGTTGATTCAC 399
Db 61 GTGTGAAGATTTCCAGTGAAGACGACTGCTCTCCCGGAGTCAATGTTGATTCAC 120
Qy 400 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGAGAGCAAGTCCGGATCATGTA 459
Db 121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGAGAGCAAGTCCGGATCATGTA 180
Qy 460 CCGCAAGTCTGTGCATCATCAGGCGGCTGTCTCATGCTCTGCGGGTACCAAGTCTT 519
Db 181 CCGCAAGTCTGTGCATCATCAGGCGGCTGTCTCATGCTCTGCGGGTACCAAGTCTT 240
Qy 520 CTGCTCCCGCAGGAAACTGAATCAGTTTGATAGCTGTGCAACACCCCTCTTTGTA 579
Db 241 CTGCTCCCGCAGGAAACTGAATCAGTTTGATAGCTGTGCAACACCCCTCTTTGTA 300
Qy 580 CGGGCAAGGCGCCAAAGAAAGGGAAGTTCGCTCGGCTCAGGCGAGGCTCCGAC 639
Db 301 CGGGCAAGGCGCCAAAGAAAGGGAAGTTCGCTCGGCTCAGGCGAGGCTCCGAC 360
Qy 640 CACCATCTGTTCTCAATTAATGACCTCTTCTCGGCACTGCTGAAGTGAAGAGATG 699

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Db 361 CACACCTCTGCTCAATATAGCCCTCTTCGCGACACTGCTAGCTGAGAGATG 420
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Qy 700 GCACCCCTCCGCAATGTTCTTCACGCCCTGCCCCACCCCTCCCTAGTGA 759
|||
Db 421 CACCCCTCCGCAATGTTCTTCACGCCCTGCCCCACCCCTCCCTAGTGA 480
|||
Qy 760 GTTCTCTGCGTCTCTTATCTGCGTAGGAGCGGAGTCCGTCTCTTGT 819
|||
Db 481 GTTCTCTGCGTCTCTTATCTGCGTAGGAGCGGAGTCCGTCTCTTGT 540
|||
Qy 820 CCTGTGCAATATATGAAAGAGCTCGTAAAGCATTCGATAATTCAGCTGAT 879
|||
Db 541 CCTGTGCAATATATGAAAGAGCTCGTAAAGCATTCGATAATTCAGCTGAT 600
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Qy 880 TTTTCAGTATGCTTGAAGAGAGGTGAGTGAAGTCAACCCCTGCTGTGTAAC 939
|||
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|||
Qy 940 CGAGTCAAGGCCAGGCTGGCAGAGTCTGCTGAGAGTCACTGAGGTGGCATCTGCC 999
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Qy 1000 TTTTGAAGCCTCCAGTGTCTCATTCATCCCTGATGGGGCATAGTTGAGACTGACA 1059
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Db 721 TTTTGAAGCCTCCAGTGTCTCATTCATCCCTGATGGGGCATAGTTGAGACTGACA 780
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Qy 1060 GTGAGAGTACGTTTTCTTAGGGCTGAGAGGCGCATGCTCCATCAAGGCTCCCTGCTG 1119
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Db 781 GTGAGAGTACGTTTTCTTAGGGCTGAGAGGCGCATGCTCCATCAAGGCTCCCTGCTG 840
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Qy 1120 ACATTCAAACTTCATGCTCTGTAAGAAACATTCCTGACAGAAATTTGGCTGTTCGCGC 1179
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Db 841 ACATTCAAACTTCATGCTCTGTAAGAAACATTCCTGACAGAAATTTGGCTGTTCGCGC 900
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Qy 1180 CTGAGTGGGCTCTAGTACTCTGAACTCAATGACTGGGACTTAGACTGGGGCTGGGCT 1239
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Db 901 CTGAGTGGGCTCTAGTACTCTGAACTCAATGACTGGGACTTAGACTGGGGCTGGGCT 960
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Qy 1240 CCCTCTGAAAAGTCTTGAAGAAATCTTCTCAGTCTCTCTGACAGAGGCTGGGCGCGG 1299
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Db 961 CCCTCTGAAAAGTCTTGAAGAAATCTTCTCAGTCTCTCTGACAGAGGCTGGGCGCGG 1020
|||
Qy 1300 ACGCCAAGACACAGCGGCGCTGCACAAAGCGGCGCTGCGGTGTGAGTGGCGCATGA 1359
|||
Db 1021 ACGCCAAGACACAGCGGCGCTGCACAAAGCGGCGCTGCGGTGTGAGTGGCGCATGA 1080
|||
Qy 1360 CGCGAGGCGCTCTGAGTGGGCTGCTGAGGAGAGGCGGAGACACAGCACCTGTC 1418
|||
Db 1081 CGCGAGGCGCTCTGAGTGGGCTGCTGAGGAGAGGCGGAGACACAGCACCTGTC 1140
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Qy 1419 ACGAAGACCCCGGAACTGCTGCGAGAGACACCGTGTACAGAGAGGGTTATGACCGAG 1478
|||
Db 1141 ACGAAGACCCCGGAACTGCTGCGAGAGACACCGTGTACAGAGAGGGTTATGACCGAG 1200
|||
Qy 1479 CTGAGAGTGAAGAAAGCTCTCCGAGAGGAGAGAGATCATGTACCCCGGAAGTAGAC 1538
|||
Db 1201 CTGAGAGTGAAGAAAGCTCTCCGAGAGGAGAGAGATCATGTACCCCGGAAGTAGAC 1260
|||
Qy 1539 CTGAGAGTGAAGAAAGCTCTCCGAGAGGAGAGAGATCATGTACCCCGGAAGTAGAC 1598
|||
Db 1261 CTGAGAGTGAAGAAAGCTCTCCGAGAGGAGAGAGATCATGTACCCCGGAAGTAGAC 1330
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Qy 1599 CAGCATACGCGCAATGTCAACAACATCAGCCCTGGCGAGACAGCAGAGAGGAGAGAC 1658
|||
Db 1321 CAGCATACGCGCAATGTCAACAACATCAGCCCTGGCGAGACAGCAGAGAGGAGAGAC 1380
|||
Qy 1659 AGAGAAAGAAAGAAAGACAGCATGTGAGACACAGTAATGATTAATATTTAG 1718
|||
Db 1381 AGAGAAAGAAAGAAAGACAGCATGTGAGAAACACAGTAATGATTAATATTTAG 1440
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Qy 1719 CCGCTCTGTGTGCTACGTAGCGGAGGAATGGTACCAATTTTCAGTGTGACTTGA 1778
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Db 1441 CCGCTGTGTCTGTGCTTACTGCGCCAGAGAAATGTTACCAATTTTTCAGTGTGACTTGA 1500
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Qy 1779 CAGCTTCTTTTGGCCACAAGACAGAGAGAAATTTAACTGTTTCAAAACCGGGGAGTTGG 1838
|||
Db 1501 CAGCTTCTTTTGGCCACAAGACAGAGAGAAATTTAACTGTTTCAAAACCGGGGAGTTGG 1560
|||
Qy 1839 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGAATTAATTAATTAATTAATTAAT 1897
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Db 1561 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGAATTAATTAATTAATTAATTAAT 1619
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RESULT 7
ABF03281
ID ABF03281 standard; cDNA; 1619 bp.
XX
AC ABF03281;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 211.
XX
KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
KW cytosolic; gene; ss.
XX
OS Homo sapiens.
XX
PN M0200239885-A2.
XX
PD 23-MAY-2002.
XX
PF 13-NOV-2001; 2001WO-US45395.
XX
PR 14-NOV-2000; 2000US-0713550.
PR 03-APR-2001; 2001US-0825284.
PR 02-OCT-2001; 2001US-0970966.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;
XX
DR WPI; 2002-500186/53.
XX
PT Novel ovarian cancer polypeptide and polynucleotide, useful for
PT detecting the presence of ovarian cancer in a patient, and in
PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
XX
PS Claim 2; Page 195; 197pp; English.
XX
CC The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
XX
XX
SQ Sequence 1619 bp; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 84.7%; Score 1606.2; DB 24; Length 1619;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1616; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

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Db 161 CGGCAAGTCGTGTGATCATGAGCGGCTGTCTCATGCCCTCGCGGGTACAGTCTT 240
Qy 520 CTGCTCCCGAGGGAAGTGAAGTCTGATGATGATGATGATGATGATGATGATGAT 579
Db 241 CTGCTCCCGAGGGAAGTGAAGTCTGATGATGATGATGATGATGATGATGATGAT 300
Qy 580 CGGCGCAAGGCGCAAGAAAGGGAAGTGTGCTGCGGCGCTGCGGCGCAAGGCGTCCGAC 639
Db 301 CGGCGCAAGGCGCAAGAAAGGGAAGTGTGCTGCGGCGCTGCGGCGCAAGGCGTCCGAC 360
Qy 640 CACATCTGTTCTCTCAATTAATGAGCCCTCTTCTGCGCACATGCTGAAGCTGAAGAGATG 699
Db 361 CACATCTGTTCTCTCAATTAATGAGCCCTCTTCTGCGCACATGCTGAAGAGATG 420
Qy 700 CCACCCCTCTCTGCAATGTTGTTCTTCCAGCCCTGCCCCAACCCCTCCCTGATGTA 759
Db 421 CCACCCCTCTCTGCAATGTTGTTCTTCCAGCCCTGCCCCAACCCCTCCCTGATGTA 480
Qy 760 GTTCTCTGCGGCTCTTCTTATCTGCGTGAAGGAGCGGAGTCCGCTGCTCTTCTTGT 819
Db 481 GTTCTCTGCGGCTCTTCTTATCTGCGTGAAGGAGCGGAGTCCGCTGCTCTTCTTGT 540
Qy 820 CCTGTGAATTAATGAAGAGCTCGTAAAGCATTTCTGAATTAATTAATGAGCTGATGAT 879
Db 541 CCTGTGAATTAATGAAGAGCTCGTAAAGCATTTCTGAATTAATTAATGAGCTGATGAT 600
Qy 880 TTTCAAGTATGTAATGAAGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 939
Db 601 TTTCAAGTATGTAATGAAGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 660
Qy 940 CGGAGTCAAGGCGCAGGCTGCGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 999
Db 661 CGGAGTCAAGGCGCAGGCTGCGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Qy 1000 TTTTGAAGGCTCGAGTGTCCATTCATCCCTGATGGGGGCAATGTTGAAGTGAAGTGA 1059
Db 721 TTTTGAAGGCTCGAGTGTCCATTCATCCCTGATGGGGGCAATGTTGAAGTGAAGTGA 780
Qy 1060 GTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1119
Db 781 GTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
Qy 1120 ACATTCAAACTTCATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1179
Db 841 ACATTCAAACTTCATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Qy 1180 CTGAGTGGGCTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1239
Db 901 CTGAGTGGGCTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 960
Qy 1240 CGCTCTGAAGAAAGTGAAGAAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1299
Db 961 CGCTCTGAAGAAAGTGAAGAAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Qy 1300 ACGCGAAGAGCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1359
Db 1021 ACGCGAAGAGCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Qy 1360 CGGCGAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1418
Db 1081 CGGCGAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Qy 1419 ACGAAGACCGCGCGAAGTGTGCGAGGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1478
Db 1141 ACGAAGACCGCGCGAAGTGTGCGAGGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Qy 1479 CTGAGGTAGAAAAAGCTCTCCGAGAGGAGGAGGAGATCATGTAGCCCGGAGTGAAGAGAC 1538
Db 1201 CTGAGGTAGAAAAAGCTCTCCGAGAGGAGGAGGAGATCATGTAGCCCGGAGTGAAGAGAC 1260
Qy 1539 CTGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1598

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Db 1261 CTGCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
Qy 1599 CAGCATACGCGCCATGTGCACAAATCAGCCCTGGGCGACACAGCAGAGGAGAGAGAC 1658
Db 1321 CAGCATACGCGCCATGTGCACAAATCAGCCCTGGGCGACACAGCAGAGGAGAGAGAC 1380
Qy 1659 AGAGAAAGAAAGAAACAGCATGAGAAACAGTAAATGAATAAACATTAATATTAG 1718
Db 1381 AGAGAAAGAAAGAAACAGCATGAGAAACAGTAAATGAATAAACATTAATATTAG 1440
Qy 1719 CCCCTCTGTTCTGCTTACTGCGCAGAGAAATGTAACAAATTTTTCAGTGTGACTGA 1778
Db 1441 CCCCTCTGTTCTGCTTACTGCGCAGAGAAATGTAACAAATTTTTCAGTGTGACTGA 1500
Qy 1779 CAGCTCTTTTGGCACAGAGAGAGAAATTAACACTGTTTCAACCCGGGAGTGTG 1838
Db 1501 CAGCTCTTTTGGCACAGAGAGAGAAATTAACACTGTTTCAACCCGGGAGTGTG 1560
Qy 1839 CTGCTTAAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAATTTTTTTTTT 1897
Db 1561 CTGCTTAAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAATTTTTTTTTT 1619

RESULT 8
ABL40345
ID ABL40345 standard; cDNA; 1619 BP.
XX
AC ABL40345;
XX
XX 28-JUN-2002 (first entry)
XX
DE Ovarian carcinoma sequence isolate 57887 extended cDNA.
XX
KM Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX
XX ss.
XX
XX Homo sapiens.
XX
PN US200204491-A1.
PD 10-JAN-2002.
XX
XX 03-APR-2001; 2001US-0825294.
PF
XX
PR 10-SEP-1999; 99US-0394374.
PR 01-MAY-2000; 2000US-0561778.
PR 15-AUG-2000; 2000US-0640173.
PR 07-SEP-2000; 2000US-0656668.
PR 14-NOV-2000; 2000US-0713550.
XX
PA (XUJ/) XU J.
PA (STOLK/) STOLK J A.
PA (ALGATE P A.
PA (FLIN/) FLIN S P.
XX
PI Xu J, Stolk JA, Algate PA, Flin SP;
DR WPL; 2002-171027/22.
XX
PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX prevention and/or treatment of cancer, especially ovarian cancer
XX
PS Claim 1a; Page 119-120; 131pp; English.
XX
XX
XX The invention relates to ovarian tumour polynucleotides and polypeptides
XX that may be utilised in cancer therapy, for example in a vaccine or
XX gene therapy. Polypeptides and polynucleotides of the invention are
XX useful for detecting a cancer in a patient, for stimulating and/or
XX expanding T-cells specific for a tumour protein, and for inhibiting the
XX development of a cancer in a patient. They are also useful for
XX stimulating an immune response in a patient, and for treating a cancer in
XX a patient and for determining the presence of a cancer in a patient.
XX The isolated polynucleotides of the invention are useful for their

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CC ability to selectively form duplex molecules with complementary stretches
CC of the entire desired gene or gene fragments, and for designing and
CC preparing ribozyme molecules for inhibiting expression of tumor
CC polypeptides in tumor cells. Polypeptides and polynucleotides of the
CC invention are also useful in recombinant DNA molecules to direct
CC expression of a polypeptide in appropriate host cells. The current
CC sequence represents the extended cDNA sequence of ovarian carcinoma
CC isolate 57887 given in record ABL48956.
XX
SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 84.7%; Score 1606.2; DB 24; Length 1619;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1616; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

```

Oy 280 GGCACCTTTTCCGATGTTCTTCTCCAGGCTTTCGCGCAAAATCCAGTGTACCA 339
Db 1 GGCACCTTTTCCGATGTTCTTCTCCAGGCTTTCGCGCAAAATCCAGTGTACCA 60

Oy 340 GTTGAGAAATTCAGCTGAACACGACGTCTCTCCCGAGTTCAATGTAATTCAC 399
Db 61 GTTGAGAAATTCAGCTGAACACGACGTCTCTCCCGAGTTCAATGTAATTCAC 120

Oy 400 GGTGAACCTTCAAGCATGTGTCAAGAAAGAGTGTGAGCAAAAGTCCGGGATCAGTA 459
Db 121 GGTGAACCTTCAAGCATGTGTCAAGAAAGAGTGTGAGCAAAAGTCCGGGATCAGTA 180

Oy 460 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCTCTGCGGGGTACAGTCTT 519
Db 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCTCTGCGGGGTACAGTCTT 240

Oy 520 CTGCTCCCGAGGAAAGTGAACCTGATGATCAGTGTGCAACACCCCTTTTGTAA 579
Db 241 CTGCTCCCGAGGAAAGTGAACCTGATGATCAGTGTGCAACACCCCTTTTGTAA 300

Oy 580 CGGCGCAAGGCGCCAAAGAGGAGTCTGTCTCTCCCGGCTCAGGCGGCTCCGAC 639
Db 301 CGGCGCAAGGCGCCAAAGAGGAGTCTGTCTCTCCCGGCTCAGGCGGCTCCGAC 360

Oy 640 CACCATCTGTTCTCAATTAAGCCCTCTCTCGGCACTGTGAAAGCTGAAGAGATG 699
Db 361 CACCATCTGTTCTCAATTAAGCCCTCTCTCGGCACTGTGAAAGCTGAAGAGATG 420

Oy 700 CCACCCCTCTCGCATTTTCTTCCAGCCCTCGGCCACACCCCCACCTCCCTGAAGTA 759
Db 421 CCACCCCTCTCGCATTTTCTTCCAGCCCTCGGCCACACCCCCACCTCCCTGAAGTA 480

Oy 760 GTTCTCTGGGTGTCTTTTATCTGGTGAAGGAGCGGAGTCCGTTCTTTGT 819
Db 481 GTTCTCTGGGTGTCTTTTATCTGGGTGAAGGAGCGGAGTCCGTTCTTTGT 540

Oy 820 CCTGTGCAAAATATGAAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGTGTGATGAT 879
Db 541 CCTGTGCAAAATATGAAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGTGTGATGAT 600

Oy 880 TTTCACTATGACTTGAAGAGAGAGTGTGAGTGAAGTCAACCCCATGTCGTGTAAAC 939
Db 601 TTTCACTATGACTTGAAGAGAGAGTGTGAGTGAAGTCAACCCCATGTCGTGTAAAC 660

Oy 940 CGGAGTCAAGGCGAGGCGTGAAGTCTGCTTAAGAGTACAGTGTGAGTGTGAGTGTGAGT 999
Db 661 CGGAGTCAAGGCGAGGCGTGAAGTCTGCTTAAGAGTACAGTGTGAGTGTGAGTGTGAGT 720

Oy 1000 TTTTGTAAAGCTCCAGTGTCTCATTCATCCCTGATGGGGCATAGTTTGAAGTGCAGA 1059
Db 721 TTTTGTAAAGCTCCAGTGTCTCATTCATCCCTGATGGGGCATAGTTTGAAGTGCAGA 780

Oy 1060 GTGAGAGTGAAGTGTCTTGAAGGCTGAGGCGCAGTGTCCCATGAAGGCTCCCTGCTTG 1119
Db 781 GTGAGAGTGAAGTGTCTTGAAGGCTGAGGCGCAGTGTCCCATGAAGGCTCCCTGCTTG 840

Oy 1120 ACATTCAAACTTCATGCTCTGAAAGACATTCCTGCGAGCATTTGGCTTTCGCGC 1179

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Db 841 ACATTCAAACTTCATGCTCTGAAAGACATTCCTGTGACAGAGAAATGGCTTTGCGGC 900
Oy 1180 CTGAGTGGGCTCTAGTACTCCAGATCTCATATGACTGAGGACTTAGACTGGGCTCGGCT 1239
Db 901 CTGAGTGGGCTCTAGTACTCCAGATCTCATATGACTGAGGACTTAGACTGGGCTCGGCT 960
Oy 1240 CGGCTGAAAAAGTCTTAAAGAAATCTTCTCAGTTCCTTGGAGAGAGTGGCGCGG 1299
Db 961 CGGCTGAAAAAGTCTTAAAGAAATCTTCTCAGTTCCTTGGAGAGAGTGGCGCGG 1020
Oy 1300 ACGGAAAGACACAGGCGCTGCACAAAGCGGCGCTGTGCTGTGAGTGGCATGTA 1359
Db 1021 ACGGAAAGACACAGGCGCTGCACAAAGCGGCGCTGTGCTGTGAGTGGCATGTA 1080
Oy 1360 CGGCGAGGCGCTTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1418
Db 1081 CGGCGAGGCGCTTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1140
Oy 1419 ACGAACAACCGCGGAAACTCTCTGAGAGACACCGTGTACAGAGCGGCTGATGACCGAG 1478
Db 1141 ACGAACAACCGCGGAAACTCTCTGAGAGACACCGTGTGTACAGAGCGGCTGATGACCGAG 1200
Oy 1479 CTGAGTGAAGAAAGTCTCTCCAGAGAGGAGAGATCATGTACCCCGGAATAGAGAC 1538
Db 1201 CTGAGTGAAGAAAGTCTCTCCAGAGAGGAGAGATCATGTACCCCGGAATAGAGAC 1260
Oy 1539 CTGCTCCAGTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1598
Db 1261 CTGCTCCAGTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1320
Oy 1599 CAGCATACGGGCAATGTCTACAGCAATCAGCCCTGGGCGAGACAGCAGAGAGGAGAGAC 1658
Db 1321 CAGCATACGGGCAATGTCTACAGCAATCAGCCCTGGGCGAGACAGCAGAGAGGAGAGAC 1380
Oy 1659 AGAGAAAAAGAAAAACACAGCATGAGAAACAGTAAATGAATTAATTAATTAATTAAT 1718
Db 1381 AGAGAAAAAGAAAAACACAGCATGAGAAACAGTAAATGAATTAATTAATTAATTAAT 1440
Oy 1719 CCCCTGTCTGTGCTGTCTTACTGTGGCGAGAAATGTTTCCAAATTTTGTAGTTGACTTGA 1778
Db 1441 CCCCTGTCTGTGCTGTCTTACTGTGGCGAGAAATGTTTCCAAATTTTGTAGTTGACTTGA 1500
Oy 1779 CAGCTTCTTTTGCACAGCAAGAGAGAAATTAACAATGTTTCAACCCGCGGAGTGTG 1838
Db 1501 CAGCTTCTTTTGCACAGCAAGAGAGAAATTAACAATGTTTCAACCCGCGGAGTGTG 1560
Oy 1839 CTGCTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAGAAAAA 1897
Db 1561 CTGCTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAGAAAAA 1619

RESULT 9
ABLA0349
ID ABLA0349 standard; cDNA; 1619 BP.
XX
XX ABLA0349;
AC
XX
XX 28-JUN-2002 (first entry)
DE
XX Ovarian carcinoma O591S nucleotide sequence.
XX
XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX ss.
XX Homo sapiens.
XX
XX US2002004491-A1.
XX
XX 10-JAN-2002.
XX
XX 03-APR-2001; 2001US-0825294.
XX
XX 10-SEP-1999; 99US-0394374.

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PR 01-MAY-2000; 2000US-0561778.
 PR 15-AUG-2000; 2000US-0640173.
 PR 07-SEP-2000; 2000US-0656668.
 PR 14-NOV-2000; 2000US-0713550.

XX (XUJ/) XU J.
 PA (STOL/) STOLK J A.
 PA (ALGA/) ALGATE P A.
 PA (FLIN/) FLING S P.

PI Xu J, Stolk JA, Algate PA, Fling SP;
 XX WPI: 2002-171027/22.

DR Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
 PT prevention and/or treatment of cancer, especially ovarian cancer -
 XX

PS Claim 1a: Page 125-126; 131pp; English.

XX The invention relates to ovarian tumour polynucleotides and polypeptides
 CC that may be utilised in cancer therapy, for example in a vaccine or
 CC gene therapy. Polypeptides and polynucleotides of the invention are
 CC useful for detecting a cancer in a patient, for stimulating and/or
 CC expanding T-cells specific for a tumour protein, and for inhibiting the
 CC development of a cancer in a patient. They are also useful for
 CC stimulating an immune response in a patient, and for treating a cancer in
 CC a patient and for determining the presence of a cancer in a patient.
 CC The isolated polynucleotides of the invention are useful for their
 CC ability to selectively form duplex molecules with complementary stretches
 CC of the entire desired gene or gene fragments, and for designing and
 CC preparing ribozyme molecules for inhibiting expression of tumour
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
 CC invention are also useful in recombinant DNA molecules to direct
 CC expression of a polypeptide in appropriate host cells. The current
 CC sequence represents the ovarian carcinoma 05915 nucleotide sequence.
 XX

Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 84.7%; Score 1606.2; DB 24; Length 1619;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1616; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 280 GGCACATTTTGGGATGTTCTTCTTCAGAGCTTGGCTGCAATCCAGTGTACCA 339
 DB 1 GGCACATTTTGGGATGTTCTTCTTCAGAGCTTGGCTGCAATCCAGTGTACCA 60
 QY 340 GTGTAGAGATTCAGCTGACCAAGACGACGCTCCCGGATTCATTTGAAATGAC 399
 DB 61 GTGTAGAGATTCAGCTGACCAAGACGACGCTCCCGGATTCATTTGAAATGAC 120
 QY 400 GGTGACGTTCAAGACATGTGTCAAGAAAGATGAGCAAAAGTCCGGGATCATGTA 459
 DB 121 GGTGACGTTCAAGACATGTGTCAAGAAAGATGAGCAAAAGTCCGGGATCATGTA 180
 QY 460 CCGCAAGTCTGTGATCATCAGCGGCTGTCTATGCCCTCTGCCGGGTACCACTCTT 519
 DB 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTATGCCCTCTGCCGGGTACCACTCTT 240
 QY 520 CTGTCTCCCGAGGAAGTCACTAGTTGATCAGTGTGCAACACCCCTTTTGA 579
 DB 241 CTGTCTCCCGAGGAAGTCACTAGTTGATCAGTGTGCAACACCCCTTTTGA 300
 QY 580 CCGGCAAGGCGCAAGAAAGGGAAGTGTGCTCGGCTCGGCTCAGGCGGATCCGAC 639
 DB 301 CCGGCAAGGCGCAAGAAAGGGAAGTGTGCTCGGCTCGGCTCAGGCGGATCCGAC 360
 QY 640 CACCATCTGTCTCTCAATTAAGCCCTCTCTCGGCAACACTGTGAAGTGAAGTGA 699
 DB 361 CACCATCTGTCTCTCAATTAAGCCCTCTCTCGGCAACACTGTGAAGTGAAGTGA 420
 QY 700 CACCCCTCTCTGATGTTGTTTCCAGGCTTCGAGCCCAACCCCTCTCTGAGTGA 759
 DB 421 CACCCCTCTCTGATGTTGTTTCCAGGCTTCGAGCCCAACCCCTCTCTGAGTGA 480

QY 760 GTTCTCTCTGGGTGCTCTTATTTCTGGTGAAGGAGCGGAGTCCGTCTCTTTTGT 819
 DB 481 GTTCTCTCTGGGTGCTCTTATTTCTGGTGAAGGAGCGGAGTCCGTCTCTTTTGT 540
 QY 820 CCTGTCAAAATTAAGAAAGCTCGTAAAGCATCTCTGAATTAATTCAGCTGACTGA 879
 DB 541 CCTGTCAAAATTAAGAAAGCTCGTAAAGCATCTCTGAATTAATTCAGCTGACTGA 600
 QY 880 TTTTCAATTAATTAAGAAAGCTCGTAAAGCATCTCTGAATTAATTCAGCTGACTGA 939
 DB 601 TTTTCAATTAATTAAGAAAGCTCGTAAAGCATCTCTGAATTAATTCAGCTGACTGA 660
 QY 940 CCGAGTCAAGGCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG 999
 DB 661 CCGAGTCAAGGCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG 720
 QY 1000 TTTTGAAGCTCTCAAGTGTCTTCCATTCCTGATGGGGGCTAGTTGAGACTGAGA 1059
 DB 721 TTTTGAAGCTCTCAAGTGTCTTCCATTCCTGATGGGGGCTAGTTGAGACTGAGA 780
 QY 1060 GTGAGAGTACGTTTCTTGAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1119
 DB 781 GTGAGAGTACGTTTCTTGAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
 QY 1120 ACATTCAACTCATGCTCTCTGAAGCAATCTCTGAGAGAAATTTGCTGCTGCGC 1179
 DB 841 ACATTCAACTCATGCTCTCTGAAGCAATCTCTGAGAGAAATTTGCTGCTGCGC 900
 QY 1180 CTGAGTTGGGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 1239
 DB 901 CTGAGTTGGGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 960
 QY 1240 CGGCTCAAAAGTCTTGAAGAAATCTTCTGAGTCTCTGAGAGAGTCTGAGGCGG 1299
 DB 961 CGGCTCAAAAGTCTTGAAGAAATCTTCTGAGTCTCTGAGAGAGTCTGAGGCGG 1020
 QY 1300 ACGGGAAGCAAGGCGGCTGCAAAAGGCGGCTGCTGCTGCTGCTGCTGCTGCTG 1359
 DB 1021 ACGGGAAGCAAGGCGGCTGCAAAAGGCGGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 QY 1360 CCGGCAAGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1418
 DB 1081 CCGGCAAGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 QY 1419 ACGAACCACCGCGAATCTCTGAGGAGACCGTGTACAGAGCGGCTGTGATGACGAG 1478
 DB 1141 ACGAACCACCGCGAATCTCTGAGGAGACCGTGTACAGAGCGGCTGTGATGACGAG 1200
 QY 1479 CTGAGTGAAGAAACGCTCTCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1538
 DB 1201 CTGAGTGAAGAAACGCTCTCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
 QY 1539 CTGTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1598
 DB 1261 CTGTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 QY 1599 CAGCATACGGCCCAATGTCAACAATCAGCCCTGGGCAAGCAGCAGCAGGAGGAGAG 1658
 DB 1321 CAGCATACGGCCCAATGTCAACAATCAGCCCTGGGCAAGCAGCAGCAGGAGGAGAG 1380
 QY 1659 AGAGAAAGAAAGAAAGCAGATGAGAAACAGTAAATGAATTAATTAATTAATTA 1718
 DB 1381 AGAGAAAGAAAGAAAGCAGATGAGAAACAGTAAATGAATTAATTAATTAATTA 1440
 QY 1719 CCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1778
 DB 1441 CCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
 QY 1779 CAGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1838
 DB 1501 CAGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560

QY 1839 CTGTGTTAAAGAACCATTAATGCTTTAGACAGTGTAAAAA 1897
 |||
 DB 1561 CTGTGTTAAAGAACCATTAATGCTTTAGACAGTGTAAAAA 1619
 |||
 RESULT 10
 ID ABRK3543 standard; cDNA: 1524 BP.
 XX ABRK3543;
 AC 08-MAY-2002 (first entry)
 XX
 DE CDNA encoding human PRO protein, Seq ID No 15.
 XX
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 breast cancer; prostate tumour; rectal tumour; liver tumour;
 pericyte cell proliferation; chondrocyte cell proliferation;
 tumour necrosis factor-alpha; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200208288-A2.
 PD 31-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US21066.
 XX
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-233646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001WO-US17092.
 XX
 PA (GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gerlitsen ME, Goddard A, Godowski PJ,
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI: 2002-172001/22.
 DR P-PSDB: AAU83599.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 XX
 XX Claim 2: Figure 15: 3599P; English.
 XX
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating

CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABRK3535-ABRK3567 represent human
 CC PRO protein coding sequences of the invention.
 XX
 SO Sequence 1524 BP; 321 A; 433 C; 435 G; 335 T; 0 other;

Query Match 80.3%; Score 1523.2; DB 24; Length 1524;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1522; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 140 GCGGCAGCAGCGCGGCCCCAGCAGCCTCGGACCCAGCCCGCTGCGAGCCGCGGAGCC 199
 |||
 DB 1 GCGGCAGCAGCGCGGCCCCAGCAGCCTCGGACCCAGCCCGCTGCGAGCCGCGGAGCC 60
 |||
 QY 200 TCCGCTGCTGCGGCTCCTGATGCGCTTGGCTTCCCGGCGCGGAGCTCCGGAGA 259
 |||
 DB 61 TCCGCTGCTGCGGCTCCTGATGCGCTTGGCTTCCCGGCGCGGAGCTCCGGAGA 120
 |||
 QY 260 ATGTGGGTCTAGGCATCGCGCACTTTTGGCGATTTCTTCCAGGCTTTGCG 319
 |||
 DB 121 ATGTGGGTCTAGGCATCGCGCACTTTTGGCGATTTCTTCCAGGCTTTGCG 180
 |||
 QY 320 CTGCAAAATCCAGTCTACAGTGTGAAGAAATTCAGCTGAACAAGCATCTCTCCGCC 379
 |||
 DB 181 CTGCAAAATCCAGTCTACAGTGTGAAGAAATTCAGCTGAACAAGCATCTCTCCGCC 240
 |||
 QY 380 GAGTTCAATTGGAATTCAGAGGTGACAGTCAAGACATGTGTGAGAAAGAAAGATGAGAG 439
 |||
 DB 241 GAGTTCAATTGGAATTCAGAGGTGACAGTCAAGACATGTGTGAGAAAGAAAGATGAGAG 300
 |||
 QY 440 CAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTCTCATCGCC 499
 |||
 DB 301 CAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTCTCATCGCC 360
 |||
 QY 500 TCTCGCGGGTACAGTCTCTGTCTCCCGAGGAACTGAATCATCATCACTGCG 559
 |||
 DB 361 TCTCGCGGGTACAGTCTCTGTCTCCCGAGGAACTGAATCATCATCACTGCG 420
 |||
 QY 560 TGCACACACCCCTTTTGAACGGGCAAGGCCAAGAAAGGGAAGTTGTGCTCGGCC 619
 |||
 DB 421 TGCACACACCCCTTTTGAACGGGCAAGGCCAAGAAAGGGAAGTTGTGCTCGGCC 480
 |||
 QY 620 CTCAGGCGAGGCTCCGACACCATCTGTCTCAAAATTAAGCCCTTCTCGGCACAC 679
 |||
 DB 481 CTCAGGCGAGGCTCCGACACCATCTGTCTCAAAATTAAGCCCTTCTCGGCACAC 540
 |||
 QY 680 TGTGGAAGCTGAAGAGATGACACCCCTCTGCAATTTCTTCACAGCCCTGCCCCAA 739
 |||
 DB 541 TGTGGAAGCTGAAGAGATGACACCCCTCTGCAATTTCTTCACAGCCCTGCCCCAA 600
 |||
 QY 740 CCCCCACCTCCCTGAGTGAAGTTCTCTGAGGTGCTTTTATTCGGGTAAGGAGCGG 799
 |||
 DB 601 CCCCCACCTCCCTGAGTGAAGTTCTCTGAGGTGCTTTTATTCGGGTAAGGAGCGG 660
 |||
 QY 800 AGTCGGTCTCTTTTGTCTCTGCAAAATGAAGAGCTCGGTAAGCAATTCGAA 859
 |||
 DB 661 AGTCGGTCTCTTTTGTCTCTGCAAAATGAAGAGCTCGGTAAGCAATTCGAA 720
 |||
 QY 860 TAAATTAGCTGACCTGAATTTTCAATATGATGATGGAAGAGAGGTGAGTGAAGTT 919
 |||
 DB 721 TAAATTAGCTGACCTGAATTTTCAATATGATGATGGAAGAGAGGTGAGTGAAGTT 780
 |||
 QY 920 CACCCCATCTCTGTGAACCGAGTGAAGCGAGGTGAGAGTGTAGAGT 979
 |||
 DB 781 CACCCCATCTCTGTGAACCGAGTGAAGCGAGGTGAGAGTGTAGAGT 840
 |||
 QY 980 CACTGAGGTGGGATCTGCTTTTGAAGCTTCAGTTCATCCCTGATGGG 1039
 |||

QY	685	AAGCTGAAGAGATGCCACCCCTCCGTGCATGTTCTTCCAGGCGCTGCCCAACCCC	744
Db	339	AAGCTGAAGAGATGCCACCCCTCCGTGCATGTTCTTCCAGGCGCTGCCCAACCCC	398
QY	745	CACCTCCCTGAGTGAATTTCTTGGGTGTCCTTTATTTCTGGGTAGGGAGCGGAGTCC	804
Db	399	CACCTCCCTGAGTGAATTTCTTGGGTGTCCTTTATTTCTGGGTAGGGAGCGGAGTCC	458
QY	805	GTTGTCCTTTTGTCTCTGTGGCAAAATATATTAAGAGCTGGTTAAGCATTTTGAATTAAT	864
Db	459	GTTGTCCTTTTGTCTCTGTGGCAAAATATTAAGAGCTGGTTAAGCATTTTGAATTAAT	518
QY	865	TCACCTGACAGTAATTTTTCAGTATGTACTTGAAGAGAGGGGGGTGAAGTTTCAACC	924
Db	519	TCACCTGACAGTAATTTTTCAGTATGTACTTGAAGAGAGGGGGGTGAAGTTTCAACC	578
QY	925	CCATGTCTGTGTAAACCGAGTCAAGGCGCAGGTCGAGAGTGCATCTTGAAGTCACTG	984
Db	579	CCATGTCTGTGTAAACCGAGTCAAGGCGCAGGTCGAGAGTGCATCTTGAAGTCACTG	638
QY	985	AGGTGGGCATCTGCTTTTGTAAAGCTCCAGTGTCCATTTCCATCTCTATGGGGCATTA	1044
Db	639	AGGTGGGCATCTGCTTTTGTAAAGCTCCAGTGTCCATTTCCATCTCTATGGGGCATTA	698
QY	1045	GTTTGAGACTGCAGAGTGAAGTGAAGTTTCTTGAAGGTCGGAGGGCCAGTTTCCACATCA	1104
Db	699	GTTTGAGACTGCAGAGTGAAGTGAAGTTTCTTGAAGGTCGGAGGGCCAGTTTCCACATCA	758
QY	1105	AGGCTCCCTGCTTGACATTTCAAACTTCATGCTCTGAAAGACCATTTCTGTGCAGCAGAT	1164
Db	759	AGGCTCCCTGCTTGACATTTCAAACTTCATGCTCTGAAAGACCATTTCTGTGCAGCAGAT	818
QY	1165	TGCGTGGTTTCGGGCTCGAATTTGGGCTCTTAGTACTGAGACTCAATGACTGGAGCTTAG	1224
Db	819	TGCGTGGTTTCGGGCTCGAATTTGGGCTCTTAGTACTGAGACTCAATGACTGGAGCTTAG	878
QY	1225	ACTGGGGCTCGGCGCTCGCTGTGAAAGGTGTTAAGAAATCTTTCAGTTCCTCTTGAG	1284
Db	879	ACTGGGGCTCGGCGCTCGCTGTGAAAGGTGTTAAGAAATCTTTCAGTTCCTCTTGAG	938
QY	1285	AGGACTGGCGCCGGGAGCGCAGAGAGCAGCGGCGCTGCACAAAGGGGGCGCTGTGGTGG	1344
Db	939	AGGACTGGCGCCGGGAGCGCAGAGAGCAGCGGCGCTGCACAAAGGGGGCGCTGTGGTGG	998
QY	1345	TGAGTGCAGTGTAGCGCGCAGGCGCTTCTGTTGGTGGCGTGTGCAGCGACGAGCGGC	1404
Db	999	TGAGTGCAGTGTAGCGCGCAGGCGCTTCTGTTGGTGGCGTGTGCAGCGACGAGCGGC	1058
QY	1405	AGCAGACACCTGAGCAAAACCCCGCGCAAACTGCTGCGAGGACACCTGTACAGAGACG	1464
Db	1059	AGCAGACACCTGAGCAAAACCCCGCGCAAACTGCTGCGAGGACACCTGTACAGAGACG	1118
QY	1465	GCTTGATGACCGAGCTGAGGTAAAGAAAGCTGCCAGAAAGGGAGAGAGATCATGTACG	1524
Db	1119	GCTTGATGACCGAGCTGAGGTAAAGAAAGCTGCCAGAAAGGGAGAGAGATCATGTACG	1178
QY	1525	CCCGGAAGTGAAGACCTGTCCAGTCTGTGCTTGGGTTGGCCCGCAGCATGATCTCTCGAA	1584
Db	1179	CCCGGAAGTGAAGACCTGTCCAGTCTGTGCTTGGGTTGGCCCGCAGCATGATCTCTCGAA	1238
QY	1585	TCTGCTTGGGCAATTCAGCAGTACAGGCCCAATGTACACATTCAGCCCTGGCGAGACAGAG	1644
Db	1239	TCTGCTTGGGCAATTCAGCAGTACAGGCCCAATGTACACATTCAGCCCTGGCGAGACAGAG	1298
QY	1645	CAGGAGGAGAGACAGAGAAAGAAAGACACAGACATGACAGACAGTAAATGAATTAANAAC	1704
Db	1299	CAGGAGGAGAGACAGAGAAAGAAAGACACAGACATGACAGACAGTAAATGAATTAANAAC	1358
QY	1705	CATTAATAATTTAGCCCTCTGTCTGTGCTTACTGCGCAGGAAATGGTACCAATTTTTC	1764
Db	1359	CATTAATAATTTAGCCCTCTGTCTGTGCTTACTGCGCAGGAAATGGTACCAATTTTTC	1418
QY	1765	AGTGTGGACTTGACAGCTTCTTTTGGCACAGACAGAGATTTTAACTGTTTCAA	1824

Db 1419 AGTGTGACTTGACACCTCTTTTCCACACGACAGAGATTAACTGTTCAA 1478

QY 1825 CCGGGGAGTTGGCTGTCTTAAAGAAAGCCATTAAATGCTTTAGACAGTGA 1878

Db 1479 CCGGGGAGTTGGCTGTCTTAAAGAAAGCCATTAAATGCTTTAGACAGTGA 1532

RESULT 12
AAD18690/c
ID AAD18690 standard; cDNA; 2528 BP.
yy

DT 18-DEC-2001 (first entry)
 XX

Human G protein coupled receptor (GPCR) 4941 cDNA

KM Human, cardiovascular; tumourigenic disorder; aberrant angiogenesis;
KM gene therapy; aberrant vascularisation; atherosclerosis; ovarian cancer
KM ischaemia/reperfusion injury; hypertension; arterial inflammation;
KM psoriasis; endothelial cell disorder; diabetic retinopathy; restenosis;
KM myocardial infarction; Graves's disease; G protein coupled receptor;
KM GPCR 42941; vasotropic; hypotensive; anti-inflammatory; cytostatic;
KM antidiabetic; antipsoriatic; leukaemia, ss

Homo sapiens

	Key	Location/Qualifiers
FH	CDS	42..1403
FT		

FT /product= "Human GPCR 4941"
FT /note= "The CDS is specifically claimed in claim 1 of
FT the specification"

PN WO200181634-A2

01-NOV-2001 PD

PF 25-APR-2001; 2001WO-US13788.

PR 26-APR-2000; 2000US-199908P.
PB 09-AUG-2000; 2000US-0635531

XX
XX
(MTT -) MTT ENRTH/ DUEBY TWO

PI Galvin KA, Rudolph-owen LA;

DR WPI; 2001-611743/70.
DR P-PSDB; AAE11751.

PT Identifying nucleic acids for the diagnosis and treatment of
PT cardiovascular and tumorigenic disorders, comprises identifying
PT protein coupled receptor (GPCR)-4941 -

PS Example 1; Flg 1; 118pp; English.

CC The present invention relates to a method for identifying a nucleic acid
CC molecule (G protein coupled receptor gene, GPCR 4941) associated with a
CC cardiovascular or tumorigenic disorder. The method comprising contacting
CC a sample containing a nucleic acid molecule with a hybridisation probe or
CC amplification primers and detecting the presence. The invention is used
CC in gene therapy. The method of the invention is used for identifying
CC nucleic acids or polypeptides associated with a cardiovascular or
CC tumorigenic disorder such as aberrant angiogenesis, aberrant
CC vascularisation, atherosclerosis, or ovarian cancer, ischaemia/
CC reperfusion injury, hypertension, restenosis, arterial inflammation,
CC endothelial cell disorders, diabetic retinopathy, psoriasis, myocardial
CC infarction, Grave's disease and leukaemia. The methods can also detect
CC mRNA or genomic DNA in a sample. The present sequence is G protein
CC coupled receptor (GPCR) 4941 cDNA

SQ Sequence 2528 BP; 516 A; 766 C; 677 G; 567 T; 2 other.

[illegible]

496

XX	ABL87898	standard; DNA; 625 BP.
XX	ABL87898:	
XX	17-MAY-2002	(first entry)
XX	Human ovarian cancer	related DNA clone SEQ ID NO:10876.
XX	Human; ovarian cancer;	ovarian tumour; cytostatic; gene; ds.
XX	Homo sapiens.	
XX	MO200192581-A2.	
XX	06-DEC-2001.	
XX	29-MAY-2001;	2001WO-US17756.
XX	26-MAY-2000;	2000US-207484P.
XX	(COBT-) CORIXA CORP.	
XX	Algate PA, Harlocker SL, Jones R;	
XX	WPI; 2002-122075/16.	
XX	Composition for therapy and diagnosis	of ovarian cancer comprising
XX	polypeptide of a ovarian tumor	polypeptide, polynucleotide encoding
XX	polypeptide, antibody specific to	polypeptide or T cell expressing
XX	polypeptide	-
XX	Claim 1; SEQ ID 10876; 489pp;	English.
XX	The present invention describes a	composition (I) comprising: carriers
XX	and immunostimulants; and a	polypeptide (II) of a ovarian tumour
XX	polypeptide encoded by a	polynucleotide (III) having a CDNA sequence
XX	(S1) from the 10912 nucleotide	sequences as given in ABL77023 to
XX	ABL87934, (III) encoding (II)	having a sequence (S2), a T cell
XX	population of (II), or antigen	presenting cells that express (II).
XX	(S1) has cytostatic activity. An	oligonucleotide (IV) that hybridises to
XX	(II) can be used for detecting	ovarian cancer in a patient's biological
XX	sample preferably serum or	ovarian tissue. The method comprises
XX	contacting a biological sample	from a patient with (IV), detecting the
XX	amount of polynucleotide	hybridising to (IV) and comparing the amount to
XX	a predetermined cutoff value	and thereby detecting ovarian cancer in the
XX	patient, where the amount of	polynucleotide hybridising to (IV) is
XX	detected preferably by	polymerase chain reaction (PCR). (I) comprising
XX	(III) and/or (II) is useful	for stimulating and/or expanding T cells
XX	specific for an ovarian	tumour protein comprising contacting T cells
XX	with (III) or (II). (III)	is useful in design and preparation of
XX	ribozyme molecules for	inhibiting expression of the tumour polypeptides
XX	and proteins in tumour	cells; and to isolate a full length gene from a
XX	suitable library e.g., a	tumour CDNA library using well known
XX	techniques.	
XX	Sequence 625 BP; 182 A;	144 C; 182 G; 116 T; 1 other.

Qy	1271	AGTTCTCTTGGACAGAGACTGCGCGCGGACGGAAAGACAAACGGGCGCTGCACAAACG	1330
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Qy	1331	GGCGCTGCGGTGGAGTGGCCATATACGCGCAGCGGCTTCTCGTGTTGGCGCTG	1390
Db	61	GGCGCTGCGGTGGAGTGGCCATATACGCGCAGCGGCTTCTCGTGTTGGCGCTG	120
Qy	1391	CAGGACAGAGCGGCGAGACACAGCACTGCGCAAGAACCCGCGCAAACTGTGCGAGAGAC	1450
Db	121	CAGGACAGAGCGGCGAGACACAGCACTGCGCAAGAACCCGCGCAAACTGTGCGAGAGAC	180
Qy	1451	CGTTACAGAGAGCGGGTTGATGACCGAGCTGAGTAGAAAAAGTCTCGAGAAAGGAG	1510
Db	181	CGTTACAGAGAGCGGGTTGATGACCGAGCTGAGTAGAAAAAGTCTCGAGAAAGGAG	240
Qy	1511	GAGATCATGTAGCCCGCGAAGTAGAAGCTCGGCCACGTGCTGGGTTGGCGCGAGC	1570
Db	241	GAGATCATGTAGCCCGCGAAGTAGAAGCTCGGCCACGTGCTGGGTTGGCGCGAGC	300
Qy	1571	CATGATCCTCCGAATCTGTTGGGCACTCCAGATACGGCCAAATGTCACAAACATACGCC	1630
Db	301	CATGATCCTCCGAATCTGTTGGGCACTCCAGATACGGCCAAATGTCACAAACATACGCC	360
Qy	1631	TGGCGACACAGCAGCAGGAGGCGAGACACAGAAAAACACAGCATGGAACACAG	1690
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Qy	1691	TAAATGATAAAAACCATTAATATTAGCCCTCTGCTGTCTGCTACTGCGCAGAAAT	1750
Db	421	TAAATGATAAAAACCATTAATATTAGCCCTCTGCTGTCTGCTACTGCGCAGAAAT	480
Qy	1751	GGTACCAATTTTCAGTGTGGACTTGACAGCTTCTTTGCCACAAGCAGAGAGATTT	1810
Db	481	GGTACCAATTTTCAGTGTGGACTTGACAGCTTCTTTGCCACAAGCAGAGAGATTT	540
Qy	1811	AACACTGTTTCAAAACCGGGGAGATTGGCGTGTAAAGAAACACATTAAATGCTTAG	1870
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Qy	1871	ACAGTGTAAAAAAGAAAAAAGAAAAA	1895
Db	601	ACAGTGTAAAAAAGAAAAAAGAAAAA	625

Search completed: November 7, 2002, 10:10:41
Job time : 384.511 secs

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Job time : 384.511 secs

Query Match	32.9%	Score 624;	DB 24;	Length 625;
Best Local Similarity	99.8%	Pred. No. 1.5e-145;		
Matches 624;	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps	0

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 17:54:48 ; Search time 2541.81 Seconds
(without alignments)
12086.984 Million cell updates/sec

Title: US-09-970-966-214

Perfect score: 1897
Sequence: 1 gcccaaccgcggagcctctg.....aaaaaaaaaaaaaaaaaa 1897

Scoring table:
OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 10

Total number of hits satisfying chosen parameters: 20126099

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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1: em_estbda:*
2: em_estbda:*
3: em_estln:*
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6: em_estln:*
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11: gb_est2:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estfun:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_hum:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	647	34.1	704	BI919074
2	631	33.3	888	BQ689771
3	627	33.1	702	BQ006545
4	597	31.5	747	BI917149
5	587	30.9	676	BE385990
6	586	30.9	696	BM547680

7	585	30.8	987	14	B068420	B068420 AGENCOURT
C	556	29.3	591	9	A1884686	A1884686 w183d07.x
C	552	29.1	606	12	BF439382	BF439382 nab33906.
C	552	29.1	948	14	B0882838	B0882838 AGENCOURT
C	546	28.8	678	9	A1936826	A1936826 w669h10.x
C	545	28.7	627	13	BM669397	BM669397 UI-E-DW1-
C	537	28.3	537	12	BF594242	BF594242 7n10d03.x
C	517	27.3	616	9	A1990500	A1990500 w40d07.x
C	516	26.4	649	10	AM590950	AM590950 h51e12.x
C	500	26.4	551	12	BE858216	BE858216 7919g07.x
C	498	26.3	608	13	BI554034	BI554034 603235426
C	489	25.8	540	12	BF939693	BF939693 nac80b12.
C	484	25.5	578	9	A1742092	A1742092 w938h03.x
C	479	25.3	534	10	BE350014	BE350014 h07g12.x
C	476	25.1	527	10	AM338938	AM338938 ha68h04.x
C	475	25.1	707	13	BI913989	BI913989 603180565
C	473	24.9	530	12	BF726459	BF726459 by06h03.y
C	472	24.9	920	9	AL538562	AL538562 AL538562
C	471	24.8	879	14	B0689033	B0689033 AGENCOURT
C	464	24.5	515	9	A1336858	A1336858 x46h05.x
C	444	23.4	690	10	AM149665	AM149665 x46h05.x
C	440	23.2	538	13	BM67957	BM67957 UI-E-DW0-
C	439	23.1	500	10	AM075598	AM075598 xb24e07.x
C	426	22.5	794	12	BE731003	BE731003 601570968
C	426	22.5	1134	12	BE730800	BE730800 601570755
C	425	22.4	467	9	A1150931	A1150931 qb53c04.x
C	424	22.4	480	10	BE336607	BE336607 bb68e04.y
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C	424	22.4	843	12	BF125134	BF125134 601762356
C	423	22.3	571	14	BM709964	BM709964 UI-E-CO1-
C	415	21.9	537	9	A1018769	A1018769 ov32e04.x
C	408	21.5	688	13	BI544761	BI544761 603242028
C	404	21.3	690	10	BI669845	BI669845 603293440
C	404	21.3	743	10	BE395797	BE395797 601310028
C	396	20.9	366	9	AA613995	AA613995 n086c08.s
C	394	20.8	452	9	A1391683	A1391683 qy93f04.x
C	390	20.6	366	9	A1499630	A1499630 t003b07.x
C	383	20.2	654	12	BE746601	BE746601 601580186
C	380	20.0	456	9	A1765236	A1765236 w172h08.x

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
603180881F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5244956 5', mRNA sequence.
ACCESSION
BI919074
VERSION
BI919074.1 GI:16200128
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 704)
NIH-MGC http://mgs.nci.nih.gov/
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Found through the I.M.A.G.E. Consortium distribution information can be
http://image.llnl.gov
Plate: LLNL1618 row: a column: 21
High quality sequence start: 4
High quality sequence stop: 702.
Location/Qualifiers

FEATURES

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Oy	1539	GAAGTAGGACCTCTCTCCAGTCTGCTTGGGTGTGGCCCGAGCCATGATCTTCGAACTCG	1588
Db	421	GAAGTAGGACCTCTCTCCAGTCTGCTTGGGTGTGGCCCGAGCCATGATCTTCGAACTCG	480
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DEFINITION	AGNCOURT_6507108 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5727798		
ACCESSION	BMS47680		
VERSION	BMS47680.1 GI:18781656		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 696) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
AUTHORS	Contact: Robert Strausberg, Ph.D.		
TITLE	Email: cgapbs-remail.nih.gov		
JOURNAL	Tissue Procurement: Invitrogen		
COMMENT	cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov High quality sequence stop: 641. Location/Qualifiers		
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	/lab_host="DH10B"		
	/note="Organ: brain; Vector: pCMV-SPORT6; Site:1: EcoRV (destroyed); Site:2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."		
BASE COUNT	188 a 160 c 197 g 134 t 17 others		
ORIGIN			
Query Match	30.9%, Score 586, DB 13, Length 696;		
Best Local Similarity	99.8%; Pred. No. 0;		
Matches 636:	Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Oy	1210	ATGATGGGAGCTTAACATCGGGCTGGGCTGCGCTCGTGAAGAAGTGTTAAGAAATCTTCT	1269
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QY	1270	CAGTTCCTCTTTCACAGAGACTGTGGCCCGGAAAGCCAAAGCAACGGGGCTGTGCACAAAGC	1329
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QY	1330	GGGCGCTGTGGTGGAGTGTGGCATGTAGCGCGAGCGCTTCTCGTGTGGTGGCTGT	1389
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QY	1390	GCAGGCAACAGCGCGCAGACACACCTCTCAGAAACACCCCGGAAACTGTGTCCAGAGACA	1449
Db	184	GCAGGCAACAGCGCGCAGACACACCTCTCAGAAACACCCCGGAAACTGTGTCCAGAGACA	243
QY	1450	CCGTGTACAGAGCGCGGTGTGATGACCGAGCTGTAGTACAAAAAGTGTCCGAGAAAGGGA	1509
Db	244	CCGTGTACAGAGCGCGGTGTGATGACCGAGCTGTAGTACAAAAAGTGTCCGAGAAAGGGA	303
QY	1510	GGAGGATCATGTAGCCCGGAAAGTGAAGACCTTCGTACAGTGTGCTTGTGGTTTGGCCGAG	1569
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DEFINITION	AGENCOURT_8301981 NIH_MGC_102 Homo sapiens cdna clone IMAGE:6275121		
ACCESSION	B0668420		
VERSION	B0668420.1	GI:21778667	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 987)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: ATCC		
	CDNA Library Preparation: Rubin Laboratory		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.llnl.gov		
	Plate: L1CM2457 row: m column: 10		
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SOURCE	location/Qualifiers		
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 /tissue_type="epidermoid carcinoma, cell line"
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 /note="Organ: salivary gland; Vector: pORF7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAC(G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin
 (University of California, Berkeley) using ZAP-cDNA
 synthesis kit (Stratagene) and Superscript II RT (Life
 Technologies). Note: this is a NIH_MGC library."
 196 a 314 C 285 g 191 t 1 others

Query Match	30.8%	Score 585	DB 14	Length 987
Best Local Similarity	100.0%	Pred. NC	0	
Matches 585	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy 19 GGTCTGTGGGCGGAGCGCGACCGAGAGACAGACACCCGACGCGGAGCCCGACG 78
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Db 11 GGTGCTGGGCGGAGCGCGACCGGAGAGACAGACACCCGACGCGGAGCCCGACG 70
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QY 79 CGGCGATGCAGGCTCCGCGAGCGGGCACCTGCGGCTCCTCTAAAGCTACGACCGTGTCTC 138
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QY 139 CGGGCAGCAGCGCGGCCCCAGCAGCCTCGGCAGCCAGCGCGCTGCAGCCGGGGAGC 198
131 CGGGCAGCAGCGCGGCCCCAGCAGCCTCGGCAGCCAGCGCGCTGCAGCCGGGGAGC 190
Db 131 CGGGCAGCAGCGCGGCCCCAGCAGCCTCGGCAGCCAGCGCGCTGCAGCCGGGGAGC 190

199 CTCGGCTGCTGCGCCCTCATGCGCTTGCCTCTCCCGGCGCCGAGACATCCGGAG 258
 191 CTTCCGCTGCTGCGCCCTCATGCGCTTGCCTCTCCCGGCGCCGAGACATCCGGAG 250

259 AATGTGGCTCCTAGGCATCGGGCAACCTTTTGGCGATTGTCTGTGCTCCAGCGTTTCC 318

QY 319 GCTGCAATCCAGTGTCTACAGTGTGAAGATTCCAGCTGAACAACAGCACTGCTCTCTCCCC 378
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379 CGAGTTTCATTGTGCAATTCACCGGTGCAACGTTCAACACATGTGTGAGAAAGAAGTGATGGA 438

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499 CTTCTGCCGGTACACAGTCTTCTGCTGCTCCCAAGGAACTGAACCTCACTTTGCATCAGCTG 558

Db 491 CTCCTGCCGGGACACAGTCTTCTGCTCCCCAGGGAACCTGAACTCAGTTTGCATCAGCTG 550

Qy 559 CTGCAACACCCCTCTTTTGTAAACGGGGCCCAAGGCCCAAGAAAAAGGG 603

Db 551 CTGCACACCCCTCTTTGTAAACGGGCCAAGGCCCAAGAAAGGGG 595

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LOCUS	A1884686		
DEFINITION			
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A1884686			
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similar to: SM:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GP39, mRNA sequence.
A1884686

KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 591)
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosentfield M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

cDNA library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGP clone distribution
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnhi.gov/brp/image/image.html
Insert length: 1462 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 444.

FEATURES	Location/Qualifiers
source	1, 591

BASE COUNT
ORIGIN

109 a 179 c 147 g 155 t 1 others

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image:2431501"
/clone_id="NCI_CGAP_Brn25"
/tissue_type="neoplastic oligodendroglioma"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - Oligo(dT) primer [5'
TGTATCCAAATCTGAAGTGGAGCGCGCCGATAGCTTTTATTTTATTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

Query Match	29.3%	Score 556	DB 9	Length 591
Best Local Similarity	100.0%	Pred. No. 0		
Matches 556	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Accession	Sequence	Length
OY	TGAAACCATTTCTCGACGACAGATTGGCTGCTTTCCGCGCTGAGTTGGGCTCTAGTGC	1199
Db	TGAAACCATTTCTCGACGACAGATTGGCTGCTTTCCGCGCTGAGTTGGGCTCTAGTGC	519

Qy	TCGAGACTCAATGACTGGAGCTTAGACTGGGGCTCGGCTCGCTCTGAAAAGTGCTTAAG	1 259
1200	TCGAGACTCAATGACTGGAGCTTAGACTGGGGCTCGGCTCGCTCTGAAAAGTGCTTAAG	
518	TCGAGACTCAATGACTGGAGCTTAGACTGGGGCTCGGCTCGCTCTGAAAAGTGCTTAAG	459

0y	1260	AAATCTTCTCAGTTCCTCTGTCGAGAGACGTGGCGCCGGAGCGGAAGAGCAACGGGGCGC	1319
0s	458		208

QY 1320 TGCACAAGCGGGCGCTGTCCGTGTGTGAGTCCGCATGTACGGCGACGGCGCTTCTCGTGG 1379
|||||

1380 TTGGCGTGTCTGACGACGAGCGGCGACACACACCTGACAGCAACACCCGCCAAATGTC 1439
 QY

DB	338	TTGGCGTGTCTGCAGCGCAGACAGCGGGCAGCAGACACACACCTTCACACCAACACCCGCGGAAATGTC	2/9
OY	1440	TGCAGACACCGTGTACAGAGAGCGGGTTGATGACCACTGAGTGTGAAAAAGCTTC	1499

Db	278	TGCGAGACACCGTGTACAGAGAGCGGGTTGATGACCGCAGCTGAGTGAGAAAAAGCTGCC	219
Dy	1500	GAGAGGGGAGGAGGATCATGTACGCCCGGAGTAGCAGCCTGTCCAGTCTGCTTGGGT	1559

Db	218	GAGAGAGGAGAGGATCATGTACGCCCCGGAGTAGAACCTCTGTCCAGTCGTGGGT	159
yy	1560	TTGGCCGAGCCATGATCCTCCGAATCTGTGTGGGCATCCAGCATACGCCCATGTGCACA	1619

1560 TTGGCCGCGAGCCATGATCCTCCGATCTGGTTGGCATCCAGCATACGGCCAATGTCACA 1619